

GenCore version 4.5  
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On protein - protein search, using sw.model

Run on: September 28, 2002, 17:53:32 ; Search time 62.3 seconds  
(without alignments)  
1201.665 Million cell updates/sec

Title: US-09-899-471-2

Sequence: 1 MPVSFLLSLALGNPVVS.....SSEAPGCEEMDGFCTTLE 674

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : A.Geneseq\_032802:\*

- 1: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:\*
- 2: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:\*
- 3: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:\*
- 4: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:\*
- 5: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:\*
- 6: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:\*
- 7: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:\*
- 8: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:\*
- 9: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:\*
- 10: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:\*
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- 18: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:\*
- 19: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:\*
- 20: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:\*
- 21: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:\*
- 22: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2352.5	65.3	692	22	Human cytokine rec
2	2339	64.9	705	22	Human PRO polypept
3	2339	64.9	705	22	Human Interleukin
4	2339	64.9	705	22	Human PRO20040. H
5	2339	64.9	705	22	Human PRO20040. H
6	2277	63.2	675	22	Human IL-17R poly
7	2263.5	62.8	688	22	Human IL-17R poly
8	1851.5	51.4	575	22	Human IL-17R poly
9	956.5	26.6	309	21	Human secreted pro
10	841.5	23.3	332	22	Human protein sequ
11	838.5	23.3	267	22	Human membrane or

12	591.5	16.4	204	22	AAE10920
13	310.5	8.6	617	21	AAV76048
14	310.5	8.6	617	22	AAE55987
15	310	8.6	667	22	AAU04957
16	167	4.6	667	17	AAU04184
17	167	4.6	864	20	AAE61271
18	167	4.6	864	19	AAE92408
19	167	4.6	864	21	AAE99935
20	167	4.6	864	21	AAE97130
21	167	4.6	864	21	AAE97180
22	167	4.6	864	21	AAE97180
23	167	4.6	864	22	AAE97180
24	167	4.6	864	22	AAE97180
25	151.5	4.2	866	17	AAE04185
26	151.5	4.2	866	19	AAE61272
27	151.5	4.2	866	20	AAE92409
28	151.5	4.2	866	21	AAE99941
29	151.5	4.2	866	21	AAE97131
30	151.5	4.2	866	21	AAE97181
31	151.5	4.2	866	21	AAE03807
32	151.5	4.2	866	22	AAE62066
33	151.5	4.2	866	22	AAE62066
34	149	4.1	330	21	AAE72754
35	149	4.1	330	22	AAE55886
36	125	3.5	1042	22	ABG26706
37	118.5	3.3	877	22	ABG28379
38	114.5	3.2	1013	22	AAE81163
39	114.5	3.2	1711	19	AAE70506
40	114.5	3.2	1711	19	AAE70507
41	108	3.0	752	22	ABE10333
42	108	3.0	997	22	ABG08088
43	105	2.9	1767	22	ABE62726
44	104.5	2.9	1149	22	AAE97640
45	104.5	2.9	1237	22	AAE97638

## ALIGNMENTS

RESULT 1

AAE61880

ID AAE61880 standard; Protein; 692 AA.

XX

AC AAE61880;

XX

DT 08-MAY-2001. (first entry)

XX

DE Human cytokine receptor zcytor14.

XX

KW Cytokine receptor; zcytor14; human; inflammation; rheumatoid arthritis;

KW antiinflammatory; gene therapy; vaccine.

XX

OS Homo sapiens.

XX

PN WO200104304-A1.

XX

PD 18-JAN-2001.

XX

PF 30-JUN-2000; 2000WO-US18383.

XX

PR 07-JUL-1999; 99US-0348854.

XX

PA (ZIMO) ZYMOGENETICS INC.

XX

PI Presnell SR, Burkhead SK, Powderder SL;

XX

DR WPI: 2001-112618/12.

XX

DR N-PSDB; AAC85027.

XX

PT New polypeptide encoding a human cytokine receptor zcytor14, for

PT treating inflammation e.g. rheumatoid arthritis

XX

PS Claim 2; Page 2; 112pp; English.

The invention provides a new human cytokine receptor designated Zcytor14. Zcytor14 can be expressed by standard recombinant methodology. The encoding nucleic acid is useful for detecting the expression of a Zcytor14 gene in a biological sample. Anti-Zcytor14 antibodies can be used to screen biological samples in vitro for the presence of Zcytor14. Proteins, polypeptides and peptides having Zcytor14 activity can be administered to a subject who lacks an adequate amount of this polypeptide, for treating inflammation and conditions such as rheumatoid arthritis. In contrast, Zcytor14 antagonists (e.g. anti-Zcytor14 antibodies) can be used to treat a subject who produces an excess of Zcytor14. Zcytor14 nucleotide sequences can also be used to provide Zcytor14 to a subject. The present sequence represents the human cytokine receptor Zcytor14.

Sequence 692 AA:

Query Match 65.3%; Score 2352.5; DB 22; Length 692;  
Best Local Similarity 67.4%; Pred. No. 2,3e-214;  
Matches 457; Conservative 66; Mismatches 136; Indels 19; Gaps 5;

1 MPVSWFLSLAIGRNVVVSLERMPDTRARCSLGLSCHMDVDVCLPSLSQAPGPV 60  
1 MPVSWFLSLAIGRNVVVSLERMPDTRARCSLGLSCHMDVDVCLPSLSQAPGPV 60  
61 LVPTRLOTELVRCPQKTCALRVVNHVLAHGHMAEPPE---AKKSELSQSRNAS 116  
61 LVPTRLOTELVRCPQKTCALRVVNHVLAHGHMAEPPE---AKKSELSQSRNAS 116  
117 LQAOVVLSTQAVPIARCALLLEVOPADLVOPGOSVGSVAVDFCEASIGAEVQIMSYTKPR 176  
117 LQAOVVLSTQAVPIARCALLLEVOPADLVOPGOSVGSVAVDFCEASIGAEVQIMSYTKPR 176  
121 LQAGVVLSTQAVPIARCALLLEVOPADLVOPGOSVGSVAVDFCEASIGAEVQIMSYTKPR 180  
121 LQAGVVLSTQAVPIARCALLLEVOPADLVOPGOSVGSVAVDFCEASIGAEVQIMSYTKPR 180  
177 YOKELNLQOQLP-----DGDNLTLTLDVSEEDFSLTLRYPPDALKSLMYKNLT 227  
177 YOKELNLQOQLP-----DGDNLTLTLDVSEEDFSLTLRYPPDALKSLMYKNLT 227  
181 YEKELNHTVQALPVLNVNSADGDVNHVNLVNSEEQHFGISLVYNGVGPQPKPWHKNLT 240  
181 YEKELNHTVQALPVLNVNSADGDVNHVNLVNSEEQHFGISLVYNGVGPQPKPWHKNLT 240  
228 GPONTITLNTDLPVPCICIOVMSLEPDSERVEFCFEREDPGHRLMILARIVLSPGWQ 287  
228 GPONTITLNTDLPVPCICIOVMSLEPDSERVEFCFEREDPGHRLMILARIVLSPGWQ 287  
241 GPQITLNTDLPVPCICIOVMSLEPDSERVEFCFEREDPGHRLMILARIVLSPGWQ 300  
241 GPQITLNTDLPVPCICIOVMSLEPDSERVEFCFEREDPGHRLMILARIVLSPGWQ 300  
288 LDAPCCLPCKVTLCWQAPDQSPQPLVPPVPPQKNATVNEPQDQVLAHHPMLCVQVSTWE 347  
288 LDAPCCLPCKVTLCWQAPDQSPQPLVPPVPPQKNATVNEPQDQVLAHHPMLCVQVSTWE 347  
301 LDAPCCLPCKVTLCWQAPDQSPQPLVPPVPPQKNATVNEPQDQVLAHHPMLCVQVSTWE 360  
301 LDAPCCLPCKVTLCWQAPDQSPQPLVPPVPPQKNATVNEPQDQVLAHHPMLCVQVSTWE 360  
348 KVOQLACASADSLGPRKDMVLVEMKTGLMNTSVCALEPGGCTPLPSMASTRARALCEEL 407  
348 KVOQLACASADSLGPRKDMVLVEMKTGLMNTSVCALEPGGCTPLPSMASTRARALCEEL 407  
361 KIQIQCETWADSLGPRKDMVLVEMKTGLMNTSVCALEPGGCTPLPSMASTRARALCEEL 420  
361 KIQIQCETWADSLGPRKDMVLVEMKTGLMNTSVCALEPGGCTPLPSMASTRARALCEEL 420  
408 LQDFRSHOCMOQLMNDNMGLMACPMKTYIHRMVLYWMLCLLAALFFFLIKKRRK 467  
408 LQDFRSHOCMOQLMNDNMGLMACPMKTYIHRMVLYWMLCLLAALFFFLIKKRRK 467  
421 LQDFRSHOCMOQLMNDNMGLMACPMKTYIHRMVLYWMLCLLAALFFFLIKKRRK 479  
421 LQDFRSHOCMOQLMNDNMGLMACPMKTYIHRMVLYWMLCLLAALFFFLIKKRRK 479  
468 AARGSRALLLHSDAGYERLVGALASALSCMPLRAVADLWSRRELISAGALAMFPHOR 527  
468 AARGSRALLLHSDAGYERLVGALASALSCMPLRAVADLWSRRELISAGALAMFPHOR 527  
480 AARGSRALLLHSDAGYERLVGALASALSCMPLRAVADLWSRRELISAGALAMFPHOR 539  
480 AARGSRALLLHSDAGYERLVGALASALSCMPLRAVADLWSRRELISAGALAMFPHOR 539  
528 RRILOEGVILLFSPAAVCOQOHTQLOVEB---GPHALAMLSVCVLPDLOGATG 584  
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585 RYGVYVDFGLHDPSPVSPFRVAPLFLPTQLPAFLDALOGGSGTSGRPAADREVERTOA 644  
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600 RYGVYVDFGLHDPSPVSPFRVAPLFLPTQLPAFLDALOGGSGTSGRPAADREVERTOA 659  
645 LRSALDSC--TSSSAPG 660  
645 LRSALDSC--TSSSAPG 660  
660 LRSALDSC--TSSSAPG 677  
660 LRSALDSC--TSSSAPG 677

RESGILT 2  
A099322

ID AAU29322 standard; Protein; 705 AA.  
XX AAU29322;  
AC AAU29322;  
XX 18-DEC-2001 (first entry)  
DT 18-DEC-2001 (first entry)  
XX Human PRO polypeptide sequence #299.  
DE Human PRO polypeptide sequence #299.  
XX PRO polypeptide: mammal; tumour; cancer; human; cattle; horse; sheep;  
KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;  
KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;  
KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.  
XX Homo sapiens.  
OS Homo sapiens.  
XX WO200168848-A2.  
PN WO200168848-A2.  
XX 20-SEP-2001.  
PD 20-SEP-2001.  
XX 28-FEB-2001; 2001MO-US06520.  
PF 28-FEB-2001; 2001MO-US06520.  
XX 01-MAR-2000; 2000MO-US05601.  
PR 01-MAR-2000; 2000MO-US05601.  
PR 02-MAR-2000; 2000MO-US05841.  
PR 03-MAR-2000; 2000US-187202P.  
PR 06-MAR-2000; 2000US-186968P.  
PR 14-MAR-2000; 2000US-189320P.  
PR 14-MAR-2000; 2000US-189320P.  
PR 15-MAR-2000; 2000MO-US06884.  
PR 15-MAR-2000; 2000MO-US06884.  
PR 21-MAR-2000; 2000US-190828P.  
PR 21-MAR-2000; 2000US-191007P.  
PR 21-MAR-2000; 2000US-191048P.  
PR 21-MAR-2000; 2000US-191314P.  
PR 28-MAR-2000; 2000US-192655P.  
PR 29-MAR-2000; 2000US-193032P.  
PR 29-MAR-2000; 2000US-193032P.  
PR 30-MAR-2000; 2000MO-US08439.  
PR 04-APR-2000; 2000US-194449P.  
PR 04-APR-2000; 2000US-194647P.  
PR 11-APR-2000; 2000US-195975P.  
PR 11-APR-2000; 2000US-196000P.  
PR 11-APR-2000; 2000US-196187P.  
PR 11-APR-2000; 2000US-196690P.  
PR 11-APR-2000; 2000US-196820P.  
PR 18-APR-2000; 2000US-198121P.  
PR 18-APR-2000; 2000US-198385P.  
PR 25-APR-2000; 2000US-199397P.  
PR 25-APR-2000; 2000US-199550P.  
PR 25-APR-2000; 2000US-199654P.  
PR 03-MAY-2000; 2000US-201516P.  
PR 17-MAY-2000; 2000MO-US13705.  
PR 22-MAY-2000; 2000MO-US14042.  
PR 30-MAY-2000; 2000MO-US14941.  
PR 02-JUN-2000; 2000MO-US15264.  
PR 05-JUN-2000; 2000US-209832P.  
PR 28-JUL-2000; 2000MO-US20710.  
PR 22-AUG-2000; 2000US-0644848.  
PR 24-AUG-2000; 2000MO-US23328.  
PR 08-NOV-2000; 2000MO-US30952.  
PR 01-DEC-2000; 2000MO-US32678.  
PR 20-DEC-2000; 2000MO-US34956.  
PA (GENTH ) GENENTECH INC.  
PI Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;  
PI Pan J, Smith V, Matanabe CK, Wood WI, Zhang Z;  
XX MPI: 2001-602746/68.  
XX N-PSDB; AAS46223.  
XX Novel nucleic acids encoding PRO polypeptides, used to diagnose the  
XX presence of tumours, such as prostate and breast tumours, in mammals and  
XX to screen for modulators of the compounds -







N-PSDB; AAF92138.

Eighty four nucleic acids encoding PRO polypeptides, useful in molecular biology, including use as hybridization probes, and in chromosome and gene mapping. -

Claim 12; Fig 162; 278pp; English.

The present sequence is a human PRO polypeptide (secreted and transmembrane). The PRO protein, and PRO agonists, PRO antagonists or anti-PRO antibodies are useful for preparation of a medicament useful in the treatment of a condition which is responsive to the PRO protein, agonists, antagonists or anti-PRO antibodies. The PRO protein may also be employed as molecular weight markers for protein electrophoresis. The PRO coding sequence has applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping.

Sequence	705 AA;
50	

Query Match	64.9%	Score 2339	DB 22	Length 705
Best Local Similarity	66.3%	Pred. No. 4	6e-213	
Matches 459; Conservative	66	Mismatches 133	Indels 34	Gaps 7

[illegible]

RESULT 5  
AAB61884

ID	Protein; 705 AA
AAB61884	standard;

AC : AAB61884 ;

DT 08-MAY-2001 (first entry)  
 XY

De chimeric zcyto14 protein #2.

KW Cytokine receptor; zcyto14; human; inflammation; rheumatoid arthritis;  
KW antiinflammatory; gene therapy; vaccine.

OS Homo sapiens

PN WO200104304-A1  
YY

PD 18-JAN-2001  
XY

PE 30-JUN-2000; 2000WU-US18383-  
XX

XX PR 07-JUL-1999; 9305-0340004-XX

(LIMC) LIMONENES AND  
XX XX

[illegible]

XX

PT New polypeptide encoding a human cytokine receptor Zcytor14, for  
XX treating inflammation e.g. rheumatoid arthritis -  
PS Claim 2, page 105-107, 112pp. English.

The invention provides a new human cytokine receptor designated zcytor14. zcytor14 can be expressed by standard recombinant methodology. The encoding nucleic acid is useful for detecting the expression of a zcytor14 gene in a biological sample. Anti-zcytor14 antibodies can be used to screen biological samples in vitro for the presence of zcytor14. Proteins, polypeptides and peptides having zcytor14 activity can be administered to a subject who lacks an adequate amount of this polypeptide, for treating inflammation and conditions such as rheumatoid arthritis. In contrast, zcytor14 antagonists (e.g. anti-zcytor14 antibodies) can be used to treat a subject who produces an excess of zcytor14. zcytor14 nucleotide sequences can also be used to provide zcytor14 to a subject. The present sequence represents a chimeric zcytor14 protein.

Sequence 705 AA;

Query Match	64.9%;	Score 2339;	DB 22;	Length 705;
Best Local Similarity	66.3%;	Pred. No. 4.6e-213;		
Matches 455;	Conservative 66;	Mismatches 133;	Indels 34;	Gaps 7

```

OY 1 MVSNEFLLISIALGRNPVYVSLERLMEPODTRKSGTSCHEMLDGBVCLPSTLSQASGPV 60
OY 1 MVSNEFLLISIALGRNPVYVSLERLMEPODTRKSGTSCHEMLDGBVCLPSTLSQASGPV 60
Db 1 mpwvffllslalgrspvvlsterlrvpddachqscslscldwdsdlclcpdlvpaaqpv 60
OY 61 LVPRRLQTELVRCPQKTDCLRNVRVYVHLAVHGMARPEP-----AGKSDELEDSRRAS 116
Db 61 laphthqtelvrlrcqctcdclrlvaahlaavhgmeepeedeekfggaadsvseeprnas 120
OY 117 LDAQVLSFOAPIRARCALLEVOVGPADLVQVQSGVSAVFCFPAASLCAEAOVIMSYTKPR 176
OY 117 LDAQVLSFOAPIRARCALLEVOVGPADLVQVQSGVSAVFCFPAASLCAEAOVIMSYTKPR 176
Db 121 lqagvvlstfgayptarcvlllevygpaaalvqfgsgvsvyvcfaaalgysevrllwysyqpr 180
OY 177 YKQELNLTQOUP-----DGDVVLTLTQVSEODSPFLILLYLRPVDAKLKSLMYKNLT 227
Db 181 ykelelnhqqdlpalpwlhvsagaadvhvlvlnseeqnlfgslaymqvqgppkprvknlt 240
OY 228 GQNTITLNTDTPVPCICIQVMSLEDESERVEFCPEREDPGAHRLMLHTARLVLSPGVMO 287
Db 228 gqntitlntdtpvpciciqvmsledeSERVEFCPEREDPGAHRLMLHTARLVLSPGVMO 287

```

241 gpglltlnhtlvpclclqvwplpdpdvtnlclpfedprahqnlqlqswl 300  
 288 LDAPCLFGKVTLCQAPDQSPCQPLVPVPPOKMATVNEPQDLVAGHPNLCVOYSTWE 347  
 301 ldpocslpaeaalcwtrpagsdcgplvpplswentvtdvletpilkhgpnlcgvnsse 360  
 348 KVOLOACSMADSLGPFKDMILVENKGTGLNMTSVCLSPSGCTPLPSMASTRARAGEEL 407  
 361 klqqlceclwadsipklkddvlllctcpqdnrslcalpsgcslpsksastrarageyl 420  
 408 LDPRSHOCMOLMNDNNGSLWACPMKXIIHRRWLVWLACLLAALFFELLKDRRK 467  
 421 lqdlqsgqclqlw-dddldgalwacpmkxyihkrwalvwlacllfaaalsllllkdhak 479  
 468 -----AARGSRFALLHSADGAGERYLVALSALSQMPLRVAVDLSRRE 513  
 480 gwllllkqdvsgaaarg-raaillysadsgferlvgaalacqlplrvavdlvsire 538  
 514 LSAHGALAMFHRRRILOEGGVVILFSPAAYAOQOMLQLOTVER---GPHDALAAML 570  
 539 lsaqgpavwfnhagrqltqeggvvvllfsgavalcsewllqdgvsqgahghdfrastl 598  
 571 SCVLPDFLGKATGKRYGVYFPGGLHPDSVSPFRVAPLFSLTQLPAPLADLOGGCSTS 630  
 599 scvlpdflqgrapsyvgacifrlhpdavpalftvpyftlpsqldflgaltqprapr 658  
 631 AGRPADRVERVTOALRSALDSC--TSSSEAPG 660  
 659 sgrlqeraegvsralqpaldsyfnppgtpapg 690

## RESULT 6

AAB61885 standard; Protein: 675 AA.

AAB61885;

08-MAY-2001 (first entry)

Chimeric zcytor14 protein #3.

Cytokine receptor; zcytor14; human; inflammation; rheumatoid arthritis; antiinflammatory; gene therapy; vaccine.

Homo sapiens.

W0200104304-A1.

18-JAN-2001.

30-JUN-2000; 2000WO-US18383.

07-JUL-1999; 99US-0348854.

(ZYMO) ZYMOGENETICS INC.

Presnell SR, Burkhead SK, Powder SL;

WPI; 2001-112618/12.

New polypeptide encoding a human cytokine receptor zcytor14, for treating inflammation e.g. rheumatoid arthritis -

Claim 2; Page 107-109; 112pp; English.

The invention provides a new human cytokine receptor designated zcytor14. zcytor14 can be expressed by standard recombinant methodology. The encoding nucleic acid is useful for detecting the expression of a zcytor14 gene in a biological sample. Anti-zcytor14 antibodies can be used to screen biological samples in vitro for the presence of zcytor14. Proteins, polypeptides and peptides having zcytor14 activity can be administered to a subject who lacks an adequate amount of this polypeptide, for treating inflammation and conditions such as rheumatoid

CC arthritis. In contrast, zcytor14 antagonists (e.g. anti-zcytor14  
 CC antibodies) can be used to treat a subject who produces an excess of  
 CC zcytor14. zcytor14 nucleotide sequences can also be used to provide  
 CC zcytor14 to a subject. The present sequence represents a chimeric  
 CC zcytor14 protein.  
 XX  
 SQ Sequence 675 AA;

Query Match 63.2%; Score 2277; DB 22; Length 675;  
 Best Local Similarity 65.9%; Pred. No. 3,4e-207;  
 Matches 447; Conservative 63; Mismatches 132; Indels 36; Gaps 6;

1 MPVSFLLSLGRNPVYSLERIMEPODTRFARCSGLSCHIMGDVLCIPGSLQSPGV 60  
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 61 LVPTFLQETELVLRCPQKDCALRRVNVVLAHGHAEPEE---AGKSDSEQESRNAS 116  
 61 lvptflqetelvlrcpqkdcalarvrvnvvlahghaepee---agksdseeqesrnas 120  
 117 LQAOVLSFOAYPIARCALLEVQVPADLVQPGQSGSAVFDCFEASLGAEOIWTSTKPR 176  
 121 lqaovlvsfoaypiarcallevqvpadlvqpgqsgsavgfdcfeaslgaevoiwtstkrpr 180  
 177 YQKELNLTQOLP-----DGDNVLLTLDVSEEDDFSLYLRRVPPDLKSLMKRLT 227  
 181 yqkelnltqolp-----dgdnvlltldvseeddfslylrrvppdlkslmlkrlt 240  
 228 GPONTTLNHTLVPCLCIQVMSLEPDSEREFCEPREDGCAHNLHRIARLSPGVQ 287  
 241 gponntlhtlvpclclqvmslepdserfcepredgcahnlhriarlspgvwq 300  
 288 LDAPCLFGKVTLCQAPDQSPCQPLVPVPPOKMATVNEPQDLVAGHPNLCVOYSTWE 347  
 301 ldpocslpaeaalcwtrpagsdcgplvpplswentvtdvletpilkhgpnlcgvnsse 343  
 348 KVOLOACSMADSLGPFKDMILVENKGTGLNMTSVCLSPSGCTPLPSMASTRARAGEEL 407  
 344 klqqlceclwadsipklkddvlllctcpqdnrslcalpsgcslpsksastrarageyl 403  
 408 LDPRSHOCMOLMNDNNGSLWACPMKXIIHRRWLVWLACLLAALFFELLKDRRK 467  
 404 lqdlqsgqclqlw-dddldgalwacpmkxyihkrwalvwlacllfaaalsllllkdhak 462  
 468 AARGSRFALLHSADGAGERYLVALSALSQMPLRVAVDLSRRELASHAGALAMFHRR 527  
 463 aargsrfallhsadgagerylvalsalsqmplrvavdlsrrelasahagalamfhrr 522  
 528 RRILOEGGVVILFSPAAYAOQOMLQLOTVER---GPHDALAAMLSCVLPDLOGRAT 584  
 523 rrlloeggvvillfspaayaoqomlqlotver---gphdalaamlscvlpdlograt 582  
 585 RYGVYFPGGLHPDSVSPFRVAPLFSLTQLPAPLADLOGGCSTGRPADRVERVTOA 644  
 583 rygvypfggllhpdsvspfrvaplfsltqlpaplaladloggcstgrpadrvervtoa 642  
 645 LRSAIDSC--TSSSEAPG 660  
 643 lrpaldsyfnppgtpapg 660

## RESULT 7

AAB61883 standard; Protein: 688 AA.

AAB61883;

08-MAY-2001 (first entry)

Chimeric zcytor14 protein #1.

Cytokine receptor; zcytor14; human; inflammation; rheumatoid arthritis;

antiinflammatory; gene therapy; vaccine.

Homo sapiens.

MO200104304-A1.

18-JAN-2001.

30-JUN-2000: 2000MO-US18383.

07-JUL-1999: 99US-0348854.

(ZYMO) ZYMOGENETICS INC.

Presnell SR, Burkhead SK, Powder SL.

WPI: 2001-112618/12.

New polypeptide encoding a human cytokine receptor designated zcytor14, for treating inflammation e.g. rheumatoid arthritis -

Claim 2: Page 102-104; 112pp: English.

The invention provides a new human cytokine receptor designated zcytor14. zcytor14 can be expressed by standard recombinant methodology. The encoding nucleic acid is useful for detecting the expression of a zcytor14 gene in a biological sample. Anti-zcytor14 antibodies can be used to screen biological samples in vitro for the presence of zcytor14. proteins, polypeptides and peptides having zcytor14 activity can be administered to a subject who lacks an adequate amount of this polypeptide, for treating inflammation and conditions such as rheumatoid arthritis. In contrast, zcytor14 antagonists (e.g. anti-zcytor14 antibodies) can be used to treat a subject who produces an excess of zcytor14. zcytor14 nucleotide sequences can also be used to provide zcytor14 to a subject. The present sequence represents a chimeric zcytor14 protein.

Sequence 688 AA:

Query Match 62.8%; Score 2263.5; DB 22; Length 688;  
Best Local Similarity 64.9%; Pred. No. 6,7e-206;  
Matches 449; Conservative 63; Mismatches 129; Indels 51; Gaps 8;

1 MPVSWFLSLALGKRPVVSLEKMEFODTARCSLGSLHMDGVLCPLGSLQSAAGV 60  
117 LQAQVYLSFGAYPIARCALLEVQPADLVQPGVSAGVAFDFEASLGAEOIWSYTKPR 176  
121 lqgqvylsfqayparcvlllevqpaalvqfsgvsyvdfeaalgsesvliwytqgr 180  
177 YQKELNLTQOLP-----DGNVLTLDVSEQDSFLIYLPRVPALKSLWTKNLT 227  
181 yqelnlntqqlpawlnvsadgnvhlvlnvseeqhfslsywqvgpprprvkhlt 240  
228 GPQNTLNHNDVLCICIQVWSLEPDSRVEFCPRPDGARNHMLHRLVLSGVQV 287  
241 gpqntlnhndvlnclclqvwslepdsvrnlclptredprahqnlwqaarltlltqswl 300  
288 LDAPFCLPGKVTLLCQMAPDSCPLVPPVPQKNATVNEPQDFOLVAGHPNLGVQVSTWE 347  
301 ldpfclpgkvtllcmaqapdscplvppvpqknatvnepqdfolvaghpnlgvqvstwe 343  
348 KVOQLSCMSADSLGPFKDDMLLVKMTKGLNNTSVCALEPDSGCTPLPSMASTRARLGEEL 407  
344 klqgqclswadslgpfkddmllvkmtkglntsvcalepdsdgctplpsmastrarlgeel 403  
408 LQDRSRHQCLQMLHMDNMGSLMACPMKXYIHRRWLVWTLACLLLAALFFLLLKDRRK 467

antiinflammatory; gene therapy; vaccine.

Homo sapiens.

MO200104304-A1.

18-JAN-2001.

30-JUN-2000: 2000MO-US18383.

07-JUL-1999: 99US-0348854.

(ZYMO) ZYMOGENETICS INC.

Presnell SR, Burkhead SK, Powder SL.

WPI: 2001-112618/12.

New polypeptide encoding a human cytokine receptor zcytor14, for treating inflammation e.g. rheumatoid arthritis -

Disclosure: Page 2-3; 112pp: English.

The invention provides a new human cytokine receptor designated zcytor14. zcytor14 can be expressed by standard recombinant methodology. The encoding nucleic acid is useful for detecting the expression of a zcytor14 gene in a biological sample. Anti-zcytor14 antibodies can be used to screen biological samples in vitro for the presence of zcytor14. proteins, polypeptides and peptides having zcytor14 activity can be administered to a subject who lacks an adequate amount of this polypeptide, for treating inflammation and conditions such as rheumatoid arthritis. In contrast, zcytor14 antagonists (e.g. anti-zcytor14 antibodies) can be used to treat a subject who produces an excess of zcytor14. zcytor14 nucleotide sequences can also be used to provide zcytor14 to a subject. The present sequence represents a variant of the human cytokine receptor zcytor14, designated zcytor14-1. This amino acid residues 1-113 of zcytor14.

Sequence 575 AA:

Query Match 62.8%; Score 2263.5; DB 22; Length 688;  
Best Local Similarity 64.9%; Pred. No. 6,7e-206;  
Matches 449; Conservative 63; Mismatches 129; Indels 51; Gaps 8;

1 MPVSWFLSLALGKRPVVSLEKMEFODTARCSLGSLHMDGVLCPLGSLQSAAGV 60  
117 LQAQVYLSFGAYPIARCALLEVQPADLVQPGVSAGVAFDFEASLGAEOIWSYTKPR 176  
121 lqgqvylsfqayparcvlllevqpaalvqfsgvsyvdfeaalgsesvliwytqgr 180  
177 YQKELNLTQOLP-----DGNVLTLDVSEQDSFLIYLPRVPALKSLWTKNLT 227  
181 yqelnlntqqlpawlnvsadgnvhlvlnvseeqhfslsywqvgpprprvkhlt 240  
228 GPQNTLNHNDVLCICIQVWSLEPDSRVEFCPRPDGARNHMLHRLVLSGVQV 287  
241 gpqntlnhndvlnclclqvwslepdsvrnlclptredprahqnlwqaarltlltqswl 300  
288 LDAPFCLPGKVTLLCQMAPDSCPLVPPVPQKNATVNEPQDFOLVAGHPNLGVQVSTWE 347  
301 ldpfclpgkvtllcmaqapdscplvppvpqknatvnepqdfolvaghpnlgvqvstwe 343  
348 KVOQLSCMSADSLGPFKDDMLLVKMTKGLNNTSVCALEPDSGCTPLPSMASTRARLGEEL 407  
344 klqgqclswadslgpfkddmllvkmtkglntsvcalepdsdgctplpsmastrarlgeel 403  
408 LQDRSRHQCLQMLHMDNMGSLMACPMKXYIHRRWLVWTLACLLLAALFFLLLKDRRK 467

PR	12-MAY-1998;	98US-0085094.
PR	12-MAY-1998;	98US-0085105.
PR	12-MAY-1998;	98US-0085180.
PR	18-MAY-1998;	98US-0085906.
PR	18-MAY-1998;	98US-0085920.
PR	18-MAY-1998;	98US-0085921.
PR	18-MAY-1998;	98US-0085922.
PR	18-MAY-1998;	98US-0085923.
PR	18-MAY-1998;	98US-0085924.
PR	18-MAY-1998;	98US-0085928.
PR	18-MAY-1998;	98US-0085925.
PR	18-MAY-1998;	98US-0085927.
PA	(HUMA-) HUMAN GENOME SCI INC.	
XX		
PI	Ruben SM, Florence K, Ni J, Rosen CA, Carter KC, Moore PA;	
PI	Olsen HS, Shi Y, Young PE, Wel F, Brewer LA, Soppet DR;	
PI	Lafleur DM, Endress GA, Ebner R;	
XX		
DR	WPI: 2000-062296/05.	
N-PFSDB; AAZ65269.		
XX		
PT	New isolated human genes and the secreted polypeptides they encode,	
PT	useful for diagnosis and treatment of e.g. cancers, neurological	
PT	disorders, immune diseases, inflammation or blood disorders	
XX		
PS	Claim 11: Page 372-373; 475pp; English.	
XX		
CC	AAZ65250 to AAZ65350 represent 97 isolated human secreted protein genes.	
CC	AAZ65124 to AAZ65223 are the secreted proteins encoded by the 97 human	
CC	genes. The gene encoding this protein was found to be on chromosome 3.	
CC	The genes and their corresponding secreted polypeptides are	
CC	useful for preventing, treating or ameliorating medical conditions,	
CC	e.g. by protein or gene therapy. Also pathological conditions can be	
CC	diagnosed by determining the amount of the new polypeptides in a sample	
CC	or by determining the presence of mutations in the new genes. Specific	
CC	uses are described for each of the 97 genes, based on which tissues they	
CC	are most highly expressed in, and include developing products for the	
CC	diagnosis or treatment of cancer, tumours, developmental abnormalities	
CC	and foetal deficiencies, blood disorders, diseases of the immune system,	
CC	autoimmune diseases, inflammation, allergies, Alzheimer's and cognitive	
CC	disorders, schizophrenia, arthritis, asthma, psoriasis, sepsis, skin	
CC	disorders, atherosclerosis, diabetes, cardiovascular disorders, kidney	
CC	disorders, digestive/endocrine disorders, infections and AIDS. The	
CC	polypeptides are also useful for identifying their binding partners.	
CC	The sequences shown in AAZ65224 to AAZ65424 represent fragments of the	
CC	secreted proteins.	
XX		
SQ	Sequence 309, AA:	
	Query Match 26.6%; Score 958.5; DB 21; Length 309;	
	Best Local Similarity 64.6%; Pred. No. 2,4e+82; Indels 29; Gaps 3;	
Matches 192; Conservative 20; Mismatches 56;		
YQ	1 MPVSFELSLALGRNVVSVLERLMPDOPARSGISCHILMDVDVLCPGLSAGAPGV 60	
DQ	1 mpvfpflslalgrsvslstlerlvpgdqcthgsglschldlclcpdipapgv 60	
YQ	61 LVPFLIGLELVRCPCIKTICALRVRRVVHLAVGHNMEPEE---AKGSDELDSRNNS 116	
DQ	61 laphlhqelvlrncqketcdclrlrvxhlavngwhepdeekfsgaadlgveepnas 120	
YQ	117 LOAGVVLSPQAFPIARCALLEVOYPADLVDPGGSVGSANVPCCFEASLSGAEOIWSYTPR 176	
DQ	121 lqagvvlstfgayplarcavllevyvpaaivgfigsvgsyvvdcafaalgsevrilwsytqr 180	
YQ	177 YOKELNLNQOLP-----GDGNLLTLIDVSEEDDFSLTYLR 212	
DQ	181 yekenhnlqqllpcrcjrlvwmsipsckalpvlnvsadgnwhlylnvseeqhfglslywn 240	
YQ	213 PVPDAKLSMTMYNKLNGPONITLNHTDLVPLCLIQVMSLEPDERVEFCPFREDPCA 269	

241 qvqppkprwhknlcpqililnhldlpolcivqwplepdsrvtsapsgrfp-ah 296

RESULT 10

AA25864 standard; Protein; 332 AA.

AA25864;

16-0CT-2001 (first entry)

Human protein sequence SEQ ID NO:1379.

Human; cancer; ulcer; HIV infection; human immunodeficiency virus; anti-inflammatory; antineoplastic; antirheumatic; immunosuppressive; antibacterial; endocrine; cardiac; central nervous system; virucide; anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia; antiaggregant; haemostatic; vulnery; antilucer; osteopathic; eczema; dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic; antiparkinsonian; infection; immunostimulant; gene therapy; antisense therapy; vaccine; inflammation; antinaphylactic; rheumatoid arthritis; septic shock; pancreatitis; cardiac dysfunction; neuropathologic disorder; cardiac anaphylaxis; autoimmune; thrombocytopenia; osteoporosis; severe combined immunodeficiency; allergic rhinitis; diabetes; multiple sclerosis; depression; Alzheimer's disease; Parkinson's disease; neurodegenerative disorder; neurological disorder.

Homo sapiens.

MO200153455-A2.

26-JUL-2001.

22-DEC-2000; 2000WO-0535017.

23-DEC-1999; 99US-0471275.

21-JAN-2000; 2000US-0488725.

25-APR-2000; 2000US-0552317.

(HYSE-) HYSEQ INC.

Tang YT, Liu C, Drmanac RT;

WPI: 2001-457603/49.

N-PSDB; AAH99805.

Isolated human polynucleotides encoding polypeptides, useful for the treatment and diagnosis of e.g. cancer, ulcers and HIV infection.

Claim 20; Page 283; 1217pp; English.

AAH99166 to AAH99904 encode the human proteins given in AA25225 to AA25963. The proteins can have activities based on the tissues and cells they are expressed in, such as: anti-inflammatory; antirheumatic; antiallergic; immunosuppressive; antibacterial; endocrine; cardiac; cardiovascular; antianaemic; antiaggregant; haemostatic; vulnery; antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic; antiparkinsonian; and immunostimulant. The proteins and polynucleotides encoding them can be used in gene therapy, antisense therapy and vaccine production. The proteins and polynucleotides are useful for screening for disorders or antagonists of a protein and for the treatment and diagnosis of disorders associated with the activity of a protein e.g. inflammation, rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction, neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal infections, autoimmunity, genetic diseases, haematopoietic disorders, anaemia, platelet disorders, thrombocytopenia, wounds, burns, ulcers, osteoporosis, severe combined immunodeficiency, eczema, allergic rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression, Alzheimer's disease, Parkinson's disease, neurodegenerative and

CC neurological disorders.

XX Sequence 332 AA;

Query Match 23.3%; Score 841.5; DB 22; Length 332;  
Best Local Similarity 62.1%; Pred. No. 3.7e-71;  
Matches 169; Conservative 22; Mismatches 52; Indels 29; Gaps 3;

1 MPVSFELSLALGRNPVYSLERMEODPARCSLGLSCHLMODVLCILGSLQASAGPV 60

2 MPVWFLSLALGRNPVYSLERMEODPARCSLGLSCHLMODVLCILGSLQASAGPV 61

61 LVPTRLQELVLRCPKTCALRVRVHLAVGHNAEPEE---AGKSPSELOESNRAS 116

62 LPTLQELVLRCPKTCALRVRVHLAVGHNAEPEE---AGKSPSELOESNRAS 121

117 LQAVYLSQAVPIARCALLERVPDVGSGVSAVDFCEASIGAEVQIMSTYKPR 176

122 LQAVYLSQAVPIARCALLERVPDVGSGVSAVDFCEASIGAEVQIMSTYKPR 181

177 YQKELNLQQLP-----DGDVVLTLQVSEODSFLLKLR 212

182 YQKELNLQQLP-----DGDVVLTLQVSEODSFLLKLR 212

213 PVPDAKSLMYNLTGPONTITNHTDLPVCLC 244

242 qvqppkprwhknlvrppsqv-hshncrplc 272

RESULT 11

AA25864 standard; Protein; 267 AA.

AA25864;

23-MAY-2001 (first entry)

Human membrane or secretory protein clone PSEC0233.

Human; secretory protein; membrane protein; vaccine; gene therapy;

rheumatoid arthritis; diabetes.

Homo sapiens.

EP1067182-A2.

10-JAN-2001.

07-JUL-2000; 2000EP-0114090.

08-JUL-1999; 99JP-0194179.

11-JAN-2000; 2000JP-0118775.

02-MAY-2000; 2000JP-0183766.

(HELI-) HELIX RES INST.

Ota T, Isogai T, Nishikawa T, Kawai S, Sugiyama T, Hayashi K;

WPI: 2001-093989/11.

N-PSDB; AAF93875.

Nucleic acids encoding secretory proteins/membrane proteins, useful in gene therapy or as candidate target molecules in drug development.

Claim 1; SEQ ID 264; 609pp + CD ROM; English.

This invention relates to nucleic acid sequences AAF93744 - AAF93916 which encode human secretory or membrane proteins represented by

AA2586317 - AA2586419. Included in the invention are primers AAF93917 - AAF94295 and AAF62232 - AAF62235 which are used to isolate the cDNA sequences of the invention. The invention also includes methods for the production of antibodies directed against the proteins, and cDNA



AAV76048;  
 27-MAR-2000 (first entry)  
 Murine skin cell protein, SEQ ID NO:303.  
 Skin; dermal papilla; keratinocyte; neonatal foreskin fibroblast; embryonic skin cell; keratinocyte stem cell; transit amplifying cell; secreted; transmembrane; inflammation; cancer; neurological disease; angiogenesis; tumour vascularisation; growth disorder; developmental disorder; skin wound; hair follicle disorder; anti-inflammatory; cytostatic; neuroprotective; vulnery.  
 Mus sp.  
 WO955865-A1.  
 04-NOV-1999.  
 29-APR-1999; 99WO-NZ00051.  
 29-APR-1998; 98US-0069726.  
 09-NOV-1998; 98US-0188930.  
 (GENE-) GENESIS RES & DEV CORP LTD.  
 Strachan L, Sleeman M, Watson JD, Onrust R, Kumble A, Murison JG;  
 WPI: 2000-072177/06.  
 N-PSDB: AAZ61753.  
 Novel polynucleotides useful for the treatment of various conditions including wounds and cancer.  
 Claim 4; Page 179-180; 235pp; English.  
 The invention relates to novel nucleic acid sequences derived from rat dermal papilla, human keratinocytes and neonatal foreskin fibroblasts, and mouse embryonic skin, keratinocyte stem cells and transit amplifying cells. Polypeptides of the invention may be used to treat inflammation, cancer and neurological diseases. The proteins may be used to stimulate the growth and motility of keratinocytes, to inhibit the growth of cancer cells, to modulate angiogenesis and tumour vascularisation, to modulate skin inflammation, to modulate epithelial cell growth and to inhibit binding of HIV-1 to leukocytes. The invention may also be used to treat growth and developmental defects, skin wounds and hair follicle disorders. Sequences AAY75942-Y76123 represent polypeptides encoded by cDNA sequences derived from several mouse, rat or human skin cell types. Sequences AAY75942-Y75947, AAY76020-Y76021, AAY76094-Y76104 and AAY76119 are proteins with an N-terminal signal sequence, indicating that they are secreted. Sequences AAY75986-Y75989, AAY76061-Y76071, AAY76106-Y76109 and AAY76121-Y76122 are proteins with one or more putative transmembrane domains.  
 Sequence 617 AA;

Query Match 8.6%; Score 310.5; DB 21; Length 617;  
 Best Local Similarity 25.7%; Pred. No. 3; le-20;  
 Matches 123; Conservative 55; Mismatches 208; Indels 93; Gaps 17;  
 224 KNLTPGNTLNTHTDLYPCICIQWLSLEPDSERVECEPEREDPGAH-RNLMHARLRVLS 282  
 183 kivsghltvdipylfipcmcleasyldetvrrkkpfgspesaygsfwgsifrttdys 242  
 283 PG---VWQDLAPCLPGKVTLCMQAPDPSPOPLVPPVPQKNAATVNEPQDFDLVAG---H 336  
 243 qhngmwalitrlcpikleaslcwtrgdptlpcetl-----patagasegwyllenvdh 296  
 337 PNLCVQSTWEKVOLOAC-----SWADSLGPFKDMILVEMKTLGNTSGVCALEPFG 388  
 297 pqicfkts-fensshvecpngsgslpwtvsmtdt-qaqqltlhfsrlyatfsaawdpg 354  
 389 C---TPPLPSMASTRARLGEELDOD-----FRSHQCKOLNNDNMGSLMACPMKTYIHR 440  
 355 lpgdtpmpypvstlsqgsvpvtldllipflrgencillwvsd-----vhta 401  
 441 WLV-----WACLLIAALFFELLKDKRRKAANGSRTALLHSADGAGYERLVGAL 493  
 402 whvylcpddapytqll-----tslsggrtvpvlllhaadseagrrlvgal 448  
 494 ASALSOM---PLRAVDLMSRRELGAHAWFHORRIQEGGVYILFSPAAVACQ 550  
 449 aellrtalgggrdvldlvegtvhtalglpjlwaarervareggvtvllwncgsp--- 505  
 551 QWLQOTVEPGRPHDALAMLSCVLPDFLOGRATGRVYGVYFDLILHDPSPSPRVAPLF 610  
 506 -----tacsqdpqaasrlrlccaaprl-----llayfsrlcakgdlprlralpry 552  
 611 SLPTQLPFLDALOGCCSTSA-----GRPADRVERVTOA-----LRALDSCSTSSSEAP 659  
 553 rllrdlprllrldaqpatlsswshlgakrcclknrlqgchllleakdkdyggslnsp 611  
 RESULT 14  
 AAB55987  
 ID AAB55987 standard; Protein: 617 AA.  
 AC AAB55987;  
 DT 08-MAR-2001 (first entry)  
 DE Skin cell protein, SEQ ID NO: 303.  
 DE Mouse; skin cell; cytostatic; anti-inflammatory; anti-HIV; neurotropic; neuroprotective; vulnery; immunomodulatory; vaccine; keratinocyte growth stimulation; cancer; angiogenesis inhibition; inflammation; neurological disease.  
 OS Mus sp.  
 PN WO200069884-A2.  
 PD 23-NOV-2000.  
 PE 15-MAY-2000; 2000WO-NZ00075.  
 PR 14-MAY-1999; 99US-0312283.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PI Watson JD, Strachan L, Onrust R, Sleeman M, Kumble A, Murison JG;  
 DR WPI: 2001-007495/01.  
 DR N-PSDB: AAC99686.  
 PT New isolated polynucleotide used in the identification of genetic disorders and encoding polypeptides used for treating inflammatory disease, cancer and neurological diseases.  
 PS Claim 4; Page 244-245; 352pp; English.  
 The present sequence is a polypeptide which is expressed in mammalian skin cells. The polypeptide is useful for stimulating keratinocyte growth and motility, inhibiting the growth of cancer cells, modulating angiogenesis, inhibiting angiogenesis and vascularisation of tumours, modulating skin inflammation, stimulating the growth of epithelial cells, inhibiting the binding of human immunodeficiency virus (HIV)-1 to leukocytes, and treating inflammatory disease, cancer and neurological diseases. The polynucleotide can be used as a marker, in the identification of genetic disorders, and for the design of oligonucleotides for examining expression patterns.  
 Sequence 617 AA;

Query Match 8.6%; Score 310.5; DB 22; Length 617;  
 Best Local Similarity 25.7%; Pred. No. 3.1e-20;  
 Matches 123; Conservative 55; Mismatches 208; Indels 93; Gaps 17;

224 KNLGPOITLNTHTLPCICIQWLSLEPDSERVEFCPPEDPGAH-RNLWHIARLVLS 282  
 183 klvsghvldlpyefllpcmcleasylgedltvrrkcfqspwpsdflvgsitfdys 242  
 283 PG---VWQLDAPCCPGKVTLCQWAPDSQPCPLVPPVPPKNAVNVEQDQVAG---H 336  
 243 qhngmvmaltlrcplkleaslcwrgqplpcetl-----pnatagesegwyllenvdh 296  
 337 PNLGVQSTWEKVOQAC-----SMADSLGPFKDDMLLVEMKGTGLNNTSVCALPESG 388  
 297 pqlcfkfs-fenssvechpgsgslpswtvsmtd-qaqqlthssrtlyafsaawdpg 354  
 389 C---TPLESMASRAARLGEELLQD-----FRSHQCMQWMDNMGSLMACPMDKYIHR 440  
 355 lgpdtmppyyslsgtqgsvpytlallpflrgencillvrsd-----vifa 401  
 441 WVLY-----WLAQLLLAALFFLLKKDRKRAAGSRTALLHSADAGYERLVAL 493  
 402 wkhvlpddapytlall-----tslgsgrtlpvlllhaadseagrtlvag 448  
 494 ASALSOM---PLRVAVDLSRRELNAHGALEWPHHQRRIIEGCVILLESPPAVACQ 550  
 449 aellrtalgggrdvldwvghvarlglpvlwaarervaregtvlllmcagpps--- 505  
 551 QWLOLQVVEPPEPHDLAAMSCVLPDFLOGRATGRVGVYFDGLHPDSVSPRVALE 610  
 506 ----tacsqgpgaastrlllcaaprpl-----llayfsrlcaxgdldprlralpry 552  
 611 SLPLQPLAFLLAGGCSNSA-----GRPADRVERVTA-----LRNALDSCTSSSEAP 659  
 553 rllrdplrlraldaqpaltlaaswshlgakrciknlegchilleaakddygststsp 611

## RESULT 15

AAU04957 standard; Protein; 667 AA.  
 AAU04957;

24-OCT-2001 (first entry)

Human Interleukin 17 receptor, IL-17RH3.

Human: Interleukin-17 receptor; IL-17RH3; agonist; antagonist;  
 PRO9877; DNA 119502-2789; systemic lupus erythematosus;  
 rheumatoid arthritis; osteoarthritis; diabetes mellitus;  
 allergic disease; asthma; demyelinating disease;  
 degenerative cartilaginous disorder; transplantation associated disease.

Homo sapiens.

Key Location/Qualifiers  
 Peptide 1..23  
 Protein /label- Signal\_peptide  
 24..667  
 Region /label- Mature\_IL\_17RH3  
 90..96  
 Region /note- "N-myristoylation site"  
 104..108  
 Region /note- "CAMP/GMP-dependent protein kinase  
 phosphorylation site"  
 318..322  
 Modified-site /note- "Asn is N-glycosylated"  
 322..329  
 Region /note- "Tyrosine kinase phosphorylation site"  
 347..351  
 Modified-site /note- "Asn is N-glycosylated"  
 358..364  
 Region

FT /note- "N-myristoylation site"  
 FT 364..368  
 FT /note- "Asn is N-glycosylated"  
 FT 453..462  
 FT /note- "Eukaryotic cobalamin-binding protein motif"  
 FT 455..472  
 FT /note- "Transmembrane domain"  
 FT 470..476  
 FT /note- "N-myristoylation site"  
 FT 482..486  
 FT /note- "Glycosaminoglycan attachment site"  
 FT 645..649  
 FT /note- "CAMP/GMP-dependent protein kinase  
 phosphorylation site"

MO200146420-A2.

28-JUN-2001.  
 20-DEC-2000; 2000MO-US34956.  
 23-DEC-1999; 99US-0172096.  
 30-DEC-1999; 99MO-US31274.  
 11-JAN-2000; 2000US-0175481.  
 18-FEB-2000; 2000MO-US04341.  
 02-MAR-2000; 2000MO-US05841.  
 21-MAR-2000; 2000US-0191007.  
 21-MAR-2000; 2000MO-US07532.  
 02-JUN-2000; 2000MO-US15287.  
 22-JUN-2000; 2000US-0213087.  
 24-AUG-2000; 2000MO-US23338.  
 24-AUG-2000; 2000MO-US23338.  
 24-OCT-2000; 2000US-0242837.  
 10-NOV-2000; 2000MO-US30873.  
 28-NOV-2000; 2000US-0253646.  
 01-DEC-2000; 2000MO-US32678.

(GETH ) GENENTECH INC.

Chen J, Filvaroff E, Fong S, Goddard A, Godowski PJ, Grimaldi CJ,  
 Gurney AL, Li H, Hillan KJ, Tumas D, Van Lookeren M, Vandlen RL,  
 Watanabe CK, Williams PM, Wood WI, Yansura DG;

WPI; 2001-451708/48.  
 N-PSDB; AAS09516.

Novel PRO polypeptides homologous to interleukin-17, useful for the  
 diagnosis and treatment of immune related disease e.g. rheumatoid  
 arthritis and diabetes -

Claim 10; Fig 16; 188pp; English.

The sequence is PRO9877 which is the human Interleukin 17 receptor,  
 IL-17RH3, encoded by DNA 119502-2789. A composition  
 containing ant/agonists to the PRO polypeptides or individual components  
 are useful for treating a mammal with an immune related disease e.g.  
 systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,  
 juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an  
 idiopathic inflammatory myopathy, Sjogren's syndrome, systemic  
 vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune  
 thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal  
 disease, a demyelinating disease, an autoimmune or immune-mediated skin  
 disease, contact dermatitis, an allergic disease e.g. food  
 hypersensitivity, asthma, a transplantation associated disease, or a  
 chronic inflammatory demyelinating polyneuropathy. Treating a  
 degenerative cartilaginous disorder comprises administering a PRO1031 or  
 PRO1122 polypeptide agonist, or antagonist to the mammal. Numerous  
 examples of the diseases and disorders are given in the specification.

Sequence 667 AA;

Query Match

8.6%; Score 310; DB 22; Length 667;



Sun Sep 29 09:32:42 2002

**us-09-899-471-2.rag**

Page 13

Best Local Similarity 28.1%; Pred. No. 3.9e-20;  
Matches 130; Conservative 56; Mismatches 214; Indels 62; Gaps 18;

```

0Y 224 KNEBPNITNTMTDVLPPCLCICIQWLSLEPSESEVEFCPPREDPCAH-RNLM---H1ARLR 279
Db 223 k1vsqnhvclpvefl1p1c1caasy1qedv1vrkkcpfgswpeaaysd1fwksvhtdys 282
0Y 280 VLSPEWQOLDAPCLCEGKXVLCMOARPOQSPQRLVPPVPOKATVNEPODF---QLVAGH 336
Db 283 qhtgmvatlt1cpr1kleaalcgndwhlt1ckd1-----pnatareasywylekvdlh 336
0Y 337 PNLCAVOVSWEKVQLOA-----CSNADSLGPRKDDMLVEMKGTGLNTSVCALEPSCG 389
Db 337 p1clckf1sgnshswcphqts1tswvmmdt1gaqql1hfsrmta1faawa1p91 395
0Y 390 ---TELPNASTRAARALGEBLLDOD---FRSHOCMOJLMDNDMSLW---ACPMOKYTH 438
Db 396 gqdt1vpruytvsqargspvs1dl1lprlpgscv1wrsd1vqfakhl1cprdsyeh 454
0Y 439 RRMVWVWLACLLAALFFELLKDKRKAARG-SR1ALLHSHADGAGERYLVGALASAL 497
Db 455 1g---111a1a11111gvlav1tcttrpgpgpgratpvl11haadseaqtr1vgalae11 512
0Y 498 SOM---PLRVAVDLMSRRELSAHGALAMFHHNORR1LOEGGV1LLFSPAANAQCOQW1Q 554
Db 513 raalgsgdv1dvlwegr1hvargr1p1w1aaatrtvaregvt11lwsga-----d 563
0Y 555 LQYVBERGHDALAAWLSCVLPDFLOCGATRGYVGVYEDGLHNPDSVPSPFRVAPLESLPT 614
Db 564 1rpsv-gpdp1raap1la-----1lhaaprt1111ayfsrlakgdlpp11ra1p1ryllr 617
0Y 615 QLPAPLDALOG---GCS2AGSRADREVERTQALRSALDSCT 653
Db 618 d1pr1ra1da1rpa1faeat1vgr1gaqr1-----qst1e1os 654

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search completed: September 28, 2002, 19:39:44
job time: 6372 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

CM protein - protein search, using sw model

Run on: September 28, 2002, 17:55:57 ; Search time 27.72 Seconds  
(Without alignments)  
593.898 Million cell updates/sec

Title: US-09-899-471-2

Perfect score: 3605  
1 MPVSWFLSLALGNRPVVS.....SSEAPCCCEWDLGPTTLE 674

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: /cgn2.6/ptodata/2/1aa/5a\_COMB.pep:\*  
2: /cgn2.6/ptodata/2/1aa/5b\_COMB.pep:\*  
3: /cgn2.6/ptodata/2/1aa/5a\_COMB.pep:\*  
4: /cgn2.6/ptodata/2/1aa/5b\_COMB.pep:\*  
5: /cgn2.6/ptodata/2/1aa/5a\_COMB.pep:\*  
6: /cgn2.6/ptodata/2/1aa/5b\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	310.5	8.6	617	4	US-09-188-930-303
2	167	4.6	864	2	US-08-620-694A-2
3	167	4.6	864	3	US-09-022-255-2
4	167	4.6	864	3	US-09-022-255-2
5	167	4.6	864	3	US-08-978-773-2
6	167	4.6	864	3	US-09-022-253-2
7	167	4.6	864	3	US-09-022-253-2
8	167	4.6	864	4	US-09-022-259-2
9	167	4.6	864	4	US-09-022-257-2
10	151.5	4.2	866	2	US-08-620-694A-10
11	151.5	4.2	866	3	US-09-022-255-10
12	151.5	4.2	866	3	US-09-022-696-10
13	151.5	4.2	866	3	US-08-978-773-4
14	151.5	4.2	866	3	US-09-022-253-10
15	151.5	4.2	866	3	US-09-022-253-10
16	151.5	4.2	866	4	US-09-022-259-10
17	151.5	4.2	866	4	US-09-022-257-10
18	149	4.1	330	4	US-09-188-930-125
19	114.5	3.2	1711	2	US-08-342-930-2
20	102.5	2.8	1498	2	US-08-404-531B-28
21	102.5	2.8	1498	3	US-08-476-900A-28
22	102.5	2.8	1498	3	US-08-488-546A-28
23	102.5	2.8	1581	2	US-08-404-531B-6
24	102.5	2.8	1581	3	US-08-476-900A-6
25	102.5	2.8	1581	3	US-08-488-546A-6
26	100	2.8	1410	3	US-09-335-409-3
27	100	2.8	1410	4	US-09-568-102-3

28	100	2.8	1410	4	US-09-567-969-3	Sequence 3, Appl1
29	100	2.8	1410	4	US-09-568-480-3	Sequence 3, Appl1
30	100	2.8	1410	4	US-09-568-486-3	Sequence 3, Appl1
31	100	2.8	1410	4	US-09-568-472-3	Sequence 3, Appl1
32	100	2.8	1447	4	US-09-041-886-25	Sequence 25, Appl1
33	100	2.8	1447	5	PCT-US94-05277-2	Sequence 2, Appl1
34	99.5	2.8	2647	2	US-08-583-562B-8	Sequence 8, Appl1
35	99.5	2.8	2647	2	US-08-779-113-8	Sequence 8, Appl1
36	97.5	2.7	1618	1	US-07-853-913-4	Sequence 4, Appl1
37	97.5	2.7	2629	2	US-09-060-836-4	Sequence 4, Appl1
38	97.5	2.7	2629	4	US-09-184-445-4	Sequence 4, Appl1
39	97.5	2.7	2629	4	US-09-261-907-2	Sequence 4, Appl1
40	95.5	2.6	2511	4	US-09-261-907-2	Sequence 2, Appl1
41	94.5	2.6	837	1	US-07-923-976-2	Sequence 2, Appl1
42	94	2.6	1004	4	US-08-916-352-2	Sequence 2, Appl1
43	92.5	2.6	3724	2	US-08-804-227C-10	Sequence 10, Appl1
44	92.5	2.6	3724	2	US-08-804-198-4	Sequence 4, Appl1
45	91.5	2.5	235	1	US-08-243-545-6	Sequence 6, Appl1

## ALIGNMENTS

RESULT 1  
US-09-188-930-303  
Sequence 303, Application US/09188930A  
Patent No. 6150502  
GENERAL INFORMATION:  
APPLICANT: Watson, James D.  
APPLICANT: Strachan, Lorna  
APPLICANT: Sileman, Matthew  
APPLICANT: Onrust, Rene  
APPLICANT: Murison, James Greg  
TITLE OF INVENTION: Compositions Isolated From Skin Cells  
FILE REFERENCE: 11000.1011C1  
CURRENT APPLICATION NUMBER: US/09/188,930A  
CURRENT FILING DATE: 1998-11-09  
NUMBER OF SEQ ID NOS: 348  
SOFTWARE: FASTSEQ for Windows Version 3.0  
SEQ ID NO 303  
LENGTH: 617  
TYPE: PRT  
ORGANISM: Mouse  
US-09-188-930-303

Query Match 8.6%; Score 310.5; DB 4; Length 617;  
Best Local Similarity 25.7%; Pred. No. 1.5e-24;  
Matches 123; Conservative 55; Mismatches 208; Indels 93; Gaps 17;

224 KNLGPRQITLNTHTDLPCLQVMSLEPDSERFCEPREDPEAH-RNLNHTIARLVLS 282  
183 KIVSGGHTVDLEPEELPCMCIEASYLOEDTVRKQKPSWPEAYGSDFOQSIPTDYS 242  
283 PG---VWOLDAPCCJPGKVTLCMOAPDQSPCLVPEYPOKNATVNEPQDQVAG---H 336  
243 OHNOMVALTLRPLKLESLCKRQDPLTFCETSS---FNATAOESGVTILENDLH 296  
337 PNLGVNSTWKEVQLOAC-----SWADSLQPFKQDMULENKTGINTSVGALBESG 388  
297 POLCFKFS-FENSSHVECPHQSGSLPSMTVSMOT-QAOQLTHFSSRTYATFASAMSDPG 354  
389 C---TLPSSMASTRARAGEELLQD-----FRSHOQMLNDMDMGMSMACPMQYTHRR 440  
355 LGPTMPVPIVSIQFGSVPTLDTLIPFLQENCLTVWRSD-----VHFA 401  
441 WVLV-----WACLLAALAEFFLLKKRRKARSGFALHSHSAGAYEELVAL 493  
402 WKHVLCPDPAVYPTQLLL-----RSLGSGRTIPVLLHAADESAQRRLVAL 448  
494 ASALSQW---PLRAVVDLMSRRELGAHALAMPHHQRRLIOEGGVVILFSPAAYACQ 550

DB 449 AELLRTALGGGRVYIVDMESTHVARIGPLPMLNAREVAREQGVILLMNCAGRS--- 505  
QY 551 QMLQLOTEBERPHDALAAMLSVLPDLQGRATGRYGVYFDGLLHPDSVSPFRVAPLF 610  
DB 506 -----TACSGDDPOAASRLTILCAAPRPL-----LTAFFSRICKAGIIPRLRALPRY 552  
QY 611 SLPTQAPALDLAGGCGSTGSA-----GRPADRVRYTQA-----LRSALDSCSTSSSEAP 659  
DB 553 RLRLDPLRLRALDAOPATLASSWSHLGAKRCLKNRLECHLLELAADDDYGGSTNSP 611

## RESULT 2

US-08-620-694A-2  
Sequence 2, Application US/08620694A  
Patent No. 5869286  
GENERAL INFORMATION:

APPLICANT: Yao, Zhengbin  
APPLICANT: Spriggs, Melanie  
APPLICANT: Fanslow, William  
TITLE OF INVENTION: No. 5869286el Receptor That Binds IL-17  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: Apple Operating System 7.5.5  
SOFTWARE: Microsoft Word for Apple, Version 6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/620,694A  
FILING DATE: 21 MARCH 1996  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/538,765  
FILING DATE: 7 AUGUST 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/410,535  
FILING DATE: 23 MARCH 1995  
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia Anne  
REGISTRATION NUMBER: 34,695  
REFERENCE/DOCKET NUMBER: 2617-B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)587-0430

INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 864 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-620-694A-2

Query Match 4.6%; Score 167; DB 2; Length 864;  
Best Local Similarity 20.3%; Pred. No. 1.1e-08;  
Matches 105; Conservative 62; Mismatches 167; Indels 104; Gaps 25;

DB 224 KNLIT--GPNITLNL-----HNDLYPCILCIQWSLEPD-----SSR 256  
DB 66 KNLITSSPNITNITVSSSTOHGELVPELVHVE-WTLOTDAIILYEGAEIAYLQINTNER 124  
DB 257 --VEFCPEFREDGCAHNLNHIARLR-VLSPG-----VMOADAPCCLGKXVILCQAPQ 307  
DB 125 LCVK--QELSMLOHKKRRKRRFSHFVVDGQETVTVHHLKPK-----IPDG 171

QY 308 SPCOP-----LVPVPQKNAATVNEPDEFQVLVAGHPNLCYQVSTWKEVLOACSWADELGP 363  
DB 172 DPNHKKIILFVPOEDSKMKMTSCVSSGLMDPRITVETLDTQHLRVDFITLNEST-PY 230  
QY 364 KDMILYEAKTGLNTSY-----CA-----LEP-- 386  
DB 231 Q---VLLSEFSDESNHSCFDVVKOIFAPROEEFHQNAVYFTLSKFFHCHHHVQVPPF 287  
QY 387 SGC-----TLPMSASTRAARLGEELLDPRSHQCMQMLMDNNGSLMACMDKY 436  
DB 288 SSCINDCLRHAVTPPCFVISTNTVTK-----PVADY 318  
QY 437 IHRNRY--LVWLAICLLLAALFFFL-----LKKDRKRAAGS----- 472  
DB 319 I-PLWYTGITLAILLVGSYIVLILICMTWLSGADQKHEGDSKINGILLPVADLTPLPL 377  
QY 473 --RTALLHSADGAGTERLYGALASAL-SQMPLRVAVDLSMRELSANGALAMFHQRR 529  
DB 378 RPRKWIIVYSADHPLYVEVYLKFAQFLITACGTEVALDLERQVISEVGMVMSKOE 437  
QY 530 ILQEGGVILFS-----PAVAQCQOQLQLOTEBERPHDALAAMLSCVL 574  
DB 438 WYSENSKIIILCSRGIOAKKAILGMAEPAPVOLRCDHW-----KPA-GDLFTAAANMIL 490  
QY 575 PDFLOGRATGRYGVYFDGLHPDSVSPFRVAPLFLSL 612  
DB 491 PDFKRPACFGTYVVCYFSGICSERDVPDLFNITSRYPL 528

## RESULT 3

US-09-022-255-2  
Sequence 2, Application US/09022255  
Patent No. 6072033  
GENERAL INFORMATION:

APPLICANT: Yao, Zhengbin  
APPLICANT: Spriggs, Melanie  
APPLICANT: Fanslow, William  
TITLE OF INVENTION: No. 6072033el Receptor That Binds IL-17  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: Apple Power Macintosh  
SOFTWARE: Microsoft Word for Apple, Version 6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/022,255  
FILING DATE:  
CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/620,694  
FILING DATE: 21 MARCH 1996  
APPLICATION NUMBER: USSN 08/538,765  
FILING DATE: 7 AUGUST 1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/410,535  
FILING DATE: 23 MARCH 1995  
ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia Anne  
REGISTRATION NUMBER: 34,695  
REFERENCE/DOCKET NUMBER: 2617-B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)587-0430

INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 864 amino acids

TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 JS-09-022-255-2

Query Match 4.6%; Score 167; DB 3; Length 864;  
 Best local similarity 20.3%; Pred. No. 1,1e-08;  
 Matches 105; Conservative 62; Mismatches 167; Indels 184; Gaps 25;

224 KNLV--GPONTLN-----HTDVPCLCIVQWSEPD-----SER 256  
 66 KNLPPSPKNIYINLSVSTOGELVPLVHVE-WTLOTASILYLEGAEISVLQINTNER 124  
 257 --VECFPRREDPGAHNRNHLRLR-VLSPG-----VMQDAPCCLPKGYTLQWAPDQ 307  
 125 LCVKF-QFLSMLOHRRKRKRRFSFSEHVDPGQREYEVTHLPK-----IPDG 171  
 308 SPCQP-----LVPPVQKNATVNEPQDFQVLVAGHPNLCVOYSTWEKYQDQACSWADSLGPF 363  
 172 DPNKSKIIIFPDCEDSKMKKTTSCVSSGLMDPNITVETLDTQHLKVDFTLWNEST-PY 230  
 364 KDMLEVMKTKGLNNTSV-----CA-----LEP-- 386  
 231 Q---VLESFSDSEHSCFEDVVKQIFAPRQEEFHORANTFTLSKFMCCHHVQVOPFE 287  
 387 SGC-----TPLPMASTRARLGBELLQDFRSHQCMQMDNDMGSIMACPMKDY 436  
 288 SSCINDCLRHAIVTPCPVISMVTPK-----PVADY 318  
 437 IHRWV--LWVACLILAALEFFL-----LLKDRRKARGS----- 472  
 319 I-PLWVGLITLIALLVGSYVILICMTWRLSGADQEKHGDSKINGILPVADLTPEPL 377  
 473 --RTALLHSADGAGYELVGAALASAL-SQMPLRVAVDMSRRELSAHGALAMFHORR 529  
 378 RPRKVMIVYSADHPLVYEVVLFKFAQLITACGEVALDLLEBVISVGVMTWSRQKE 437  
 530 ILQEGVVIILFS-----PAVAOCQOMIQLQVEGPHALAAMLSCVL 574  
 438 MVSNSKIIILICSGTQAKKAKAILGMAEPAYOLKCDHW-----KPA-GDLFTAAAMNML 490  
 575 PDFLOGRATGRVGVYFDGLLHPDSVSPFRVAPLESL 612  
 491 PDFKRPACFGTYVVCYFSGICSERDVPDLFNITSRPL 528

RESULT 4  
 S-09-022-696-2  
 Sequence 2, Application US/09022696  
 Patent No. 6072037

## GENERAL INFORMATION:

APPLICANT: Yao, Zhengbin  
 APPLICANT: Spriggs, Melanie  
 APPLICANT: Fanslow, William  
 TITLE OF INVENTION: No. 6072037el Receptor That Blinds IL-17  
 NUMBER OF SEQUENCES: 10

## CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunex Corporation  
 STREET: 51 University Street  
 CITY: Seattle  
 STATE: WA  
 COUNTRY: USA  
 ZIP: 98101

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
 COMPUTER: Apple Power Macintosh  
 OPERATING SYSTEM: Apple Operating System 7.5.5  
 SOFTWARE: Microsoft Word for Apple, Version 6.0.1  
 CURRENT APPLICATION DATA:  
 FILING DATE:  
 APPLICATION NUMBER: US/09/022.696  
 CLASSIFICATION:

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/620,694  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: USSN 08/410,535  
 FILING DATE: 23 MARCH 1995  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Perkins, Patricia Anne  
 REGISTRATION NUMBER: 34,695  
 REFERENCE/DOCKET NUMBER: 2617-B  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (206)587-0430  
 TELEFAX: (206)  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 864 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-09-022-696-2

Query Match 4.6%; Score 167; DB 3; Length 864;  
 Best local similarity 20.3%; Pred. No. 1,1e-08;  
 Matches 105; Conservative 62; Mismatches 167; Indels 184; Gaps 25;

224 KNLV--GPONTLN-----HTDVPCLCIVQWSEPD-----SER 256  
 66 KNLPPSPKNIYINLSVSTOGELVPLVHVE-WTLOTASILYLEGAEISVLQINTNER 124  
 257 --VECFPRREDPGAHNRNHLRLR-VLSPG-----VMQDAPCCLPKGYTLQWAPDQ 307  
 125 LCVKF-QFLSMLOHRRKRKRRFSFSEHVDPGQREYEVTHLPK-----IPDG 171  
 308 SPCQP-----LVPPVQKNATVNEPQDFQVLVAGHPNLCVOYSTWEKYQDQACSWADSLGPF 363  
 172 DPNKSKIIIFPDCEDSKMKKTTSCVSSGLMDPNITVETLDTQHLKVDFTLWNEST-PY 230  
 364 KDMLEVMKTKGLNNTSV-----CA-----LEP-- 386  
 231 Q---VLESFSDSEHSCFEDVVKQIFAPRQEEFHORANTFTLSKFMCCHHVQVOPFE 287  
 387 SGC-----TPLPMASTRARLGBELLQDFRSHQCMQMDNDMGSIMACPMKDY 436  
 288 SSCINDCLRHAIVTPCPVISMVTPK-----PVADY 318  
 437 IHRWV--LWVACLILAALEFFL-----LLKDRRKARGS----- 472  
 319 I-PLWVGLITLIALLVGSYVILICMTWRLSGADQEKHGDSKINGILPVADLTPEPL 377  
 473 --RTALLHSADGAGYELVGAALASAL-SQMPLRVAVDMSRRELSAHGALAMFHORR 529  
 378 RPRKVMIVYSADHPLVYEVVLFKFAQLITACGEVALDLLEBVISVGVMTWSRQKE 437  
 530 ILQEGVVIILFS-----PAVAOCQOMIQLQVEGPHALAAMLSCVL 574  
 438 MVSNSKIIILICSGTQAKKAKAILGMAEPAYOLKCDHW-----KPA-GDLFTAAAMNML 490  
 575 PDFLOGRATGRVGVYFDGLLHPDSVSPFRVAPLESL 612  
 491 PDFKRPACFGTYVVCYFSGICSERDVPDLFNITSRPL 528

RESULT 5  
 US-08-978-773-2  
 Sequence 2, Application US/08978773  
 Patent No. 6083906  
 GENERAL INFORMATION:  
 APPLICANT: Trout, Anthony  
 TITLE OF INVENTION: Method of Regulating Nitric Oxide Production  
 NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple PowerMacintosh  
OPERATING SYSTEM: Apple Operating System 7.5.5  
SOFTWARE: Microsoft Word for PowerMacintosh, Version 6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/978,773

FILING DATE:  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 60/052,525  
FILING DATE: 27 NOVEMBER 1996  
CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia Anne  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 2673-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)

INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 864 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
S-08-978-773-2

Query Match: 4.6%; Score 167; DB 3; Length 864;  
Best Local Similarity 20.3%; Pred. No. 1.1e-08;  
Matches 105; Conservative 62; Mismatches 167; Indels 184; Gaps 25;

224 KNTL--GPNITLN-----HTDLPVPCICIOVMSLEPD-----SER 256  
66 KNTLSSPKNIIYINLSVSTOGELVPLVHVE-WTLOTDAISILYLEGAELSVLQANTNER 124  
257 --VEFCPRFREDGARNIMHIARLR-VISPG-----VWOLDAPCCLPGRVTLQWAPDQ 307  
125 LCVKF--QELSMLOHHRKMRSEFSHFVVDPGQYEYTVHHLPRP-----IPDG 171  
308 SPOCP---LVPVPQKATYNEPDQFQVAGHPNLCVOVSTWEKYOLQACSNADSLGPF 363  
172 DPNHKSIIIFVPCDEDSKMKMTTSCVSSGSLMDPNITVETLDTQHLKVDFTLMNEST-PY 230  
364 KDDMLVEMKTGLNNTSV-----CA-----LEP-- 386  
231 Q---VLLSEFSDSENHSCFDVYKQIFAPROEERHORANVTFTLSKPHWCCHNHVOVOPFF 287  
387 SGC-----TLPMSASTRAARLGEELLQDFRSHOCMOLMNDNMGLMPCMDKY 436  
288 SSCINDCLRHAVTPCPYISNTTVPK-----PVADY 318  
437 IHRWV--LVWLACILLAALEFFL-----LLKDRKRAAGS----- 472  
319 I-PLWVYGLTLILAILVGSIVILYICMTWRISGADQEKHGDSKINGILPVADLTGPPL 377  
473 --FTALLHSADGAYEELVGLASAL--SQMPLRYAVUDLMSRELSSAHGALMWHHR 529  
378 RPRKRWIVYSADHPLUYEVVLFKFAOFLITACSTEVALLDLLEBOYISEVGWTVWSRKOE 437  
530 ILDEGVVILLES-----PAAVAQCOQMLQLOTFVEGPRHDLAAMLSCVL 574  
438 MVSNSKIIILCSRGTOAKWKAKIILQMAEPAVQLRCDHM-----KPA-GDLFTAAANMIL 490  
575 PDLFGRATGATGYVGVYDGLLHPDSVSPFRVAPLESL 612

Db 491 PDFKRPACFGTYVVCYFSGICSERDVPDLFNITSRPL 528

RESULT 6

US-09-022-253-2  
Sequence 2, Application US/09022253  
Patent No. 6096305  
GENERAL INFORMATION:  
APPLICANT: Yao, Zhenqin  
APPLICANT: Spriggs, William  
APPLICANT: Fanslow, William  
TITLE OF INVENTION: No. 6096305el Receptor That Binds IL-17  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Power Macintosh  
OPERATING SYSTEM: Apple Operating System 7.5.5  
SOFTWARE: Microsoft Word for Apple, Version 6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/022,253  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/620,694  
FILING DATE: 21-MARCH-1996  
APPLICATION NUMBER: USSN 08/538,765  
FILING DATE: 7 AUGUST 1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/410,535  
FILING DATE: 23 MARCH 1995

ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia Anne  
REGISTRATION NUMBER: 34,695  
REFERENCE/DOCKET NUMBER: 2617-B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 864 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-022-253-2

Query Match: 4.6%; Score 167; DB 3; Length 864;  
Best Local Similarity 20.3%; Pred. No. 1.1e-08;  
Matches 105; Conservative 62; Mismatches 167; Indels 184; Gaps 25;

224 KNTL--GPNITLN-----HTDLPVPCICIOVMSLEPD-----SER 256  
66 KNTLSSPKNIIYINLSVSTOGELVPLVHVE-WTLOTDAISILYLEGAELSVLQANTNER 124  
257 --VEFCPRFREDGARNIMHIARLR-VISPG-----VWOLDAPCCLPGRVTLQWAPDQ 307  
125 LCVKF--QELSMLOHHRKMRSEFSHFVVDPGQYEYTVHHLPRP-----IPDG 171  
308 SPOCP---LVPVPQKATYNEPDQFQVAGHPNLCVOVSTWEKYOLQACSNADSLGPF 363  
172 DPNHKSIIIFVPCDEDSKMKMTTSCVSSGSLMDPNITVETLDTQHLKVDFTLMNEST-PY 230  
364 KDDMLVEMKTGLNNTSV-----CA-----LEP-- 386



$\frac{d}{dt} \left( \frac{1}{2} \dot{\theta}^2 \right) = \frac{1}{2} \dot{\theta}^2$

---

575 PDLGRATGRVGVYFDGLHPDVPSPFRVAPLESL 612  
111 : 111 : 111 : 111 : 111 : 111 :  
b 491 PDLGRATGRVGVYFDGLHPDVPSPFRVAPLESL 612

RESULT 10  
15-08-620-694A-10  
Sequence 10, Application US/08620694A  
Patent No. 5869286

GENERAL INFORMATION:

APPLICANT: Yao, Zhengbin  
APPLICANT: Spriggs, Melanie  
APPLICANT: Fanslow, William  
TITLE OF INVENTION: No. 5869286el Receptor That Binds IL-17  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: Apple Power Macintosh  
SOFTWARE: Microsoft Word for Apple, Version 6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/620,694A  
FILING DATE: 21 MARCH 1996  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/538,765  
FILING DATE: 7 AUGUST 1995  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/410,535  
FILING DATE: 23 MARCH 1995  
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia Anne  
REGISTRATION NUMBER: 34,695  
REFERENCE/DOCKET NUMBER: 2617-B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 866 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
08-620-694A-10

Query Match 4.28; Score 151.5; DB 2; Length 866;  
Best Local Similarity 19.28; Pred. No. 5.4e-07;  
Matches 142; Conservative 73; Mismatches 206; Indels 317; Gaps 34;

55 SAGP-----VLVP-----TRLOTELVLRCPQKTDCAIRVRVVVLAHVGMAEPE 100  
: 111 : 111 : 111 : 111 : 111 : 111 :  
10 AVBGRLLGLLLGLVLAFGASRLDLHDAVCSQP---GLNCYKNSTCLDSDWIHPR 66  
: 111 : 111 : 111 : 111 : 111 : 111 :  
101 EAGKSDSEIQESNNAIQAVVIF-----QAVPIARCALLLEVQVPAVLVQGVSGVSAVF 156  
: 111 : 111 : 111 : 111 : 111 : 111 :  
67 -----NLTPSSPKDQIOLHFAHTQOGDLFPVAH---IEVTLQD----- 103  
: 111 : 111 : 111 : 111 : 111 : 111 :  
157 DCEASTL-----GAEVOI-----WSTI-----KPRROKEL 181  
: 111 : 111 : 111 : 111 : 111 : 111 :  
104 -----ASILYLEGELSVLQNTNERLCVRFEEFLSKLRHHRRMREFSHFVVDPDDEYEV 159  
: 111 : 111 : 111 : 111 : 111 : 111 :  
182 -----NLTOQLPDGDNVLLTLDVSEEDSFLLYLRLRVPD-----ALKSILWYKN 225  
: 111 : 111 : 111 : 111 : 111 : 111 :

Db 160 TVHHLKPIPDGD-----PNHOSKNL-----VPDCEHAKKVTTPCKSSGLMDPN 206  
OY 226 LTGPONTLTNHTDVLPCLOIOWSLPEPDERVEFC-----PREDPGNHR 270  
Db 207 IT-----VETLEAHLQVAFSLTLMNESTHYQILTLSPHMEHSCFE 247  
OY 271 NLMHIALRLRVLSPGWQDAPCCLEKVTLCWQAPQSPQPLVPPVPOKNATVNEPODF 330  
Db 248 HMHHI-----PAPR-----PEEF 260  
OY 331 Q-----LVAGHPNLGVOSTWEKVOLOACSNWADSLGPFKDMILVEMKGLNNTSVCL 384  
Db 261 HQRNMTLTLANLKCCR-----HOVQIO-----PF-----FSSCLND-----CL 295  
OY 385 EPSGCTPLPSMASTRBAARLGEELLQDFRSHOCQMLNNDMGSLMACPMCKYIHRMYLV 444  
Db 296 RNSATVSCPEMPDT-----PEPIDY-----VYMEIT 326  
OY 445 WLACLLLAALFFLLKKRKAARG-----RTALILH 479  
Db 327 GISLLVGSVI-----LTIQVMTWRLAGPSEKYSDDTKYTDGLPAPADILPPLKPKRWIY 384  
OY 480 SADGAGYERLYGALAS-ALSCMPLRAVADLMSRRELASGALAMFHRRRIIOEGGVYI 538  
Db 385 SADHPLVYDVYLKRAQFILLTACGTEVALDLLEQALISEAGVMTWGRQKQEMESNSKIT 444  
OY 539 LIESPAVVAOCQWL-----QLOTVBERP-HDALAMLSCLVLPDLQGRATGRVGVYF 591  
Db 445 VLCSRGTRAKQALLGRGAPVRLCDHGRKPVGDLPFAANMMLPDLFRAPCGFYVVCYE 504  
OY 592 DGLHPSVSPFRVAPFSLPTQIPAF-----IDALGGCSTSGAPRDRERVTQ-- 643  
Db 505 SEVSCDDVDPLFGAAPPYPLMDREVEYFRIDLEMFQPG-----RMHRVVELS 554  
OY 644 -----ALRSALD 650  
Db 555 GDNVLRSPGGRQLRALD 572

RESULT 11  
US-09-022-255-10  
Sequence 10, Application US/09022255  
Patent No. 6072033  
GENERAL INFORMATION:  
APPLICANT: Yao, Zhengbin  
APPLICANT: Spriggs, Melanie  
APPLICANT: Fanslow, William  
TITLE OF INVENTION: No. 6072033el Receptor That Binds IL-17  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: Apple Power Macintosh  
SOFTWARE: Microsoft Word for Apple, Version 6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/022,255  
FILING DATE:  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/620,694  
FILING DATE: 21 MARCH 1996  
APPLICATION NUMBER: USSN 08/538,765  
FILING DATE: 7 AUGUST 1995  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/410,535  
FILING DATE: 23 MARCH 1995



ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia Anne  
REGISTRATION NUMBER: 34,695  
REFERENCE/DOCKET NUMBER: 2617-B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)

INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 866 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-022-255-10

Query Match 4.2% Score 151.5; DB 3; Length 866;  
Best Local Similarity 19.2% Pred. No. 5.4e-07;  
Matches 142; Conservative 73; Mismatches 206; Indels 317; Gaps 34;

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55 SAPGP-----VLVP-----TRIQTELVLRCPQKTCALRVVYVHILAVHGMARE 100
10 AVRPRLGLLLLLGLVLPAGGASLRLDLRALVCSQP---GLKCTYKNSCTCLDSWIMHR 66
101 EAGKSELDSESRNASLQAOVYLSF---QAYPIARCALLEVOPADLVOPGOSVGSAYF 156
67 -----NLTPSSPKDQIQQLHFATQGGDLPPVAH---IEWTLQTD----- 103
157 DCFEASL---GAEQVQI-----WSTY-----KRYQKEL 181
104 ---ASTLYLEGAEISVLQNLNTERLCVAFEEFLSKLRHHRRWRFTFSHFVVDQDEYEV 159
182-----NLITQOLPFGDNVILTLVDSEODFSFLTLRLRPYD-----ALKSLMYKN 225
160 TVNHLPRPIPDG-----PNHOSKNFL-----VPDCEHARKKVTTPCMSSGSLMDPN 206
226 LTGPQNTLNLHTDLVPCICIQWLSLEPDSERVEFC-----PFREDPGANR 270
207 IT-----VETLEAHQLRVSFILMNSTHYQILLTSPFHENHSCFE 247
271 NLNMIARLVLSPGWQDAPRCCLRGKYLICQAPROSCQPLVPPRPQKATVNEPODF 330
248 HMMHT-----PAPR-----DEEF 260
331 Q-----LVAGHPNLQVQSTWEKYLQACSWADSLGPFKDMILYEMKGLNNTSCAL 384
261 HORSNVTLTLNKLGGCCR---HOVOIQ-----PF-----FSSCLND-----CL 295
385 EPSCGCTLPSSASTRAARLGEELLQDFRSHQCMQWMDNDMGSIMACPMDKYIHRRLVLY 444
296 RHSATVSCPEMPDT-----PEPIPDY-----MPLW-----VYWFIT 326
445 WLAGCLLAALEFFLLKKDRKARGS-----RTALLH 479
327 GISLILVGSYV---LLIYQMTWRLAPGSEKYSDDTKYTDGLPRAADLIPPLKPKRWIY 384
480 SADGAGERYLVALAS---ALSOMPLRAVADLMSRRELSTAGALAMFHHORRIIOEGGVI 538
385 SADHPLVVDVYLKRAQFLITACGTVALDLEEQAISLSEAGVMTWVGROKDEWESNKTII 444
539 LLESPAVALQOCQWL-----OLQTEBERP---HDAIAMLSCVLPDEFLOGRATGRYGVYE 591
445 VLCSRGTRAKQALLIGRGAHYRLRCDHGKRVGDLFTFAANMMLIPDFKRPACFGYVVCYF 504
592 DGLLHPDSVSPFRVAVPLFSLPTQLPAP-----LDALOGGCGSTSGRPRADVERVYQ-- 643
505 SEVSCDGDVDPDLFAAPRYPLMDREEVYFRIQDLEMFOPG-----RMHRVGLS 554
644 -----ALRSALD 650
555 GDMYLRSPGKQLRAALD 572
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RESULT 12

US-09-022-696-10

; Sequence 10, Application US/09022696

; Patent No. 6072037

; GENERAL INFORMATION:

; APPLICANT: Yao, Zhengbin

; APPLICANT: Spriggs, Melanie

; APPLICANT: Fanslow, William

; TITLE OF INVENTION: NO. 6072037e1 Receptor That Binds IL-17

; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Immunex Corporation

; STREET: 51 University Street

; City: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98101

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: Apple Power Macintosh

; SOFTWARE: Microsoft Word for Apple, Version 6.0.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/022,696

; FILING DATE:

; CLASSIFICATION:

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: 08/620,694

; FILING DATE:

; CLASSIFICATION:

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: USN 08/410,535

; FILING DATE: 23 MARCH 1995

; CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia Anne

REGISTRATION NUMBER: 34,695

REFERENCE/DOCKET NUMBER: 2617-B

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206)587-0430

TELEFAX: (206)

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 866 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-022-696-10

Query Match

Best Local Similarity 4.2% Score 151.5; DB 3; Length 866;  
Matches 142; Conservative 73; Mismatches 206; Indels 317; Gaps 34;

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55 SAPGP-----VLVP-----TRIQTELVLRCPQKTCALRVVYVHILAVHGMARE 100
10 AVRPRLGLLLLLGLVLPAGGASLRLDLRALVCSQP---GLKCTYKNSCTCLDSWIMHR 66
101 EAGKSELDSESRNASLQAOVYLSF---QAYPIARCALLEVOPADLVOPGOSVGSAYF 156
67 -----NLTPSSPKDQIQQLHFATQGGDLPPVAH---IEWTLQTD----- 103
157 DCFEASL---GAEQVQI-----WSTY-----KRYQKEL 181
104 ---ASTLYLEGAEISVLQNLNTERLCVAFEEFLSKLRHHRRWRFTFSHFVVDQDEYEV 159
182-----NLITQOLPFGDNVILTLVDSEODFSFLTLRLRPYD-----ALKSLMYKN 225
160 TVNHLPRPIPDG-----PNHOSKNFL-----VPDCEHARKKVTTPCMSSGSLMDPN 206
226 LTGPQNTLNLHTDLVPCICIQWLSLEPDSERVEFC-----PFREDPGANR 270
207 IT-----VETLEAHQLRVSFILMNSTHYQILLTSPFHENHSCFE 247
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QY 271 NMHTARLRLVSPGVWQDAPCCLPGRKVTLCWQAPDQSPCQPLVPVPQKNATVNEPODF 330  
 DB 248 HHHH-----PAPR-----PEEF 260  
 QY 331 Q-----LVAGHPNLCVQVSTWEKVQIACSWADSLGPFKDMILVEMKTGLNNTSVCA 384  
 DB 261 HORSNVTLLRLNKGCCR-----HOVOIQ-----FSSCLND-----CL 295  
 QY 385 EPGGCTPLPSMASTRARLGEELLQDFRSHOCQMLMNDNMGSLMACPMCKYIHRRLV 444  
 DB 296 RHSAIVSCPEMDT-----PEPIPDY-----MPLM-----VYWFIT 326  
 QY 445 WLACLLAAALFFELLKKDRKARGS-----RTALLH 479  
 DB 327 GISILLVGSVI-----LLIYCMTRILAGPSEKYSDDTKYTGCLPRADLIPPLKPKRWIIT 384  
 QY 480 SADGAGYERLVGALAS-ALSQMPLRAVADLMSRRELSSAGALAMFHRRRILOEGGVI 538  
 DB 385 SADHPLLYDVVLFKFAQFLITACGTEVALDLLEQALISEAGVMTWVGROKQEVESNKKI 444  
 QY 539 LLESPAANAQCCQWL-----QLOTEVPGP-HDALAAMLSCVLPDFLOGRATGRVGYVF 591  
 DB 445 VLCSGRTAKWQALLGKAPVRLKCDHGKPYGDLFTAAAMNMLPDKRPACFGTYVVCYF 504  
 QY 592 DGLLHPDVSPSPRVAPLPSLPQLPAF-----LDALQGGCSTSGRPRADRYERTQ-- 643  
 DB 505 SEVSCDGVDPDLFGAARPRPLMDRFEERYFRIDLEMFQPG-----RMRHVGELS 554  
 QY 644 -----ALRSALD 650  
 DB 555 GDNYLRSFGROLRAALD 572

## RESULT 13

IS-08-978-773-4  
 Sequence 4, Application US/08978773  
 Patent No. 6083906

## GENERAL INFORMATION:

APPLICANT: TROUT, Anthony  
 TITLE OF INVENTION: Method of Regulating Nitric Oxide Production  
 NUMBER OF SEQUENCES: 4

## CORRESPONDENCE ADDRESSES:

ADDRESSEE: Immunex Corporation  
 STREET: 51 University Street  
 CITY: Seattle  
 STATE: WA  
 COUNTRY: USA

ZIP: 98101

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: Apple Macintosh  
 SOFTWARE: Microsoft Word for Macintosh, Version 6.0.1

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/978,773  
 FILING DATE:

CLASSIFICATION: 530

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: USSN 60/052,525  
 FILING DATE: 27 NOVEMBER 1996

## CLASSIFICATION: 530

## ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia Anne  
 REGISTRATION NUMBER: 34,693  
 REFERENCE/DOCKET NUMBER: 2623-A  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (206) 587-0430  
 TELEFAX: (206)

## INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 866 amino acids  
 TYPE: amino acid

TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-978-773-4

Query Match 4.28; Score 151.5; DB 3; Length 866;  
 Best Local Similarity 19.28; Pred. No. 5.4e-07;  
 Matches 142; Conservative 73; Mismatches 206; Indels 317; Gaps 34;

QY 55 SAGP-----VYVP-----TRLOTELVRCQKTCALRRVYVHLAVGHAAPE 100  
 DB 10 AVPGPLGLILLGLVLAAPGASLRLDHRALVCSOP-----GLNCTVKNSTCLDSDWTHPR 66  
 QY 101 EAKGSESEIQUESRNASIQAVYLSF-----QAVPIARCALLEVOVPADVQPGSGSAVF 156  
 DB 67 -----NLTPSSPKDQIQHAFHTQGGDLFPVAH-----IEMTLQTD----- 103  
 QY 157 DCREASL-----GAEVQI-----WSYT-----KPRYQEL 181  
 DB 104 -----ASILYLEGAEISVLIQNTNERLCVREFELSKIRHHRRMRFTFSHFVYDPPQDEYEV 159  
 QY 182 -----NLQOLPDGDNVLLTLDVSEEDPSFLYLKRVPD-----ALKSLMYKN 225  
 DB 160 TVHHLEKPIPDGD-----PNHOSKNFL-----VPDEHARKVYTPCMSGSLMDPN 206  
 QY 226 LKGPQNTLHTDLPCLCIQVMSLEPDSERVEFC-----PPREDGAHR 270  
 DB 207 IT-----VETLEAHQLAVSFTLMNETHYQILLISFPHEHNSCEE 247  
 QY 271 NMHTARLRLVSPGVWQDAPCCLPGRKVTLCWQAPDQSPCQPLVPVPQKNATVNEPODF 330  
 DB 248 HHHH-----PAPR-----PEEF 260  
 QY 331 Q-----LVAGHPNLCVQVSTWEKVQIACSWADSLGPFKDMILVEMKTGLNNTSVCA 384  
 DB 261 HORSNVTLLRLNKGCCR-----HOVOIQ-----FSSCLND-----CL 295  
 QY 385 EPGGCTPLPSMASTRARLGEELLQDFRSHOCQMLMNDNMGSLMACPMCKYIHRRLV 444  
 DB 296 RHSAIVSCPEMDT-----PEPIPDY-----MPLM-----VYWFIT 326  
 QY 445 WLACLLAAALFFELLKKDRKARGS-----RTALLH 479  
 DB 327 GISILLVGSVI-----LLIYCMTRILAGPSEKYSDDTKYTGCLPRADLIPPLKPKRWIIT 384  
 QY 480 SADGAGYERLVGALAS-ALSQMPLRAVADLMSRRELSSAGALAMFHRRRILOEGGVI 538  
 DB 385 SADHPLLYDVVLFKFAQFLITACGTEVALDLLEQALISEAGVMTWVGROKQEVESNKKI 444  
 QY 539 LLESPAANAQCCQWL-----QLOTEVPGP-HDALAAMLSCVLPDFLOGRATGRVGYVF 591  
 DB 445 VLCSGRTAKWQALLGKAPVRLKCDHGKPYGDLFTAAAMNMLPDKRPACFGTYVVCYF 504  
 QY 592 DGLLHPDVSPSPRVAPLPSLPQLPAF-----LDALQGGCSTSGRPRADRYERTQ-- 643  
 DB 505 SEVSCDGVDPDLFGAARPRPLMDRFEERYFRIDLEMFQPG-----RMRHVGELS 554  
 QY 644 -----ALRSALD 650  
 DB 555 GDNYLRSFGROLRAALD 572

## RESULT 14

US-09-022-253-10  
 Sequence 10, Application US/09022253  
 Patent No. 6096305

## GENERAL INFORMATION:

APPLICANT: Yao, Zhengbin  
 APPLICANT: Spriggs, William  
 APPLICANT: Ranslow, William  
 TITLE OF INVENTION: No. 6096305e1 Receptor That Binds IL-17  
 NUMBER OF SEQUENCES: 10  
 CORRESPONDENCE ADDRESSES:

```

01 385 EPSGCTPLPSMASTRARARGEEELLOFRRSHQCMOLMNDNNGSLWACPMDKYIHRRWLV 444
02 296 RNSATVSCSEMDT-----PEPIPD-----MLM-----YWFIT 326
03 445 WLACILLAALFEFLLKKDRRAARG-----FTALLH 479
04 327 GISILVGSVI--LLIVCMTRLAGSESEKSDDTKYTDGJLPAADLIPPLPKRWIIT 384
05 480 SMDGAGYEPLVGLAS-ALSQMLRVAVDLMSRRELSHGALAMPHHQRRLIOEGSVI 538
06 385 SADHPLHYDVVVKFAQFLLTACGTEVALDLLEDAISAGVMTWGRQOEWEVNSKIT 444
07 539 LIFSPAIVAQCOQWL-----OLQTVBGP-HDMLAAMLSCLVLPFLOGRATGRYGVYE 592
08 445 VLCSRCTRAKWLALLRGAPAVRLRCDHGKPYGDLFTAAAMNMLPDKRACSTYYVCYF 504
09 592 DELIHPDVSPEPRVAPLFLSLPQLPAF-----LDALQGCSTAGRPADRYERYTQ-- 643
10 505 SEVSCGQDVDPDLFGAAPRYPLMDRFEVEYFRIDLEMPQG-----RMRVGEIS 554
11 644 -----ALRSALD 650
12 555 GDNVLRSPGGRQLRAALD 572
13
14 RESULT 15
15 US-09-022-260-10
16 ; Sequence 10, Application US/09022260
17 ; Patent No. 6100235
18 ; GENERAL INFORMATION:
19 APPLICANT: Yao, Zhengbin
20 APPLICANT: Spriggs, Melanie
21 APPLICANT: Fanslow, William
22 TITLE OF INVENTION: No. 6100235el Receptor That Binds IL-17
23 NUMBER OF SEQUENCES: 10
24 CORRESPONDENCE ADDRESS:
25 ADDRESSEE: Immunex Corporation
26 STREET: 51 University Street
27 CITY: Seattle
28 STATE: WA
29 COUNTRY: USA
30 ZIP: 98101
31
32 COMPUTER READABLE FORM:
33 MEDIUM TYPE: Floppy disk
34 COMPUTER: Apple Power Macintosh
35 OPERATING SYSTEM: Apple Operating System 7.5.5
36 SOFTWARE: Microsoft Word for Apple, Version 6.0.1
37 CURRENT APPLICATION DATA:
38 APPLICATION NUMBER: US/09/022,260
39 FILING DATE:
40 CLASSIFICATION:
41 PRIOR APPLICATION DATA:
42 APPLICATION NUMBER: 08/620,694
43 FILING DATE:
44 CLASSIFICATION:
45 PRIOR APPLICATION DATA:
46 APPLICATION NUMBER: USN 08/410,535
47 FILING DATE: 23 MARCH 1995
48
49 ATTORNEY/AGENT INFORMATION:
50 NAME: Perkins, Patricia Anne
51 REGISTRATION NUMBER: 34,695
52 REFERENCE/DOCKET NUMBER: 2617-B
53 TELECOMMUNICATION INFORMATION:
54 TELEPHONE: (206)587-0430
55 TELEFAX: (206)
56
57 INFORMATION FOR SEQ ID NO: 10:
58 SEQUENCE CHARACTERISTICS:
59 LENGTH: 866 amino acids
60 TYPE: amino acid
61 TOPOLOGY: linear
62 MOLECULE TYPE: protein
63
64 US-09-022-260-10

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Sun Sep 29 09:32:43 2002

us-09-899-471-2.rai

Page 11

Query Match	4.2%	Score 11.5;	DB 3;	Length 866;
Best Local Similarity	19.2%	Pred. No. 5,4e-07;		
Matches 142;	Conservative 73;	Mismatches 206;	Indels 317;	Gaps 34;

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55 SAGP-----VLP-----TRLOEYLRCQKTDCLRVRYVHLAVHGAERE 100
10 AVGPRLGLLLLLGLVLA PGASLRLLDHRALVCSOP---GLNCTYKNSCTLDDSMHPR 66
101 EAGKSDSELOESRNASIAQAVULSF-----QAVPIKCALLEVQVADLVQPGOSVSAVF 156
67 -----NLTPSSPKDQIQIHLRHAHQOGLRPVAH---IEWTQTD----- 103
157 DCEASL-----GAEVOI-----WSY-----KPYOKEL 181
104 ---ASILYLEGALVELVLOINTNERLCVRFEFLSKLRHHNRMRFTFSHFVVDPOEYEV 159
182 ---NLQOOLRQGNVLLTLDVSEODPSFLLYLRVPD-----ALKSILMYKN 225
160 TVHHLEKPIPDG-----PMSKNFL-----VPCEHARMKVTTPCMSGSLMDPN 206
226 LTGPONITNHTLVPCICIQVWSLEPDSERVEFC-----PREDGAR 270
207 IT-----VELLEHOLRVSTLLMNESTHYQILTSFPMENHSCE 247
271 NLMHTARLVLSPGWOLAPCCLPKVTLQWADPDSFCOPLVRPPOKNATVNEPOFE 330
248 NMHHI-----PAH-----PEEF 260
331 Q-----LVAGHNILCVOWSTWEKYOLOACSMADSLDPFKODMLVEMKGTGLNNTSYAL 384
261 HORSNVTTLRLNKGCCR---HOVOIQ-----FSSCLND---CL 295
385 EPSGCTPLPSMASTRAARLGEELLDOFRSHOCQMOMDNDNGSLMACPMOXYIHRWVLY 444
296 RHSATVSCPEMDT-----PEIIPY-----HPLW-----YVWFIT 326
445 WILACLLLAALFFFLILKKDRKKANGS-----RTALEH 479
327 GISILVGSVI---LIVCMTWRLAGGSEKYSDDTKYTDGLRPADLLPPLKPKRWIIT 384
480 SADGAGEYELVALAS-ALSQMPLRVAVULMSRELSAHGALAMFHQORRIIOEGVVI 538
385 SADHLYLVYVULKFOELFLACGTEVALDLLEBOAISCAVMVTWGROKORMVESNSKII 444
539 LIFSRAVAACQOML-----OLQTVEPGP-HBALAAMLSCVLPDFOGRATGKYVYGF 591
445 VLSRGSTAKMOMALLGRGAPVRLRCDHGKRPVGDLEFRAMMMIILPDEFKRPACFGYVUYCF 504
592 DGLLHPDSVSPFRRVAPLFSLETPQLPAF-----IDLQGGCSTSAGRPADRVRYTO- 643
505 SEVSCDGDVPDLFGAAPRPRLMDREEEYVFRIQDLEMFQG-----RMHRVGEIS 554
644 -----ALRSALD 650
555 GDNVLRBSGROLRALD 572

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Arch completed: September 28, 2002, 19:40:27  
 Time: 6270 sec

GenCore version 4.5  
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protein - protein search, using sw model

Search time 72.7 Seconds  
1603.832 Million cell updates/sec

US-09-899-471-2

Sequence: 1 MPVSWFLSLALGRNPVVS.....SSAPGCCCEMDLPCPTTLE 674

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5

Number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0  
Minimum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- 1: SP:archaea:\*
- 2: SP:bacteria:\*
- 3: SP:fungi:\*
- 4: SP:human:\*
- 5: SP:invertebrate:\*
- 6: SP:mammal:\*
- 7: SP:mhc:\*
- 8: SP:organelle:\*
- 9: SP:phage:\*
- 10: SP:plant:\*
- 11: SP:rodent:\*
- 12: SP:virus:\*
- 13: SP:vertebrate:\*
- 14: SP:unclassified:\*
- 15: SP:viirus:\*
- 16: SP:bacteriopl:\*
- 17: SP:archaeop:\*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Rank	Score	Query Match	Length	DB ID	Description
1	2471	68.5	567	11 099J43	099J43 mus musculu
2	1749.5	48.5	538	4 09BR97	09BR97 homo sapien
3	167	4.6	864	11 060943	060943 mus musculu
4	151.5	4.2	866	4 043844	043844 homo sapien
5	151.5	4.2	866	4 096F46	096F46 homo sapien
6	114.5	3.2	1013	16 053499	053499 mycobacteri
7	110.5	3.1	2012	4 09BX84	09BX84 homo sapien
8	110	3.1	2910	11 055225	055225 mus musculu
9	108.5	3.0	361	3 060150	060150 schizosacch
10	108.5	3.0	1072	4 09Y4G7	09Y4G7 homo sapien
11	106.5	3.0	478	16 09RY89	09RY89 delinococcus
12	106.5	3.0	589	10 094G03	094G03 flaveria pr
13	106.5	3.0	1248	4 09UJ61	09UJ61 homo sapien
14	106	2.9	756	10 093XR9	093XR9 bruguliera g
15	106	2.9	1693	2 09RL2	09RL2 agrobacteri
16	105.5	2.9	698	16 09PBH5	09PBH5 xylella fas

17	105	2.9	1767	5 09W4F5	09W4F5 drosophila
18	105	2.9	1767	5 024495	024495 drosophila
19	104.5	2.9	549	10 09FV22	09FV22 cinamomum
20	104.5	2.9	581	10 094BW5	094BW5 cinamomum
21	104.5	2.9	864	4 043297	043297 homo sapien
22	104.5	2.9	1237	4 09UNC9	09UNC9 homo sapien
23	104.5	2.9	1248	4 09UBZ5	09UBZ5 homo sapien
24	104.5	2.9	3021	12 081258	081258 hepatitis c
25	103.5	2.9	383	5 09VIT5	09VIT5 hepatitis c
26	103.5	2.9	936	13 09BS71	09BS71 gallus gall
27	103	2.9	851	5 09U2S3	09U2S3 caenorhabdi
28	103	2.9	906	16 09HX92	09HX92 pseudomonas
29	102.5	2.8	758	4 09NKR9	09NKR9 homo sapien
30	102.5	2.8	1239	13 09DEP4	09DEP4 xenopus lae
31	102.5	2.8	1418	13 09BSW6	09BSW6 xenopus lae
32	102	2.8	509	11 008907	008907 mus musculu
33	102	2.8	758	6 09N2H2	09N2H2 sus scrofa
34	102	2.8	955	4 096DN2	096DN2 homo sapien
35	102	2.8	3021	12 068870	068870 hepatitis c
36	101.5	2.8	610	4 014775	014775 homo sapien
37	100.5	2.8	2270	4 09NSJ3	09NSJ3 homo sapien
38	100	2.8	3013	12 092530	092530 hepatitis c
39	100	2.8	3019	12 092529	092529 hepatitis c
40	99.5	2.8	589	10 094G02	094G02 flaveria pr
41	99.5	2.8	1114	11 09JKW7	09JKW7 mus musculu
42	99	2.7	932	11 09D2V7	09D2V7 mus musculu
43	99	2.7	1002	11 091VB4	091VB4 mus musculu
44	99	2.7	1617	13 073905	073905 gallus gall
45	99	2.7	2308	5 09VDJ9	09VDJ9 drosophila

ALIGNMENTS

RESULT	1	PRELIMINARY	PRT	567 AA.
099J43	099J43	099J43		
AC	01-JUN-2001	(TREMBLrel. 17, Created)		
DT	01-JUN-2001	(TREMBLrel. 17, Last sequence update)		
DT	01-DEC-2001	(TREMBLrel. 19, Last annotation update)		
DE	HYPOTHEICAL	62.8 KDA PROTEIN.		
OS	Mus musculus (Mouse)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.			
OX	NCBI_TaxID=10090;			
RN	(1)			
RP	SEQUENCE FROM N.A.			
RA	Strausberg R.			
RL	Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.			
DR	EMBL: BC004759; AAH04759.1;			
KW	Hypothetical protein.			
SO	SEQUENCE 567 AA; 62798 MW; C1AAB79E2006BID CRC64;			
Query Match	68.5%; Score 2471; DB 11; Length 567;			
Best Local Similarity	94.7%; Pred. No. 7.3e-247			
Matches	463; Conservative 0; Mismatch 2; Indels 24; Gaps 1;			
QY	1	MPVSWFLSLALGRNPVVSLERLMEPODTRARCSIGLSCHLMDGVICLPGLSASGPV 60		
DB	1	MPVSWFLSLALGRNPVVSLERLMEPODTRARCSIGLSCHLMDGVICLPGLSASGPV 60		
QY	61	LVPTRLQTELVLRCPKTDALRVVVVHLAVHGMABPEEAGKSDSELRNASTLQAO 120		
DB	61	LVPTRLQTELVLRCPKTDALRVVVVHLAVHGMABPEEAGKSDSELRNASTLQAO 120		
QY	121	VWLSQAVPIARCALLLEVQVADLVQGVSGSAVDFCFEASLGAEOVITWSTKPRYQKE 180		
DB	121	VWLSQAVPIARCALLLEVQVADLVQGVSGSAVDFCFEASLGAEOVITWSTKPRYQKE 180		
QY	181	INLTLQOLP-----DGDVTLTLDVSEQDFSLILYLRPYD 216		
DB	181	INLTLQOLP-----DGDVTLTLDVSEQDFSLILYLRPYD 216		

181 LNLTOOLPDCRGLEVDSDIOSCWYLPWLNSTDDGNVLLTLDVSEEDSEFLYLRLPVPD 240  
 217 ALKSLMYKNLGTGQNTLNTDLPVCCIOYWSLEPDSERVECFPREPGAHRLNHLA 276  
 241 AKSLMYKNLGTGQNTLNTDLPVCCIOYWSLEPDSERVECFPREPGAHRLNHLA 300  
 277 RLRLVSPGWQDAPCCLPKVTLCQAPDPSQOPVLPVPOKATVNEPQDFOLVAGH 336  
 301 RLRLVSPGWQDAPCCLPKVTLCQAPDPSQOPVLPVPOKATVNEPQDFOLVAGH 360  
 337 PNLGVQVSTWEKVOLOACSMADSLGPEKDMLLVEMKTGLNNTSVCALEPSCGTPSPMA 396  
 361 PNLGVQVSTWEKVOLOACSMADSLGPEKDMLLVEMKTGLNNTSVCALEPSCGTPSPMA 420  
 397 STRARLGEELLQDFRSHQCMQMDNDNMGSLACPMKTYHRRVLYVLACILLAAALF 456  
 421 STRARLGEELLQDFRSHQCMQMDNDNMGSLACPMKTYHRRVLYVLACILLAAALF 480  
 457 FELLKKDR 465  
 481 FELLKKDR 489

ESULT 2  
 9BR97 PRELIMINARY: PRT: 538 AA.  
 09BR97: 01-JUN-2001 (TREMBLrel. 17, Created)  
 01-JUN-2001 (TREMBLrel. 17, last sequence update)  
 01-DEC-2001 (TREMBLrel. 19, last annotation update)  
 HYPOTHEICAL. 59.1 KDA PROTEIN.  
 Homo sapiens (Human)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 NCBI\_TaxID=9606;  
 (1)  
 SEQUENCE FROM N.A.  
 TISSUE-ENOMERIAL ADENOCARCINOMA;  
 Strausberg R.;  
 Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
 EMBL; BC006411; AA06411.1;  
 Hypothetical protein.  
 SEQUENCE 538 AA: 59127 MW: 65E6344DA6A5AFD2 CRC64;

Query Match 48.5%; Score 1749.5; DB 4; Length 538;  
 Best Local Similarity 65.2%; Pred. No. 6.5e-149;  
 Matches 339; Conservative 51; Mismatches 107; Indels 23; Gaps 5;

1 MPVSFLLSLALGRNPNVYSLERLMEPQDARCSIGLSCHLMDGVDLPGSLQSAAPGV 60  
 1 MPVPFLLSLALGRNPNVYSLERLMEPQDARCSIGLSCHLMDGVDLPGSLQSAAPGV 60  
 61 LVPRLQTELVLRCPOKTDCAALRVVYVHLAVHGMWAEPEE---AGKSDSELQESRNAS 116  
 61 LVPRLQTELVLRCPOKTDCAALRVVYVHLAVHGMWAEPEE---AGKSDSELQESRNAS 116  
 61 LAPRLQTELVLRCPOKTDCAALRVVYVHLAVHGMWAEPEE---AGKSDSELQESRNAS 120  
 117 LQAVVLSQAPAPLACALLEVQPADLVQPGSVGSAVFCFPAKSLAEVQIWSYTKR 176  
 121 LQAVVLSQAPAPLACALLEVQPADLVQPGSVGSAVFCFPAKSLAEVQIWSYTKR 180  
 177 YOKELNLTQOLP-----DGDNVLLTLDVSEEDSEFLYLRLPVPDALKSLMYKNL 227  
 181 YOKELNLTQOLP-----DGDNVLLTLDVSEEDSEFLYLRLPVPDALKSLMYKNL 240  
 228 GPONITLNTDLPVCCIOYWSLEPDSERVECFPREPGAHRLNHLA 287  
 241 GPONITLNTDLPVCCIOYWSLEPDSERVECFPREPGAHRLNHLA 300  
 288 LDAPCCLGKVTLCQAPDPSQOPVLPVPOKATVNEPQDFOLVAGH 347  
 301 LDAPCCLGKVTLCQAPDPSQOPVLPVPOKATVNEPQDFOLVAGH 360

QY 348 KYOLACSMADSLGPEKDMLLVEMKTGLNNTSVCALEPSCGTPSPMASTRARLGEEL 407  
 DB 361 KLOLQELMADSLGPEKDMLLVEMKTGLNNTSVCALEPSCGTPSPMASTRARLGEEL 420  
 QY 408 LQDFRSHQCMQMDNDNMGSLACPMKTYHRRVLYVLACILLAAALFELLKKDR 467  
 DB 421 LQDFRSHQCMQMDNDNMGSLACPMKTYHRRVLYVLACILLAAALFELLKKDR 477  
 QY 468 AARGSFALLHSDAGYERLY-----GALASALSGMP 501  
 DB 478 -AKGWLRLKQDVRSGGEWQALGGPPGSGQACASSPLP 516

RESULT 3  
 060943 PRELIMINARY: PRT: 864 AA.  
 AC 060943: 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)  
 DE INTERLEUKIN 17 RECEPTOR.  
 GN IL17R.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 CX NCBI\_TaxID=10090;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-THYMOMA E14.  
 RX MEDLINE=96111968; PubMed=8777726;  
 RA Yeo Z., Fanslow W.C., Seidlin M.F., Rousseau A.M., Painter S.L.,  
 RT Comeau M.R., Cohen J.I., Spitznagel M.K.;  
 RT "Herpesvirus Saimiri encodes a new cytokine, IL-17, which binds to a  
 RT novel cytokine receptor."  
 RL Immunity 3:811-821(1995).  
 DR EMBL; U31993; AAC52357.1;  
 DR MGI; MGI:107399; 11117r.  
 KW Receptor.  
 SO SEQUENCE 864 AA: 97807 MW: 343FD51AA687DA31 CRC64;

Query Match 4.6%; Score 167; DB 11; Length 864;  
 Best Local Similarity 20.3%; Pred. No. 4.3e-06;  
 Matches 105; Conservative 62; Mismatches 167; Indels 184; Gaps 25;

QY 224 KNLTL--GPONITLN-----HTDLPVCCIOYWSLEPD-----SER 256  
 DB 66 KNLTFSPKNTIYINLSVSSQHGELVPLVHVE-WTLDASILVLEGAEISVLQINTNER 124  
 QY 257 --VERCFREDPGAHRLNHLA 307  
 DB 125 LCVKF-QFLSMLOHARRMFSFSHFVVDGQEVYVNHLPKP-----IPDG 171  
 QY 308 SPCOP--LVPVPOKATVNEPQDFOLVAGH 363  
 DB 172 DENHKSILTFVDCESKAKMTTSCVSSGSLMDPNTVEITDQHLKRVDFTLNNEST-PY 230  
 QY 364 KDDMLVEMKTGLNNTSV-----CA-----LEP-- 386  
 DB 231 Q---VLLSEFSSEHNSCDFVQKIFARQOEFGQANVTFTLSFKHNCNHHVQVQPF 287  
 QY 387 SGC-----TLPASASTRAARLGEELLQDFRSHQCMQMDNDNMGSLACPMKTY 436  
 DB 288 SSCLNDCLRHAVTVPCVPSINTVTPK-----PVADY 318  
 QY 437 IHRNV--LVNLAALAAALFFFL-----LKKDRRKARG-- 472  
 DB 319 I-PLVWYGLITLAILLVGSAIVYLITMTWRLSGADDEKDDSKINILPVAADITPPPL 377  
 QY 473 --RTALLHSADGAGERYLVGALASAL--SOMPLKVAVDLWSRRELISAHGALAMFHRORR 529  
 DB 378 RPRKWIYVYSAHPIVVEYVLKFAQELITACGTEVALDILEQYVISEGVMTWVSROKE 437

QY 480 SAGAGCTEELTGALAS-ALSCMPLEAVAYDMSRRELSAHCLALMFHHQRKILDEBGVYI 538  
 Db 385 SAHPHLYVDVYLKFRQELLTACGTEVALDLLEQALSEAGVMTWVGROKQDMVNSKRII 444  
 QY 539 LIFSFAVVAOCQML-----OLQTVPEPGR-HDALAAMLSCTLPDFLOGRATGRVGYVF 591  
 Db 445 VLCSGRGRAMQALGGRAPVRLRODHGFRVGDLEFRAAMMILPDEFRRPACFGTYVCFE 504  
 QY 592 DGLHLPDSVSPFVAPLFLSLPTQLPAF-----IDLALGCGCSTSAGRPRADRVETVTC-- 643  
 Db 505 SEVSCDDVDLEDFGAAPRYPLMDRFEVEYFRIQDLEMFQPG-----RMHRVGEIS 554  
 QY 644 -----ALNSALD 650  
 Db 555 GDNLYRSPGGKOLRAALD 572  
 RESULT 5  
 Q96F46 PRELIMINARY; PRT: 866 AA.  
 AC Q96F46  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE SIMILAR TO INTERLEUKIN 17 RECEPTOR.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI-TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=UTERUS, AND LEIOMYOSARCOMA;  
 RA Strausberg R.,  
 RL Submitted (JUL-2001) to the EMBL/Genbank/DDBJ databases.  
 DR EMBL; BC011624; AAH11624.1;  
 KW Receptor.  
 SQ SEQUENCE 866 AA; 96131 MM; 28330BED230B0C9 CRC64;  
 Query Match 4.2%; Score 151.5; DB 4; Length 866;  
 Best Local Similarity 19.2%; Pred. No. 0.00011;  
 Matches 142; Conservative 73; Mismatches 206; Indels 317; Gaps 34  
 QY 55 SARGP-----VLVP-----TRLOTELYLRCPQKTDICALRVYVYHILAVHGMARE 100  
 Db 10 AWPGLGLGLLLGLLGLVLAIPGASLRLDLHRAALVYCSOP--GLMCTVKNSTCLDQSWIHR 66  
 QY 101 EAGKSDSELOESRNASLOAVLVSF--QAVPIARCALLEVQVPADLVQPGQSVGSAVF 156  
 Db 67 NLPSSPKDQIQHFAHTQOGDLFPVAH--IEKTLQTD----- 103  
 QY 157 DCFEASL---GAEOVI-----WSYT-----KRYQKEI 181  
 Db 104 ---ASILYLEGAEISVQLNTNTERLCVRFELSKLRHHRMRFFSHFVVPDQDEYEV 159  
 QY 182 ---NLQOOLRGGNVLLTDVSEBODSFLLRYRPD-----ALKSLMTKN 225  
 Db 160 TVNHLEKRPDPGD-----PNHOSKNFL--VPDCEHARKVYTPPCSSGSLMDPN 206  
 QY 226 LTPGPNITLNTHTLVPCICLOVMSLEPSEVEFC-----PREDPGAHR 270  
 Db 207 IT-----VETLEAHQLRVSTFLMNSTHVIQLITSPHNENHSCFE 247  
 QY 271 NIMHTARLVLSGWMOLDAPCCLPKGVTLQWAPDQSCQPLVPRPQKNATVNEBDF 330  
 Db 248 NMHNI-----PAPR-----PEEF 260  
 QY 331 Q-----LVAGHNILCYQVSTWKEVVOLOACSMADSLSPKDKMLLVEMKGLNNTSVAL 384  
 Db 261 HORSNVTLRLNRKGCGR--HOVOID--PF-----FSSCLND---CL 295  
 QY 385 EFSGCTPESMASTRARLGEELLQDFESHQCMOLANDNMGSIACPMDKYTHRRVYLV 444

296 RHSAWVSCPEMPD-----DEPIDY-----MPLM-----VYMFIT 326  
 445 WACCLLAALAEFFLLKKDRKAARG-----RTALLH 479  
 327 GISILLVGSVY--LLIYCMTRNLAPGSEKSDPKRYTDGLPYADLLPPLKPRKWIY 384  
 480 SAGAGERYLVGALAS--ALSQMPLRVAVDIMSRRELHANGALAMFHQRRILOEGSVI 538  
 385 SAHPLVYDVYVLAKEPFLINACGEVALDLEEQALISEAGVMTWGRQKQEWESNKKI 444  
 539 LIESPAVAOCQOML-----OLQTEBERP--HDALAAMLSCVLPDFLOGRATRGVGF 591  
 445 VLCSRGTRAKWQALLGSGAPVRLRCDHGRPVDDLFTANMMILPDKRPRACFTYVYCF 504  
 592 DGLLHPDSVSPFVAPLFSLEPTQLPAF-----IDALQGCSTSGRPRADRYERTQ-- 643  
 505 SEVSCDQDVPDLFEAARPYPLMDREVEYFRIDLEMFGPG-----RMHVGELS 554  
 644 -----ALRSALD 650  
 555 GDNVYLSPGGRQRLRALD 572

RESULT 6 PRELIMINARY; PRT: 1013 AA.

053499: 01-JUN-1998 (Tremblrel. 06, Created)  
 01-JUN-1998 (Tremblrel. 06, last sequence update)  
 01-DEC-2001 (Tremblrel. 19, last annotation update)  
 HELZ OR RV2101 OR MTVO20 01.  
 Mycobacterium tuberculosis.  
 Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
 Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
 NCBI\_TaxID=1773;

SEQUENCE FROM N.A.  
 STRAIN=H37RV;  
 MEDLINE=98295987; PubMed=9634230;  
 Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,  
 Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,  
 Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,  
 Davies R., Devlin K., Fellwell T., Gentles S., Hamlin N., Holtroyd S.,  
 Horsby T., Jagsels K., Krogh A., McLean J., Moule S., Murphy L.,  
 Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,  
 Rutter S., Seeger K., Skelton S., Squares S., Squares R.,  
 Sultston J.E., Taylor K., Whitehead S., Barrell B.G.;  
 "Deciphering the biology of Mycobacterium tuberculosis from the  
 complete genome sequence."  
 Nature 393:537-544(1998).  
 -1. SIMILARITY: TO HELICASE C-TERMINAL DOMAIN.  
 EMBL; AL021924; CAI17284.1;  
 Tuberculin; RV2101;  
 InterPro; IPR001410; DEAD.  
 InterPro; IPR001650; Helicase\_C.  
 InterPro; IPR000330; SNF2\_N.  
 Pfam; PF00271; helicase\_C1.  
 Pfam; PF00176; SNF2\_N.1.  
 SMART; SM00487; DEXDC; 1.  
 SMART; SM00490; HELIC; 1.  
 ATP-binding; Complete proteome; Helicase.  
 SEQUENCE 1013 AA; 111029 MW; 601FDF1DB5CABEF1 CRC64;

Query Match 3.28; Score 114.5; DB 16; Length 1013;  
 Best Local Similarity 20.48; Pred. No. 0.28; Mismatches 232; Indels 251; Gaps 33;  
 Matches 143; Conservative .75;

90 LAVHGWAE--EAGKSDSELDSESNASIQAVVLSQAVPIARCALLEVOVPADL--- 144  
 2 LVLRHGWNSGGRMLAEADSDLL---VKSPSQALRSARPHFA-----APADLLNG 49

QY 145 VQSGSVSAVFDCFEASLGAEVQIMSTYKPKYQKELNTQQLPDGDNVLLTLDVSEED 204  
 DB 50 IHGK-----PATAVILLPSLSAPLD 71  
 QY 205 FSPFLYLRPVVDALKSLWKYNLTGPONITLNHD--LVPLCLIQVMSLEPSEVEREPCFR 263  
 DB 72 SPELIRLAPRAA-----RTDDPLAMTVPVVDLDPTPALAALFQOP 113  
 QY 264 EDGAFHNLMIHIALRVLPSPGWQDAPCCLPGKY-----TLGV-----QAPDS 308  
 DB 114 PDVRYGASVDYLAEIAYARELVE-----RGVLPQLRDTGHAACRPVYLGHDV 166  
 QY 309 PCQPLV---PPVQKNATVNEPQDFOLVA-----GHPNLQV 342  
 DB 167 AMSLVSAAMPVCAEYGVGHDPHELATSLDAMVAVPAALSPMDLLPRGRSKHRA 226  
 QY 343 VSTW-----EKVQLOACS--WAD-----SLGPKDMILVEAKTGLNNTS 380  
 DB 227 VEAMLDALTCPRDGRFDEPDELALAEALRPWDVIGIGVAPARATFRLESEVENET- 285  
 QY 381 VCALPEPGCTPLPMSASTRAARLGEELLQDFRSHOC-----QLMNDNMGSLMACPMKY 436  
 DB 286 -----PAG-----SLMRL--EFLQSTQDPSILVPAEQAMND--GSL----- 319  
 QY 437 IHRWV---LWVLAALLAEFFLLKKDRKAARGSRALLHSDAGYERLVGA 492  
 DB 320 --RRMLDRPOEILITELGRASRIPELV-----PALPTAPCSGLELDADGA--YRFLSG 369  
 QY 493 LASALSMPLRVAVDIMSRRRELHANGALAMFHQRRILOEGSVIILPSP--AAVAQO 550  
 DB 370 TAAVLDEAGFGVILPSW-----W---DRRRL--GLVLSAYTPVDGVYKAS 411  
 QY 551 QMLQLOVE-----PGPHDALAAMLSCVLP-----DFLOG 580  
 DB 412 KFGREQLYVERWELAVGDPLSEEEIALTEKSPILRLRGQVADTEQMRGLEPLER 471  
 QY 581 RATGRYVGVTFDGLL--HPDSVPFVAPLFSLEPTQLPAFDALQGCSTSGRPRADRY 638  
 DB 472 KPTGRKTTAEILALAAASHPDVDVPLEVTAV-----RADGMIGDLILAGAAASLQPLDP 526  
 QY 639 ERYTQALRSALDSCTS-----SSEARGCCEMDLGPCTTLE 674  
 DB 527 DGTATILRPYQKGLAMWLAFSLSSLGSLGSLADMDGLKTVQ 567

RESULT 7 PRELIMINARY; PRT: 2012 AA.

09BX84;  
 01-JUN-2001 (Tremblrel. 17, Created)  
 01-OCT-2001 (Tremblrel. 17, last sequence update)  
 01-OCT-2001 (Tremblrel. 18, last annotation update)  
 DE CHANNEL-KINASE 2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=KIDNEY;  
 RX MEDLINE=99147092; PubMed=10021370;  
 RA Ryzanov A.G., Pavur K.S., Dorovkov M.V.;  
 RT "Alpha-kinases: a new class of protein kinases with a novel catalytic  
 domain."  
 RL Curr. Biol. 9:R43-R45(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=KIDNEY;  
 RA Ryzanov A.G., Pavur K.S., Petrov A.N., Dorovkov M.V., Ryzanov A.G.;  
 RT "Novel type of signaling molecules: protein kinases covalently linked  
 to ion channels."



MOI. Biol. 0-0-0(2001).  
 DR EMBL: AF350881; AAK31202.1;  
 DR InterPro: IPR000636; Cation\_chan\_non\_11g.  
 DR InterPro: IPR002111; Cat\_channel\_TPL.  
 DR Pfam: PF00520; Ion\_trans; 1.  
 DR Kinase.  
 KW SEQUENCE 2012 AA; 230493 MW; 8AD583235D8080AF CRC64;

Query Match 3.1%; Score 110.5; DB 4; Length 2012;  
 Best Local Similarity 19.6%; Pred. No. 1.7;  
 Matches 138; Conservative 84; Mismatches 269; Indels 213; Gaps 30;

1 MPVSFLLSLAGRPVVSLEFLMEPDAR-----CSIGLS 38  
 1268 MPSS-LKRLSLAGRRPPRORCALLETNSKREATVNRNDQERQETSSIVSGVSPNRQ 1326  
 39 CHLMDGVLCPLGSIQASAPVLPTRLCQELVLRQ-----KIDCALRRVVYHLA-- 91  
 1327 AHSKYGQFLVPSNLKR-----VPSAEVLPLSRPSVDVLALEDQIQEVEVLHTGQ 1380  
 92 --VHGMA--EPEBAGKSDSEIQRNASIAQAVLSFOAYPIARCALLEVOVPADLVQ 146  
 1381 TPVVSQMASVDEPKKEHEPIAHLDDQDAQVLPITLSCTPEPMTSSPLS---QAKIQ 1437  
 147 PGQSVGSAVPDFCEASLGAEOIWSYTK-----PRYQKELNLQQLPDCGN 192  
 1438 TGGGVYNNAF-----SEGDEGVFSIKKKMQTCLPSTCDSSRSRQKQAKQDSSLSGN 1492  
 193 VLLVLDSEEDDFLLVLRPPDALKSLMYKMLTGQNTLTNTDLVPCICIQWLSLP 252  
 1493 STRSAQSECEVQ--PWLP--NTSFMINPLRRYRPPARSHS-----FRFHK 1536  
 253 DSEVEFCPEFREDPGAHRLMHLARLVSPGVQDLAPCLLPKVTLCMQAPDPSQCP 312  
 1537 EEKLMKICKIKNLSSSE-----IGQAM-- 1560  
 313 LVPPVPOKNATVNEPDQFLVAGHPN--LCVOVSTWEKVOLOACSNADSLGPFKDMIL 369  
 1561 ---VKAKMLT---KDRLSKKKKNTGLOVYIT---VANCSDQDNPREGENSI 1607  
 370 VEMTGLNNTVCALEPGSCPTLPMSASTRAARLGEELD--DF--RSHQCM--QLMND 422  
 1608 SEEYSKMWFTVSKSHGVVEYIHQ--KMKTKEIGQCAIDISDYLKSHODLSKSNLWS 1666  
 423 -----DNMGLMACPMKYIHRRWLVWLACILLAALEFFILKKDR 465  
 1667 RSTMLNNSLSKSSIGVDKISLSLSPQEPHHYSAT-----ER 1705  
 466 RKAARSGRTALLSHSADAGYERLVGALASALQMPLRVAVDLSRRELSA----- 516  
 1706 NMLRLSOTIPTPOLPAGGEITYVRLSES--SPLMDKSMSSMSQGRAMIQLVLSREE 1764  
 517 -HGAL-----AMFHQRRILOBGV--VILLESAPAAVQCOQLQLOTVERGPHDAL 566  
 1765 MDGGLRRAMRVVSTWSEDD--ILKPGOVFIYKSLPEVVRVTHKIFQESTV----- 1813  
 567 AAMLSCVLPDFLGATGRGVGVYFDGLLHPDSVSPFRAPLE 610  
 1814 ---LHLGLREIQQRAAKL--ITYFNQVKPOTIPTYPRLEVF 1852

RESULT 8  
 55225 PRELIMINARY; PRT: 2910 AA.

01-JUN-1998 (Tremblrel. 06, Created)  
 01-JUN-1998 (Tremblrel. 06, Last sequence update)  
 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
 OTOGELIN.  
 OTOG.  
 Mus musculus (Mouse).  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID-10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BALB/C;  
 RX MEDLINE-98070772; PubMed-9405633;  
 RA Cohen-Salmon M., El-Amraoui A., Leibovici M., Petit C.;  
 RT "Otogelin: A glycoprotein specific to the acellular membranes of the  
 inner ear."  
 RL Proc. Natl. Acad. Sci. U.S.A. 94:14450-14455(1997).  
 DR EMBL: U96411; AAB9361.1;  
 DR HSSP; P56682; ICV.  
 DR MGD; MGI:1202064; Olog.  
 DR InterPro: IPR002086; Aldehyde\_dehydr.  
 DR InterPro: IPR000359; Cys\_knot.  
 DR InterPro: IPR002919; TIL.  
 DR InterPro: IPR001846; VWD.  
 DR Pfam; PF01826; TIL; 3.  
 DR Pfam; PF00094; vwd; 4.  
 DR SMART; SM00041; CT; 1.  
 DR SMART; SM00214; VWC; 1.  
 DR SMART; SM00216; VWD; 4.  
 DR PROSITE; PS00070; ALDEHYDE\_DEHYDR\_CYS; UNKNOWN\_1.  
 DR PROSITE; PS01225; CTCK\_2; 1.  
 SEQUENCE 2910 AA; 313410 MW; 7270FC61A23264CD CRC64;

Query Match 3.1%; Score 110; DB 11; Length 2910;  
 Best Local Similarity 20.8%; Pred. No. 3.1;  
 Matches 54; Conservative 31; Mismatches 82; Indels 92; Gaps 13;

QY 214 VPDALKSLMYKMLTGQNTLTNTDLVPCICIQWLSLEPS-----ERVECCPR 263  
 DB 2427 VPRALGETWNSLSG-----CCQOCCCAPPTIIPVLDLPCGPPRESCP-- 2469  
 QY 264 EDPGARMLMHLARLVSPGVQDLAPCLLPKVTLCMQAPDPSQCPPLVPVQKNAT 323  
 DB 2470 -----RGEVYILDP---TEDPCL-GSVCV---NQTLEGLAPTCRPGHSL 2510  
 QY 324 VNEPDQFLVAGH-----PMLCVOSTWEKVOLOACSNADSLGPFKDMILVEMKTLINN 378  
 DB 2511 ITHQEDSCPSYSCQCDGCLC-----EAEQVPTC-----REDQILLEGSLG-- 2552  
 QY 379 TSVCALEPGSC---TLPMSASTRA-----ARLGEELDQFRSHQ----- 415  
 DB 2553 DSCCTSYFCGGGECSDPMPECEGEGALTVHRNTTELCCPLYOCVCENFRCPVOCGMCTS 2612  
 QY 416 CMQLMNDNMGSLMACPMD 434  
 DB 2613 LVEVWSPRCPCPYKSCED 2631

RESULT 9  
 060150 PRELIMINARY; PRT: 361 AA.  
 AC 060150;  
 DT 01-AUG-1998 (Tremblrel. 07, Created)  
 DT 01-AUG-1998 (Tremblrel. 07, Last sequence update)  
 DT 01-AUG-1998 (Tremblrel. 07, Last annotation update)  
 DE HYPOTHEICAL 40.1 KDA PROTEIN.  
 GN SPBC18H10.20C.  
 OS Schizosaccharomyces pombe (Fission yeast).  
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;  
 OC Schizosaccharomycetes.  
 OX NCBI\_TaxID-4896;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-972H;  
 RA Lyne M., Rajandream M.A., Barrell B.G., Badcock K., Churcher C.M.;  
 RL Submitted (MAR-1998) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AL022304; CAA18417.1;

44 GDVLC LPSLQ-----SAPGVLVPTRIQTELVLRCPQKTDICALRVRWVHLLA 91

QY 287 QLDAPCGKVTLCWQARDQSPQRLVPPVQKNATVNEPQDFQLVAGHPNLCVQVST<sup>TM</sup> 346

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134 LARAPGOLPGTVPAHSVLYAOEASALSAPAGDGLTLH-----LGSGD---RLAHW 182
135 EKVOLOACSNADSLGPFDDMLVEMKTC--LANTSCALPESGCTPLPSMASTRARIG 404
183 QGRLV---SWR-SLGP--NMOLLVDETSPVSGQLALRPD---LP--ASER----- 225
405 EELLQDRSHQCMLNDNDNGSLWACPMDKYTHRRVWLWLAACLLAALFFLLKKD 464
226 -QELFTVGGQLOLVFSGD-----YLLRRR 250
465 -----RRKAARSTFALLHSADGAGYERLYGALASALSOMPLRVAVLMSRRRLS 515
251 ADAAQTRHLRLALIGRACALLLPBQHGRLRLARTLRLRGDP-----PRADDP 302
516 AHGALAMFH-----HORRLIQEGGVILLFSPAAYVACCOMLQLOTFBERPHDALAM 569
303 ASGOVAFAPQPAECLAARSLQLRLEPLGRSPAPVA-----HEAQVAQ 347
570 LSCVLPDLQGRATGRVGYVEDGLHPDSVSPFRVA---PLFSL---PTQLPA---FL 620
348 ALHLRP-----HTAAQVQAALHAASAPLEALATDPLVGRAPPLPATGHEI 399
621 DALQGCSTAGRPADRYERYTQALRSAL 649
400 VFPLGPDPLEVRLEPGRDLTLRPDYRAEL 428

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## RESULT 12

```

094G03 PRELIMINARY: PRT: 589 AA.
094G03:
01-DEC-2001 (Tremblrel. 19, Created)
01-DEC-2001 (Tremblrel. 19, Last sequence update)
01-DEC-2001 (Tremblrel. 19, Last annotation update)
PUTATIVE CYTOSOLIC NADP-MALIC ENZYME (EC 1.1.1.40).
CYTMEA.
Flaveria pringlei.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; easterids II; Asterales; Asteroideae; Asteroideae;
Helentidae; Flaveria.
NCBI_TaxID=4226;
[1]
SEQUENCE FROM N.A.
Lal L.B., Nelson T.;
"Expression of the cytosolic NADP-malic enzyme genes in Flaveria.";
Submitted (JUL-2000) to the EMBL/Genbank/DBJ databases.
EMBL: AF288920; FAK83073.1;
Oxidoreductase.
SEQUENCE 589 AA: 65124 MW: AB3AGFB01BBF95A CRC64:

```

Query Match 3.0%; Score 106.5; DB 10; Length 589;

Best Local Similarity 17.8%; Pred. No. 0.71;

Matches 106; Conservative 70; Mismatches 182; Indels 237; Gaps 26;

```

135 LLEVQVPADLVNQGSGVAVFCFESLAGEVQ---WS-----YT---KRYQKELN 182
136 LKQMGESVVDSSAVGGVDVYGEDRASEDLITPWTVSASGYTLRLPHNNKGLA 64
183 LTQQLPDDGNVLLTLDVSEQDFSLYLRLVVPDLAKSLMWKNLNGPQITLNTHTLVPC 242
65 FTER-----ERDSHYLGLLPPAVATQELQEKLM--QNRISYEVPL--H 105
243 LCIQVWSLEPDSERVECPREDPGAHNRNLMHIALRYLSPGWOLDACCLPGKTYLWC 302
106 RYVAMMELEERNERLEY-----KLIDNVEEL-----LPVYT--- 138
303 QAPDQSPQPLVPFPYQKNTV--NEPDQVLAVAGHPNLCVOV--STWEKYOLOACSNADSL 360
139 -----PTVGEACQKYGSIKRPQGLYISLKEKGLIEVLRLMPPFNINQIVYVTDG- 188

```

```

QY 361 GPFKDDMLVEMKTCGLNN-----TSVCALEPSCCTPLPSMASTRARL- 403
DB 189 -----ERLIGLGDGCGMGIPVKIALVATLALGVAPSAFLPTIDVTNNOKLL 238
QY 404 -----GELL---QDRSHQCML----- 419
DB 239 DDEFTIGLRKATGKEYTDLLEEFMSAYKONGEYLVQEPEDANNAFLAKYRTSH 298
QY 420 --WDDNDNGSLWACPMDKYTHRRVWLWLAACLLAALFFELLKKRRKAARSGRTALL 477
DB 299 LVFNDDIGT-----ASVVLAGVLSKLL-----GGSIDHTLFL 334
QY 478 LHSAD--GAGYERLYGALASALSOMPLRVA--VDLM-----SRRLSAHGALAMFH 525
DB 335 LGAGEAGTGAIELIALEISTKANIPIDEARKITWLDKGLVSSRKETLOHFKPMANE 394
QY 526 -----ORRLIQEGGVILLFSPAAYVAC-- 549
DB 395 HEPLSTLIDANKAIRPSVLIGTSVQOTFTQNVVEAANERPLIMASPTSOAECTA 454
QY 550 ---QWLOLOTV-----EPGPHDALAAMLSCVLPDLQGRATGRVGYVEDGL 594
DB 455 EQAYTWTQGRAIFFSSGSPDPYEYNGNL-----FIRGOANNAYI---FPGL 497

```

## RESULT 13

QY 090J61 PRELIMINARY: PRT: 1248 AA.

AC 090J61:

DT 01-MAY-2000 (Tremblrel. 13, Created)

DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)

DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)

DE APOPTOTIC PROTEASE ACTIVATING FACTOR 1.

GN APAF-1.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Hahn C., Duerkop H., Stein H.;

\*Sequence of Apaf-1 in L.428.\*;

Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.

-1. SIMILARITY: CONTAINS 11 WD REPEATS (TRP-ASP DOMAINS).

EMBL: AJ243009; CAB55585.1; -

HSSP: 014727; ICY5.

InterPro: IPR001315; CARD.

InterPro: IPR000767; Disease\_resist.

InterPro: IPR002182; NB-ARC.

InterPro: IPR001680; WD40.

PFam: PF00619; CARD; 1.

PFam: PF00931; NB-ARC; 1.

PFam: PF00400; WD40; 11.

PRINTS: PRO0364; DISEASESERSIST.

SMART: SM00320; WD40; 11.

PROSITE: PS50209; CARD; 1.

PROSITE: PS00678; WD\_REPEATS\_1; UNKNOWN.

PROSITE: PS50082; WD\_REPEATS\_2; 9.

PROSITE: PS50294; WD\_REPEATS\_REGION; 1.

Protease Repeat; WD repeat.

SEQUENCE 1248 AA: 141728 MW: DDA72856D5C8F37 CRC64:

Query Match 3.0%; Score 106.5; DB 4; Length 1248;

Best Local Similarity 19.1%; Pred. No. 2;

Matches 112; Conservative 64; Mismatches 188; Indels 221; Gaps 27;

```

QY 79 DCALRVVVVHLAVHGH-----WAPEEAGKSDSELQ--SRNASIQ--QVLSFOY-- 128
DB 537 DCAVSENFQELSLNGHLGNQFPNINQVQLGCEPETSIVYQQAQAOEYVNGHLYLE 596
QY 129 -----PLARCALLLEVQVPADLV-----QPGSGVGSANVD---CFEASIG----- 164

```

597 WINKKINTNLSCLVVRPHPTDVAHYNACFSEDEGRIASCGADKTLQVFAETGKLEIKAH 656  
165 -----AEVOIMS-----YTKPROKELNLTQOLPDGDVNL 195  
657 EDEVLCACSTDDFAITCSVDKAKKIMNSMTGELVHTYDEHSEOVNCHPTNSSHLL 716  
196 TLDSVSEODSFLLYLRVPDALKSLMYKNLTGPONITLHNTLVPLCLCIQVMSLEPDS 255  
717 ATGSS-----DCFLKMLDNOKECRNTMGHTN----- 744  
256 RVEFCFPREDPGAHNLMHARLRYLSPGWOLDAPCCLEPGVTLQWADPSCOPLP 315  
745 SVNHCFSPD-----KILASCSADGTLKL-WDATSANERKSI-- 781  
316 PVPQKATVNEPQDFOLVAGHPNLCVOYSTWEKVOLOACSW-ADS-----LGP 362  
782 NVKQFPLNEDPODM-----EVIYKCCSWSADGARIMAAKKKIFLEA 825  
363 FKDDMLVEKGTGLNNT-SVCALEPSCGTPLEPSMASTRARALGELLQDRSHOCMOAN 421  
826 IHTSGLLGELHTGHSTIOYCDFSPQNLAVVAL-----SOYCVELMN 868  
422 DDMGSLMACPMCKYIHRMYLVMLACLLLAALFEFLLLKDRRAAGSRRTALLHSA 481  
869 TDSRSKVADCRG-----HLNV-----HG-----VWFSP 892  
482 DCGYERLVALASALQMPRAVAVDLMSRRELSAGALAMPHORRRIIOEGVILLF 541  
893 DGSSF-----LTSSDDO-----TIRMETKKYCNNSAV-MLKQEVVYQENEMVVL- 938  
542 SPAAVACCOOOLQOTVEPDPHAL--NAAMLSCVLPDLOGRATG 584  
939 ---AVDHIR-LQLVNGRTGOIDYLTGAOVSCCCLSPHLQYIAFG 979  
ESULT 14  
93XR9  
093XR9 PRELIMINARY; PRT: 756 AA.  
01-DEC-2001 (Tremblrel. 19, Created)  
01-DEC-2001 (Tremblrel. 19, Last sequence update)  
01-DEC-2001 (Tremblrel. 19, Last annotation update)  
BG55 PROTEIN.  
Bruguiera gymnorhiza.  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
eurosids I; Malpighiales; Rhizophoraceae; Bruguiera.  
NCBI\_TaxID=39984;  
[1]  
SEQUENCE FROM N.A.  
TISSUE=LEAF;  
Banazai T., Hershkovits G., Katcoff D.J., Hanagata N., Dubinsky Z.,  
Karube I.;  
Identification of mRNA transcripts differentially expressed in  
response to high salinity by means of differential display in the  
mangrove plant, Bruguiera gymnorhiza.  
Submitted (May-2001) to the EMBL/Genbank/DBJ databases.  
EMBL: AB061795; BAB55653.1;  
SEQUENCE 756 AA; 84482 MW; 1597F3D46C3E0809 CRC64;

Db 84 NGDIVSRCKQSRNMLEOSLDQIQTMVPVILAAEISQVIDDLVAKFVLDH--SDEAGK 141  
QY 105 SDSELOE---SRNASLOAOV-VLSQAVPIARCALLEVOYPAALNPOGOSGSAVPCFE 160  
Db 142 AVRELLDOHTMSDSDVESEIKVLRPA-----SRLCITTPKOLLIERKSI----- 186  
QY 161 ASLGAEOIWSYTKPRYOKELNLTQOLPDGDVNLTLDSVSEODSFLLYLRVPDALKS 220  
Db 187 -----KLVKVR-----DN-----DPKKILLYLHL-----LKK 213  
QY 221 LMYKNLGPONITLNH-----TDLVC-ICIOV-----SLPDSERVE 258  
Db 214 -YGNSTLGEQENLNSQOELEFADGSSVSQAFAVGPCACKQIVARAKMSNIPAPPE 272  
QY 259 F-CFPR-----DPCAHNLMHARLRYLSPG-----WOLDAPCCLEPGVTLQWADPDS 308  
Db 273 YKPLSKRLMYP-----VVIASGTFERIM-----IQKFDEGND 308  
QY 309 PC-----QPLVPVPQKATVNEPQDFOLVAGHPNLCVOYSTWEKVOLOACSWADS 359  
Db 309 TCEPTLVKLDHOSLMPNTALKLISKWCEKGVTLIDPN---SOAFOSLDTSTSYA-S 363  
QY 360 LGPKDDMLL-----VEMKGLNNTSVCALEP-----SGCTPLPSMAST- 398  
Db 364 FGISMNDLHLPLDISNVLSGSSDASYCSDSPRTKIAERSMISMQRNGYSAPFSRANTN 423  
QY 399 -----RAARLGE-----ELQDRSHOCMOIWNDDMGSLMACPMCKYIHRMYLVML 446  
Db 424 KTCIDPLFSRLAKLGESKCEMEDVKSHL-----BDNVQPFHHSIENERVE 469  
QY 447 ACILLAALFEFLLLK---DPRKAAGSRRTALLHSDAG-----YERVLGALAS 495  
Db 470 -----PLIFLDRAKQHDVRAORAGSKLLAEVSKRSGISMLHEDFDLLASMLDS 522  
QY 496 ALSQMPLRV---AVDLSRRELSAGALAMPHH---QRRRIIOEGVILLFSPAAYQ 548  
Db 523 ELVEBALAILVELSDKRSKRITASGALVYIIRIDSEEEEOEGAVRILHNSNNEV 582  
QY 549 COQWLOQOTVEPDPHALAAMLSCVLPDLOGRATGRYGV 589  
Db 583 CSQILSINCIPK-----LVFPINQOLASHCMQL 611  
RESULT 15  
ID 09R6L2 PRELIMINARY; PRT: 1693 AA.  
AC 09R6L2;  
DT 01-MAY-2000 (Tremblrel. 13, Created)  
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
DE TIORE47 PROTEIN.  
GN TIORE47.  
OS Agrobacterium tumefaciens.  
OC plasmid pTI-SAKURA.  
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;  
OC Rhizobiaceae; Rhizobium.  
OX NCBI\_TaxID=358;  
ON (1)  
RP SEQUENCE FROM N.A.  
RC STRAIN-MAFF301001;  
RX MEDLINE-20184752; PubMed-10721727;  
RA Katoh A., Hattori Y., Uraji M., Ohta N., Iwata K., Murata K.,  
Suzuki K., Yoshida K.;  
RT "Complete nucleotide sequence of a plant tumor-inducing Ti plasmid."  
RL Gene 242:331-336(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-MAFF301001;  
RX MEDLINE-98193120; PubMed-9524202;  
RA Suzuki K., Ohta N., Hattori Y., Uraji M., Katoh A., Yoshida K.;  
RT "Novel structural difference between nopaline- and octopline- type trbJ  
gene: construction of genetic and physical map and sequencing of  
trbJ/tral and rep gene clusters of a new Ti plasmid pTI-SAKURA.";

BLochlm. Biophys. Acta 1396:1-7(1998).  
[3]  
SEQUENCE FROM N.A.  
RC STRAIN-MAFF301001;  
RT Hattori Y., Suzuki K., Ohta N., Uraji M., Katoh A., Yoshida K.;  
RT "Genome structure of pTI-SAKURA(I): Strategy for DNA sequencing of a  
RT Japanese cherry-ti plasmid."  
RT Nucleic Acids Symp. Ser. 37:159-160(1998).  
[4]  
SEQUENCE FROM N.A.  
RC STRAIN-MAFF301001;  
RT Ohta N., Suzuki K., Hattori Y., Uraji M., Katoh A., Yoshida K.;  
RT "Genome structure of pTI-SAKURA (II): Characteristics of T-DNA."  
RT Nucleic Acids Symp. Ser. 39:185-186(1998).  
[5]  
SEQUENCE FROM N.A.  
RC STRAIN-MAFF301001;  
RT Uraji M., Suzuki K., Ohta N., Hattori Y., Katoh A., Yoshida K.;  
RT "Genome structure of pTI-SAKURA (IV): Characteristics of tra region."  
RT Nucleic Acids Symp. Ser. 39:187-188(1998).  
[6]  
SEQUENCE FROM N.A.  
RC STRAIN-MAFF301001;  
RT Hattori Y., Suzuki K., Ohta N., Uraji M., Katoh A., Yoshida K.;  
RT "Genome structure of pTI-SAKURA (V): Complete nucleotide sequence of  
RT plasmid pTI-SAKURA's vir region in Agrobacterium tumefaciens."  
RT Nucleic Acids Symp. Ser. 39:265-266(1998).  
RC EMBL: AB016260; BAA87672.1;  
RC HSSP: P14385; 2ADM.  
RC InterPro: IPR001650; Helicase\_C.  
RC InterPro: IPR002296; N12N6\_mltifase.  
RC InterPro: IPR002032; N6\_Mtase.  
RC InterPro: IPR000051; SAM\_bind.  
RC Pfam: PF00271; Helicase\_C; 1.  
RC PRINTS: PR00507; N12N6MTFRASE.  
RC PROSITE: PS00092; N6\_MTASE; UNKNOWN\_1.  
RC ATP-binding: Helicase; Plasmid.  
RC SEQUENCE 1693 AA; 187978 MW; 0DD679AFBE6514BE CRC64;

Query Match 2.9% Score 106; DB 2; Length 1693;  
Best local similarity 19.4%; Pred. No. 3.4; Mismatches 159; Indels 254; Gaps 32;  
Matches 115; Conservative 66;  
79 DCALRVVVLAVHGM-AEPEEAGKSDSELOESRNASLOAQVLSFOAYPIARCALLE 137  
414 DLVVALSAVHLPEGHGDETEI-DLDELEATDA-----P 450  
138 VOVPADLVQGSV--GSAVDFCEASLGAEOVWSTYRKYOKELNLTQOLPDGDVNL 195  
451 VDLPSD-----RHVREGSFFPDNARGLM-----QVIDGEPAVAL 483  
196 TL-----DYSEEDFSFLKLRVPDALKSLM-----YKMLT----- 227  
484 KYKGRNADGILEHVRIRLIPRDVREVLAQKQELDRPMKDLQVRLVAMGSFYRDF 543  
228 GPONITLNTDLVPCLOVNSLEPDS-----RYEFCFEREDGARRNLMIARL 278  
544 GP-----INHRTV-----SITDEPESGETRESHRPNLOFPADDP-----DCMLVASI 586  
279 RVLSPGVQWLDAPCCLEPGKVTLCMQAPDQSPCOPLVPVPQKNATVNEPQDFQVLVAGHPN 338  
587 E-----DYDLENDTAKPGAIR-----TERVISPPAPV-----ITSADA 621  
339 LCVQVSTWEKVOQAC-----SW--ADSL--GPFKDMT 368  
622 LAVVNLNENGRVNDLHIAELLHRDPDDVVAELGSAIFRDPADSGMWADAVLSCFVRDLK 681  
369 LVEMKTGILN--NTSVCLSPSGCTPLPSPMASTRARLG-----ELLQDF 411  
682 VAEEAALADPYNRNRYAL--AGVQPVDLRPSDITARLGAPWIPADVVAFAVEKMGTDI 739  
412 RSHQCML--WDD--NMGSLMACPMKYYIHRNRYLVWLACLLAALFFELLKKDRRK 467

Db 740 RIHMEELASWVTEARQGLACTSE-----W-----GTDKRR 773  
OY 468 A-----ARGSRALLHS-ADGAGYERLVGALASALCOMPLRAVD-----LWS----- 510  
Db 774 AGELISDALNSRVPQJFDFTIRGDSERRVNLVVDTEAAKEKELKIKDAQRMWISDPDR 833  
OY 511 -----RRELS-----AGCALMFHHQR--RILOEGGAVI 538  
Db 834 DELARYNDNFNNIAPRKESGDHLNLPAGSAGFVLYGHQKRGIMRISSGSTYL 887

Search completed: September 28, 2002, 19:42:54  
Job time: 1007 sec

10

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

protein - protein search, using sw model

on: September 28, 2002, 19:38:52 ; Search time 24.51 Seconds  
(without alignments)  
1064.748 Million cell updates/sec

US-09-899-471-2  
3605  
1 MPVSFWLSTLALGRNPVVS.....SSEAPGCCCEMDLGPCTTLE 674

ing table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

ched: 105224 seqs, 38719550 residues

1 number of hits satisfying chosen parameters: 105224

um DB seq length: 0

um DB seq length: 200000000

Processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

ase : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Score	Query	Match	Length	ID	Description
116.5	3.2	1711	1	PTPO_RAT	06612 rat mus norv
105.5	2.9	1451	1	A2M2_MOUSE	P28666 mus musculu
105	2.9	443	1	W70T_RAT	035828 rat mus norv
104.5	2.9	1248	1	APAF_HUMAN	014727 homo sapien
103.5	2.9	3707	1	PCBM_MOUSE	005793 mus musculu
100.5	2.8	1062	1	NAL2_HUMAN	09nx02 homo sapien
100	2.8	1447	1	DCC_HUMAN	P43146 homo sapien
99.5	2.8	2647	1	ABR2_HUMAN	P21333 homo sapien
99	2.7	922	1	W70T_MOUSE	Q9d2v7 mus musculu
99	2.7	2437	1	MOTC_BRARE	P46530 brachydantio
98.5	2.7	1447	1	DCC_MOUSE	P70211 mus musculu
97.5	2.7	1618	1	NEST_HUMAN	P48681 homo sapien
97	2.7	963	1	URB4_HUMAN	Q13107 homo sapien
96.5	2.7	1476	1	RVR3_HUMAN	Q15413 homo sapien
96.5	2.7	837	1	A2M1_MOUSE	P28665 mus musculu
94.5	2.6	1587	1	GCSR_MOUSE	P40223 mus musculu
94	2.6	962	1	URB4_MOUSE	Q9y6n6 homo sapien
93.5	2.6	204	1	C267_HUMAN	P55123 mus musculu
93.5	2.6	1914	1	STCK_EMENT	P58512 homo sapien
93.5	2.6	2390	1	SPCP_HUMAN	000706 emeticella
92.5	2.6	1249	1	APAF_RAT	Q15020 homo sapien
92	2.6	398	1	GSP1_KLEPN	Q9epv5 rattus norv
92	2.6	1912	1	PTPD_HUMAN	P15751 klebsiella
91.5	2.5	235	1	FLJ3_HUMAN	P23468 homo sapien
91.5	2.5	461	1	NIFN_KLEPN	P49771 homo sapien
91.5	2.5	486	1	ABR3_HUMAN	P08738 klebsiella
91.5	2.5	880	1	TYO3_MOUSE	Q55144 homo sapien
91.5	2.5	890	1	TYO3_HUMAN	P55144 mus musculu
91.5	2.5	1073	1	VAS5_SCHPO	Q06418 homo sapien
91	2.5	1208	1	RCO4_HUMAN	Q10141 schizosach
91	2.5	362	1	CKRA_HUMAN	Q94761 homo sapien
91	2.5	505	1	CXAA_MOUSE	P46092 homo sapien
91	2.5	505	1	CXAA_MOUSE	Q9wus4 mus musculu

34	91	2.5	1104	1	NFX1_HUMAN	Q12986 homo sapien
35	91	2.5	1189	1	HAIR_HUMAN	O43593 homo sapien
36	91	2.5	3695	1	IMA5_HUMAN	O15230 homo sapien
37	91	2.5	3065	1	EPPL_HUMAN	P58107 homo sapien
38	90.5	2.5	385	1	YEHY_ECOLI	P33361 escherichia
39	90.5	2.5	458	1	MOC_RABIT	P03988 oryctolagus
40	90.5	2.5	479	1	MUCM_RABIT	P04321 oryctolagus
41	90.5	2.5	690	1	KATR_SCHRO	Q10156 schizosach
42	90.5	2.5	880	1	TYO3_RAT	P55146 rattus norv
43	90	2.5	337	1	ICAL_MOUSE	P13597 mus musculu
44	90	2.5	796	1	SG2N_MOUSE	Q9erg2 mus musculu
45	90	2.5	1928	1	LPN_RAT	Q02401 rattus norv

## ALIGNMENTS

RESULT	1	STANDARD:	PRT:	1711 AA.
PTPO_RAT				
ID	PTPO_RAT			
AC	06612:			
DT	01-NOV-1997	(Rel. 35, Created)		
DT	01-NOV-1997	(Rel. 35, last sequence update)		
DT	15-JUL-1999	(Rel. 38, last annotation update)		
DE	Osteosteticular protein tyrosine phosphatase precursor (EC 3.1.3.48)			
DE	(OSF-PTP)			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.			
OX	NCBI_TaxID=101116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISUP-Osteosarcoma;			
RX	MEDLINE=95074080; PubMed=7527035;			
RA	Mauro L.J., Olmsted E.A., Skrobacz B.M., Mourey R.J., Davis A.R.,			
RA	Dixon J.E.;			
RT	"Identification of a hormonally regulated protein tyrosine			
RT	phosphatase associated with bone and testicular differentiation.";			
RL	J. Biol. Chem. 269:30659-30667(1994).			
CC	-1- FUNCTION: MAY FUNCTION IN SIGNALING PATHWAYS DURING BONE			
CC	REMODELING, AS WELL AS SERVE A BROADER ROLE IN CELL INTERACTIONS			
CC	ASSOCIATED WITH DIFFERENTIATION IN BONE AND TESTIS. OPTIMAL PH FOR			
CC	PHOSPHATASE ACTIVITY IS 5.6.			
CC	-1- ASSOCIATED WITH DIFFERENTIATION IN BONE AND TESTIS.			
CC	-1- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O -> protein			
CC	tyrosine + phosphate.			
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein.			
CC	-1- ALTERNATIVE PRODUCTS: A PRESUMED ALTERNATE TRANSCRIPT OF 4.8-5.0			
CC	KILOBASES, WHICH MAY LACK PTP DOMAINS, IS PRESENT IN PROLIFERATING			
CC	OSTEOBLASTS, BUT NOT DETECTABLE AT OTHER STAGES.			
CC	-1- TISSUE SPECIFICITY: BONE AND TESTIS. IN THE LATTER, RESTRICTED TO			
CC	THE BASAL PORTION OF THE SEMINIFEROUS TUBULE.			
CC	-1- DEVELOPMENTAL STAGE: UP-REGULATED IN DIFFERENTIATING CULTURES OF			
CC	PRIMARY OSTEOBLASTS AND DOWN-REGULATED IN LATE STAGE MINERALIZING			
CC	CULTURES. IN TESTIS, EXPRESSION IS HIGHEST BETWEEN STAGES I AND			
CC	VII WHEN MATURING SPERMATIDS REMAIN BURIED WITHIN THE SEPTOLI			
CC	EPITHELIUM.			
CC	-1- INDUCTION: BY PARATHYROID HORMONE AND CYCLIC AMP ANALOGS.			
CC	-1- PTM: THE CYTOPLASMIC DOMAIN CONTAINS POTENTIAL PHOSPHORYLATION			
CC	SITES.			
CC	-1- SIMILARITY: CONTAINS 2 PROTEIN-TYROSINE PHOSPHATASE DOMAINS.			
CC	-1- SIMILARITY: CONTAINS 10 FIBRONECTIN TYPE III-LIKE DOMAINS.			
CC	-1- THIS SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
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CC	entities requires a license agreement (See <a href="http://www.isb-sdb.ch/announce/">http://www.isb-sdb.ch/announce/</a>			
CC	or send an email to <a href="mailto:license@isb-sdb.ch">license@isb-sdb.ch</a> ).			
CC	EMBL: L36884; AAA63911.1; -			
DR	HSP; P18052; TYFO.			

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Query Match          3.2%  Score 116.5;  DB 1;  Length 1711;
Best Local Similarity 20.7%  Pred. No. 0.33;
Matches 150;  Conservative 80;  Mismatches 227;  Indels 267;  Gaps
43  DGVVLCPEGSLOSA-----DGPVVPVPRQLREL-VLNCPRK-----TDC 80
    || || || || || || || || || || || || || || || || || ||
333 DGYVLRKSGPHESTSTLGPBECNAVFPEP-LPQGHYTLQLKVLGAPYDAWEGSTMALES 39
    || || || || || || || || || || || || || || || || || ||
81 ALRVVVVHLAVHGMALPEEAGKSDSELDSESNASLOAQVYLSFOAIPARCAILEYOV 14
    || || || || || || || || || || || || || || || || || ||
392 AALPREVPGARL---WLDGLEAKR-----QGRALLLYSD-----DAPGSLGNLSV 43
    || || || || || || || || || || || || || || || || || ||
141 PALDLYO-----PGQ-----SYGSANVFDCPEASGAEVQLMSTYKPRKQKLTNTQOLPD 18
    || || || || || || || || || || || || || || || || || ||
435 PSCGHYHIFCGVLPGAHYRADYASTDSDISOSIG-----YHSPLEPSLEY----- 48
    || || || || || || || || || || || || || || || || || ||
190 GDNVLLTLVDSEEDFELLVLRFPDAL---KSLATYKNLT-----GPONITLNH 23
    || || || || || || || || || || || || || || || || || ||

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DB	482	-----	ISRSSPSDLTIAMGPARGOLEGKVTWHQDSGQSPGDLVDLGPDTLSLT	532
OY	237	TDLYP	CLCIQW-----SLRPSERVECP-----PREDPGARHMLH-----	274
DB	533	KSLVPGSGCYTVSAAMAGNLDSDSK	HSCTRPAPPTNLISGRADHAPAAKASVYHPGG	592
OY	275	-----	IARLYV-----SPGV-----W-OLDRPCLPGKVTUQCMARDSPCQPIV	314
DB	593	RDAPHMLRYLRPPTLSEKVLPRFADQNFMAQLRACGEFOYUJLTMGSSERS	-----	646
OY	315	PRVPOKATVNEPODFOLVAGHPNLCTVOVSTWEKVOLOACSMWDSIGREFKDMILVEMKT	374	
DB	647	-----	SAATGWT-----PSAPTL-VNVTSDAPQLQY-SNAHYVG-----	681
OY	375	GLANTSYCALREPSCTPLPSAASRAALGEBLLODFRSHQCMQNLNDDNMGSLMACPMD	434	
DB	682	GSRRYOYTLTYOESTRTATISMP-----	KEDTSEGLTPGT	718
OY	435	KYIHRRLVWMLACILLLAA-----	LEFFILKKDRKRAANGSRALLHNSDAGYEYLV	490
DB	719	KY-----	KEVISMAGLYTAAANVSATYPLTNE-----LLVSMQASAVYNLAW	765
OY	491	-----	GALASALS-----OMPLRAYVDLSMRRELSAHGALAMFHHRRIILEGGV	536
DB	766	PSGLPGGACHAQLSDAGHLSMEQPLKIGELFMYLRLPGHTISMSVRCRAPPLQASTH	825	
OY	537	VILLFSPAANAQCOQMLQLOVPEGP	HDAL-----AAMLS-----CVLPDELIQ	579
DB	826	LVVL-----	SEBGPVEDVLCHPREATYDALMTMPAGDVYCLV-----	864
OY	580	GRATGRV-----	GYVE-----DGLHPDSVP-SPERVAPLPSLTOLPAFLDALQGGC	627
DB	865	-----	VERHLYPBGGHFHVQVNTSGDALLPLNLPPTSTYLS-----LVTLGRMSRMSRAVLVC	920
OY	628	STSA	631	
DB	921	STSA	924	
RESULT 2				
A2M2_MOUSE	A2M2_MOUSE	STANDARD;	PRT; 1451 AA.	
AC	P28666;			
DT	01-DEC-1992	(Rel. 24, Created)		
DT	01-DEC-1992	(Rel. 24, Last sequence update)		
DT	01-NOV-1997	(Rel. 35, Last annotation update)		
DE	Murino globulin 2 precursor (Mug2).			
OS	MUG2 OR MUG-2.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxId=10090;			
RP	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Liver;			
RC	MEDLINE=91358495; PubMed=1840592;			
RA	Overbeugh L.; Torrekens S.; van Leuven F.; van den Berghe H.;			
RT	"Molecular characterization of the murine globulins."			
RL	J. Biol. Chem. 266:16903-16910(1991).			
CC	-I- FUNCTION: A PROTEINASE ACTIVATES THE INHIBITOR BY SPECIFIC			
CC	PROTEOLYSIS IN THE BAIT REGION, WHICH, BY AN UNKNOWN MECHANISM			
CC	LEADS TO REACTION AT THE CYS161N1-GLUTAMYL INTERNAL THIOL ESTER			
CC	SITE AND TO A CONFORMATIONAL CHANGE, WHEREBY THE PROTEINASE IS			
CC	TRAPPED AND/OR COVALENTLY BOUND TO THE INHIBITOR. WHILE IN THE			
CC	TETRAMERIC PROTEINASE INHIBITORS STERIC INHIBITOR IS SUFFICIENTLY			
CC	STRONG, MONOMERIC FORMS NEED A COVALENT LINKAGE BETWEEN THE			
CC	ACTIVATED GLUTAMYL RESIDUE OF THE ORIGINAL THIOL ESTER AND A			
CC	TERMINAL AMINO GROUP OF A LYSINE OR ANOTHER NUCLEOPHILIC GROUP ON			
CC	THE PROTEINASE, FOR INHIBITION TO BE EFFECTIVE.			
CC	-I- SUBUNIT: MONOMER.			
CC	-I- TISSUE SPECIFICITY: PLASMA.			
CC	-I- SIMILARITY: TO OTHER PROTEINS OF THE ALPHA-2-MACROGLOBULIN FAMILY,			
CC	INCLUDING COMPLEMENT COMPONENTS C3, C4, AND C5.			



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EMBL: M65238; AAA73041.1; -  
PIR: B41185; B41185.  
HSSP: P01023; 1BVB.  
MGP: MGI:99836; MUG2.  
InterPro: IPR002890; Alpha\_2\_macroglabin.  
Pfam: PF00207; A2M; 2.  
Pfam: PF01835; A2M; N; 1.  
PROSITE: PS00477; ALPHA\_2\_MACROGLABIN; 1.  
Serine protease inhibitor; Glycoprotein; Plasma; Bait region; Signal;  
Multigene family.  
SIGNAL 1 27 BY SIMILARITY.  
CHAIN 1 27 MURINOGLABIN 2.  
DOMAIN 677 734 BAIT REGION (APPROXIMATELY).  
DISULFID 48 86 BY SIMILARITY.  
DISULFID 251 276 BY SIMILARITY.  
DISULFID 269 288 BY SIMILARITY.  
DISULFID 461 555 BY SIMILARITY.  
DISULFID 587 773 BY SIMILARITY.  
DISULFID 634 680 BY SIMILARITY.  
DISULFID 849 885 BY SIMILARITY.  
DISULFID 923 1274 BY SIMILARITY.  
DISULFID 1081 1104 BY SIMILARITY.  
DISULFID 1298 1444 BY SIMILARITY.  
THIOLEST 974 977 BY SIMILARITY.  
CARBOHYD 55 55 N-LINKED (GLCNAC... ) (POTENTIAL).  
CARBOHYD 294 294 N-LINKED (GLCNAC... ) (POTENTIAL).  
CARBOHYD 313 313 N-LINKED (GLCNAC... ) (POTENTIAL).  
CARBOHYD 500 500 N-LINKED (GLCNAC... ) (POTENTIAL).  
CARBOHYD 749 749 N-LINKED (GLCNAC... ) (POTENTIAL).  
CARBOHYD 776 776 N-LINKED (GLCNAC... ) (POTENTIAL).  
CARBOHYD 871 871 N-LINKED (GLCNAC... ) (POTENTIAL).  
CARBOHYD 1401 1401 N-LINKED (GLCNAC... ) (POTENTIAL).  
SEQUENCE 1451 AA; 162368 MW; 982A82EFAA6258F6 CRC64.

Query Match 2.9%; Score 105.5; DB 1; Length 1451;  
Best Local Similarity 20.4%; Pred. No. 2.5;  
Matches 76; Conservative 48; Mismatches 159; Indels 89; Gaps 17;

67 QTELVLCRQ-----KIDCALRVVYHLAV-----HGMAPEEA--- 102  
454 ETSSILPCNQITVQAHFLIKGDLGVLEFYLVMAQSIIGNTGHVPEGAPEK 513  
103 GKSPSELDSESNASDAQVYVLSQAPPIARCALLEVOVPADLVPGOSVGSVAVDCEAS 162  
514 GNFDLE-----IPVFSNAPMAKMLYTTILPDGEVI--ADSVNFEIEKLRNK 559  
163 LGAEVQIMSYTKPRYKELNLTQQLPDGDNVLTLDVSEBDFSLYLRLPVDALSKSM 222  
560 VDLSSSS--SQSLPACSTRQVYAS--POSICGLRAVDOS-----VLLIKP--EDELSPSM 609  
223 YKNLTGPONTLNTHTDLPV-----CLCIQVMSLEPDSERVEFCPPREDPAHR-- 270  
610 IYNLPGMQ-----HNKFISSLSSEDRDCILYSSWAE--KHTDWPVHGREKRYRIV 661  
271 ---NLNHLARLVLSPGVQDLAPCLLP--GKVTLCWQAPDQSPQO-----PLVPPVPOK 320  
662 EDMQLAKFTNLIKIKIPKICFDSAPMGPRGKFDLAFSSVSGTLQKSSSKRPQPEPRE 721  
321 NATVNEPQDFOLVAGHPNLCYGVSTWEKQVQOLACSNV-----DSLCPFFKDDMLIVEAK 373  
722 DPEKDPDLAEITRIKTFPEETWV-----WDIVTVNSTGVAEVEVTPTTTEWAKAGALCLSD 777

OY 374 TGLNNTSYSCALE 385  
DB 778 TGLGLSSVFLQ 789

RESULT 3  
W70T\_RAT STANDARD; PRT: 443 AA.  
ID W70T\_RAT  
AC O35828;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 01-MAR-2002 (Rel. 41, Last annotation update)  
DE 70 kDa WD-repeat tumor rejection antigen (Fragment).  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=WISTAR;  
RX PubMed-9703019;  
RA Muralikrishna T., Begum Z., Swamy C.V., Khar A.;  
RT Molecular cloning and characterization of a tumor rejection antigen  
from rat histiocytoma, AK-5.\*  
RL DNA Cell Biol. 17:603-612(1998).  
CC -1- SIMILARITY: CONTAINS AT LEAST 4 WD REPEATS (TRP-ASP DOMAINS).  
CC -1- SIMILARITY: BELONGS TO THE CORONIN FAMILY OF WD-REPEAT PROTEINS.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).CC EMBL: Y15054; CAA75339.1; -  
CC InterPro: IPR001680; WD40.  
CC Pfam: PF00400; WD40; 3.  
CC SMART, SM00320; WD40; 3.  
CC PROSITE: PS00678; WD\_REPEATS\_1; 1.  
CC PROSITE: PS00682; WD\_REPEATS\_2; 2.  
CC PROSITE: PS50294; WD\_REPEATS\_REGION; 1.  
KW Repeat: WD repeat.  
FT NON\_TER 1 1  
FT REPEAT 61 103 WD 1.  
FT REPEAT 111 151 WD 2.  
FT REPEAT 154 193 WD 3.  
FT REPEAT 247 287 WD 4.  
SQ SEQUENCE 443 AA; 48902 MW; 6469C18BF8FA7F0B CRC64.

Query Match 2.9%; Score 105; DB 1; Length 443;  
Best Local Similarity 20.0%; Pred. No. 0.56;  
Matches 91; Conservative 50; Mismatches 137; Indels 176; Gaps 21;

OY 60 VLVPRLQTELVLCRQKID--CALRVVYVHLAVHGMAPEEAGKSDSELSHNSAL 117  
DB 2 IRVPCNTLKGMLNTTGESDGFPCANRLRVAVPLLSG----- 38  
OY 118 QAQVLSFGAYPIARCALLEVOVPADL-----VQPGDSVGSVAVDCEAS 164  
DB 39 -----GOVAVLELQKPRGLPDTGLPTLQNGAAVMDLVWDFDPRLAVAGED 85  
OY 165 AEVQIMSYTKPRYKELNLTQQLPDGDNVLTLDVSEBDFSLYLRLPVDALSKSM 224  
DB 86 ARIRLM-----GOVAVLELQKPRGLPDTGLPTLQNGAAVMDLVWDFDPRLAVAGED 85  
OY 225 NLGPGONTLNTHTDLPV-----PC-----LCIQVMSLEPDSERVEFCPPREDPG 267  
DB 102 -LTTPETVLTGHTEKIYSLRHFPLADVLASSSYDLTIRINDIARTQDLRL-----QG 154  
OY 268 AHRNLMHLARLVLSPGVQDLAPCLLP--GKVTLCWQAPDQSPQOPLVPPVPO--KNATVNE 326

155 HODQIFSLA-----WSPQKQD-ARVCKDGRVAV--YDPRSSPLPLQDGFQPCGRGAASS 207  
Y 327 PDQFQVAGBNLCVOYST-----WEKVLQACSWADSLGP-----FDDMLLYE 371  
b 208 GCVMVYVCMVLTVAEVSASCSWLMWQKA-IQHC-MASTVAPSTLLPSYPDTGLV- 264  
Y 372 MKTGLNITSYCALE-----PSCGTPLPMSASTRAARLGE 405  
b 265 LITGKGRTRFLVLEVEAPFLFECNSTSPDPHKGFIILPTECDIQDVEFARCLRLRO 324  
b 406 ELIAD--FRSHQCMQNMND--NMGSLMACPM 434  
b 325 TSLPVAFRLEPRVKEFQDDVEPTAVTWASALD 358

SEQUENCE FROM N.A. (ISOFORM 3), AND PARTIAL SEQUENCE.  
TISSUE-Cervical carcinoma.  
MEDLINE-97410306; PubMed-9267021;  
Zou H., Henzel W.J., Liu X., Lutschg A., Wang X.;  
Apaf-1, a human protein homologous to C. elegans CED-4, participates  
in cytochrome c-dependent activation of caspase-3.\*;  
Cell 90:405-413(1997).

SEQUENCE FROM N.A. (ISOFORMS 1; 4 AND 5).  
TISSUE-peripheral blood, heart, and cervical carcinoma;  
MEDLINE-99373149; PubMed-10441496;  
Hahn C., Hirsch B., Jahnke D., Duerkop H., Stein H.;  
Three new types of Apaf-1 in mammalian cells.\*;  
Biochem. Biophys. Res. Commun. 261:746-749(1999).

SEQUENCE FROM N.A. (ISOFORM 2).  
TISSUE-T-cell;  
MEDLINE-9932765; PubMed-10364241;  
Salah A., Srinivasula S.M., Acharya S., Fishel R., Alnemri E.S.;  
Cytochrome c and dATP-mediated oligomerization of Apaf-1 is a  
prerequisite for procaspase-9 activation.\*;  
J. Biol. Chem. 274:17941-17945(1999).

SEQUENCE FROM N.A. (ISOFORM 1).  
TISSUE-Kidney;  
Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
[5]  
SEQUENCE OF 385-1248 FROM N.A. (ISOFORM 1).  
TISSUE-Brain;  
MEDLINE-98116655; PubMed-9455477;  
Ishikawa K.-I., Nagase T., Nakajima D., Seki N., Ohira M.,  
Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;  
Prediction of the coding sequences of unidentified human genes. VIII.  
78 new cDNA clones from brain which code for large proteins in  
vitro.\*;  
DNA Res. 4:307-313(1997).

SEQUENCE OF 810-864 AND 866-883 FROM N.A.  
Roberts D.L., Dalgleish R., Cohen G.M., MacFarlane M.;  
The mammalian CED4 homologue, Apaf1, exists as two distinct forms in

RT human cells.\*;  
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.  
RN [7]  
RA SEQUENCE OF 1-138 FROM N.A. (ISOFORM 1/4/5).  
RP Won M., Lee J.-W., Oh H.-H., Kim D.-U., Chung K.-S., Lee M.,  
RA Yoo H.-S.\*;  
RT "Cloning of variant Apaf1.\*"  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
RN [8]  
RP APAF-1-MEDIATED OLIGOMERIZATION.  
RX MEDLINE-98315378; PubMed-9651578;  
RA Srinivasula S.M., Ahmad M., Fernandes-Alnemri T., Alnemri E.S.;  
RT "Autoactivation of procaspase-9 by Apaf-1-mediated oligomerization.\*";  
RL Mol. Cell 1:949-957(1998).  
RN [9]  
RX INDUCTION BY E2F AND p53.  
RA MEDLINE-21283226; PubMed-11389439;  
RA Moroni M.C., Hickman E.S., Denchi E.L., Capra G., Colli E.,  
RA Cecconi F., Mueller H., Helin K.;  
RT "Apaf-1 is a transcriptional target for E2F and p53.\*";  
RL Nat. Cell Biol. 3:552-558(2001).  
RN [10]  
RX X-RAY CRYSTALLOGRAPHY (1.3 ANGSTROMS) OF 1-97.  
RA MEDLINE-20013059; PubMed-10543941;  
RA Vaughn D.E., Rodriguez J., Lazebnik Y., Joshua-Tor L.;  
RT "Crystal structure of Apaf-1 caspase recruitment domain: an alpha-  
RT helical Greek key fold for apoptotic signaling.\*";  
RL J. Mol. Biol. 293:439-447(1999).  
RN [11]  
RX STRUCTURE BY NMR OF 1-97.  
RA MEDLINE-20047184; PubMed-10578182;  
RA Day C.L., Dupont C., Lackmann M., Vaux D.L., Hinds M.G.;  
RT "Solution structure and mutagenesis of the caspase recruitment domain  
RT (CARD) from Apaf-1.\*";  
RL Cell Death Differ. 6:1125-1132(1999).  
CC -1- FUNCTION: Oligomeric Apaf-1 mediates the cytochrome c-dependent  
CC autocatalytic activation of pro-caspase 9 (Apaf-3), leading to the  
CC activation of caspase-3 and apoptosis. This activation requires  
CC ATP.  
CC -1- SUBUNIT: Monomer. Oligomerizes upon binding of cytochrome c and  
CC dATP. Oligomeric Apaf-1 and pro-caspase-9 bind to each other via  
CC their respective NH2-terminal CARD domains and consecutively  
CC mature caspase-9 is released from the complex.  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -1- ALTERNATIVE PRODUCTS: 5 isoforms; 1/Apaf-1X (shown here), 2/Apaf-  
CC 1L, 3/Apaf-1S, 4/Apaf-1M and 5/Apaf-1XS; are produced by  
CC alternative splicing.  
CC -1- TISSUE SPECIFICITY: Ubiquitous. Highest levels of expression in  
CC adult spleen and peripheral blood leukocytes, and in fetal brain,  
CC kidney and lung. Isoform 1 is expressed in heart, kidney and  
CC liver.  
CC -1- INDUCTION: By E2F and p53 in apoptotic neurons.  
CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.  
CC -1- SIMILARITY: CONTAINS 13 WD REPEATS (TRP-ASP DOMAINS).  
CC -1- SIMILARITY: CONTAINS 1 NB-ARC DOMAIN.\*  
CC -1- CAUTION: Ref.7 sequence differs from that shown due to a  
CC frameshift in position 109.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
CC -----  
DR EMBL: AF013263; AAC51678.1; -  
DR EMBL: AJ243003; CAB55579.1; -  
DR EMBL: AJ243004; CAB55580.1; -  
DR EMBL: AJ243005; CAB55581.1; -  
DR EMBL: AJ243006; CAB55582.1; -  
DR EMBL: AJ243007; CAB55583.1; -  
DR EMBL: AJ243008; CAB55584.1; -

Query Match	2.98; Score 104.5; DB 1; Length 1248;
Best Local Similarity	19.18; Pred. No. 2.5;
Matches 112;	Conservative 64; Mismatches 188; Indels 221; Gaps 27;
QY 79 DCLLRVAVVYHLAVGH-----WAPPEAGKSDSELOE-SRNASTLOA-OVYLSFOAY--	128
DB 537 DCAVSENFQOELSINGHLGRQFPENIVOLGICEPETSSEYVQAOKIAQKOEVDNGMLEYE	596
QY 129 -----PIARCALLLEVOYADLV-----OPGQSVGAVPD-----CEASLG-----	164
DB 597 WIKKNTNTNLSRLVVRHTDVAYHACFSEDDGRIASCAGDKTLQVRAETGEKILEITKAH	656
QY 165 -----AEVOIMS-----YTKPRYKEINTLQOLPDGDVLL	195
DB 657 EDEVLCAAFSTDDEFIATCSYDKKVKYKINMSMGELVHTYDEHSEQVNCCHFTSSHHLL	716
QY 196 TLDVSEPODSFLLYLKRPVPAKLSLWKNTLTGPONTITLNHDVLPCLCIQVWSLEPDE	255
DB 717 ANGSS-----DCFLKMLDNLQKCRNTMGHTN-----	744
QY 256 RVEEFCFEEDPGAHRLNLMHARLRYLSPGVQMLDAPCLPGVYTLQMOAPDQSPQPLVP	315
DB 745 SVNHCFSPD-----KLASCSADGTLKL-WDATSANERKSI--	781
QY 316 PVPQKNATVNEPODEFOLVAGHPNLCVOYSTWEKVOLQACSW-ADS-----LGP	362
DB 782 NVKQFPLNLEDPQEDM-----EVLYKCCSWSDAGRIWAAKNKIFLFD	825
QY 363 FKDDMLLVKKTGLNNT-SVCALERPSCGPLPSMASTRARLGEELLQDFRSHQOQLMN	421
DB 826 HTSGLLGHETHGHSHSTIQYCDSPQNHLLAVALL-----SOYCEVLNN	868
QY 422 DDNMGSLMACPMKYIHRRWLVWMLACLLLAALFFELLKKDRRAANGSRFALLHSA	481
DB 869 TDSRSKVAACRG-----HLSNV-----HG-----VWFSP	892
QY 482 DGAGTERLVGALASALSQMLPRAVAVDMSRRELNSAGALAMFHHQRRRLIOEGSVILLF	541
DB 893 DSSSF-----LTSDDQ-----TIRLWETKKVCNKSNAV-MLKQEDVYVQENEVAVL--	938
QY 542 SPAANAQCCOMLOLOQVYEPGRHAL-AAATLSCTVLPDLQCATG	584
DB 939 ---AVDHIRR-LQLINGRTGQIDYLTLEAQSVCCLSPHLOYIAFG	979
RESULT 5	
PGBM_MOUSE	
ID	STANDARD; PRT; 3707 AA.
AC 005793;	
DT 01-NOV-1995 (Rel. 32, Created)	
DT 01-NOV-1995 (Rel. 32, Last sequence update)	
DT 01-MAR-2002 (Rel. 41, Last annotation update)	
DE Basement membrane-specific heparan sulfate proteoglycan core	
DE protein precursor (HSPG) (Perlecan) (PLC)	
GN HSPG2.	
OS Mus musculus (Mouse).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC Mammalia; Euteria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
OX NCBI_TaxID=1090;	
XX [1]	
RN SEQUENCE FROM N.A.	
RP TISSUE=Melanoma;	
RC MEDLINE=92078153; PubMed=1744087;	
RA Noonan D.M., Fulle A., Valente P., Cai S., Horiigan E., Sasaki M.,	
RA Yamada Y., Hassell J.R.;	
RT "The complete sequence of perlecan, a basement membrane heparan	
RT sulfate proteoglycan, reveals extensive similarity with laminin A	
RT chain, low density lipoprotein receptor, and the neural cell adhesion	
RT molecule."	
RT J. Biol. Chem. 266:22939-22947(1991).	
RN [2]	
RP SEQUENCE OF 940-1601 AND 1870-2600 FROM N.A., AND PARTIAL SEQUENCE.	
RX MEDLINE=89034110; PubMed=2972708;	

Noonan D.M., Horigan E.A., Ledbetter S.R., Vogeli G., Sasaki M., Yamada Y., Hassell J.R.;  
 Identification of cDNA clones encoding different domains of the basement membrane heparan sulfate proteoglycan.\*;

J. Biol. Chem. 263:16379-16387(1988).

- 1- FUNCTION: THIS PROTEIN IS AN INTEGRAL COMPONENT OF BASEMENT MEMBRANES. IT IS RESPONSIBLE FOR THE FIXED NEGATIVE ELECTROSTATIC CHARGE AND IS INVOLVED IN THE CHARGE-SELECTIVE ULTRAFILTRATION PROPERTIES. IT INTERACTS WITH OTHER BASEMENT MEMBRANE COMPONENTS SUCH AS LAMININ AND COLLAGEN TYPE IV AND SERVES AS AN ATTACHMENT SUBSTRATE FOR CELLS.
- 1- SUBUNIT: PURIFIED PERLECAN HAS A STRONG TENDENCY TO AGGREGATE IN DIMERS OR STELLATE STRUCTURES.
- 1- SUBCELLULAR LOCATION: Extracellular.
- 1- TISSUE SPECIFICITY: FOUND IN THE BASEMENT MEMBRANES.
- 1- PTM: CONTAINS THREE HEPARAN SULFATE CHAINS AS WELL AS N-LINKED AND O-LINKED OLIGOSACCHARIDES.
- 1- SIMILARITY: CONTAINS 4 LDL-RECEPTOR CLASS A DOMAINS.
- 1- SIMILARITY: CONTAINS 10.5 LAMININ EGF-LIKE DOMAINS.
- 1- SIMILARITY: CONTAINS 15 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
- 1- SIMILARITY: CONTAINS 3 LAMININ G-LIKE DOMAINS.
- 1- SIMILARITY: CONTAINS 1 SEA DOMAIN.

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EMBL: M77174; AAA39911.1; -;  
 EMBL: J04054; AAA39899.1; -;  
 EMBL: J04055; AAA39912.1; -;  
 HSSP: Q07954; 1CR8P.  
 MGD: MGI:96257; HSP92.  
 InterPro: IPR000561; EGF-like.  
 InterPro: IPR000742; EGF\_2.  
 InterPro: IPR001438; EGF\_11.  
 InterPro: IPR003006; Ig\_MHC.  
 InterPro: IPR003598; Ig\_C2.  
 InterPro: IPR002172; LDL\_recept\_A.  
 InterPro: IPR000034; Laminin\_B.  
 InterPro: IPR002049; Laminin\_EGF.  
 InterPro: IPR001791; Laminin\_G.  
 InterPro: IPR000082; SEA.  
 Pfam: PF00047; Ig\_15.  
 Pfam: PF00052; Laminin\_B; 3.  
 Pfam: PF00053; Laminin\_EGF; 8.  
 Pfam: PF00054; Laminin\_G; 3.  
 Pfam: PF00057; LDL\_recept\_a; 4.  
 Pfam: PF01390; SEA; 1.  
 PRINTS: PR00010; EGFBL00D.  
 ProDom: PD003031; Laminin\_B; 3.  
 SMART: SM00180; EGF\_Lam; 7.  
 SMART: SM00001; EGF\_Like; 6.  
 SMART: SM00408; IGC2; 14.  
 SMART: SM00192; LDLa; 4.  
 SMART: SM00281; Lamb; 3.  
 SMART: SM00282; Lamb; 3.  
 SMART: SM00200; SEA; 1.  
 PROSITE: PS00022; EGF\_1; 8.  
 PROSITE: PS01186; EGF\_2; 5.  
 PROSITE: PS01248; LAMININ\_TYPE\_EGF; 11.  
 PROSITE: PS50025; LAM\_G\_DOMAIN; 3.  
 PROSITE: PS01209; LDLRA\_1; 4.  
 PROSITE: PS50068; LDLRA\_2; 4.  
 PROSITE: PS50024; SEA; 1.  
 Signal: Basement membrane; Proteoglycan; Repeat; Glycoprotein; Heparan sulfate; Laminin EGF-like domain; Immunoglobulin domain; Extracellular matrix; EGF-like domain.

FT	SIGNAL	1	21	POTENTIAL.
FT	CHAIN	22	3707	BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN.
FT	DOMAIN	80	194	SEA.
FT	DOMAIN	195	234	LDL-RECEPTOR CLASS A 1.
FT	DOMAIN	281	319	LDL-RECEPTOR CLASS A 2.
FT	DOMAIN	320	359	LDL-RECEPTOR CLASS A 3.
FT	DOMAIN	360	403	LDL-RECEPTOR CLASS A 4.
FT	DOMAIN	404	504	IG-LIKE C2-TYPE DOMAIN 1.
FT	DOMAIN	521	530	LAMININ EGF-LIKE 1 (N-TERMINAL).
FT	DOMAIN	531	730	LAMININ EGF-LIKE 1 (N-TERMINAL).
FT	DOMAIN	731	763	LAMININ EGF-LIKE 1 (C-TERMINAL).
FT	DOMAIN	764	813	LAMININ EGF-LIKE 2.
FT	DOMAIN	814	871	LAMININ EGF-LIKE 3.
FT	DOMAIN	879	923	LAMININ EGF-LIKE 4 (INCOMPLETE).
FT	DOMAIN	924	933	LAMININ EGF-LIKE 5 (N-TERMINAL).
FT	DOMAIN	934	1125	LAMININ EGF-LIKE 5 (C-TERMINAL).
FT	DOMAIN	1126	1158	LAMININ EGF-LIKE 5 (C-TERMINAL).
FT	DOMAIN	1159	1208	LAMININ EGF-LIKE 6.
FT	DOMAIN	1209	1265	LAMININ EGF-LIKE 7.
FT	DOMAIN	1275	1324	LAMININ EGF-LIKE 8.
FT	DOMAIN	1325	1334	LAMININ EGF-LIKE 9 (N-TERMINAL).
FT	DOMAIN	1335	1529	LAMININ EGF-LIKE 9 (N-TERMINAL).
FT	DOMAIN	1530	1562	LAMININ EGF-LIKE 9 (C-TERMINAL).
FT	DOMAIN	1563	1612	LAMININ EGF-LIKE 10.
FT	DOMAIN	1613	1670	LAMININ EGF-LIKE 11.
FT	DOMAIN	1677	1771	IG-LIKE C2-TYPE DOMAIN 2.
FT	DOMAIN	1772	1865	IG-LIKE C2-TYPE DOMAIN 3.
FT	DOMAIN	1866	1954	IG-LIKE C2-TYPE DOMAIN 4.
FT	DOMAIN	1955	2049	IG-LIKE C2-TYPE DOMAIN 5.
FT	DOMAIN	2050	2148	IG-LIKE C2-TYPE DOMAIN 6.
FT	DOMAIN	2149	2244	IG-LIKE C2-TYPE DOMAIN 7.
FT	DOMAIN	2245	2343	IG-LIKE C2-TYPE DOMAIN 8.
FT	DOMAIN	2344	2436	IG-LIKE C2-TYPE DOMAIN 9.
FT	DOMAIN	2437	2532	IG-LIKE C2-TYPE DOMAIN 10.
FT	DOMAIN	2533	2619	IG-LIKE C2-TYPE DOMAIN 11.
FT	DOMAIN	2620	2720	IG-LIKE C2-TYPE DOMAIN 12.
FT	DOMAIN	2721	2809	IG-LIKE C2-TYPE DOMAIN 13.
FT	DOMAIN	2810	2895	IG-LIKE C2-TYPE DOMAIN 14.
FT	DOMAIN	2896	2980	IG-LIKE C2-TYPE DOMAIN 15.
FT	DOMAIN	2984	3162	LAMININ G-LIKE 1.
FT	DOMAIN	3163	3241	EGF-LIKE.
FT	DOMAIN	3245	3425	LAMININ G-LIKE 2.
FT	DOMAIN	3518	3705	LAMININ G-LIKE 3.
FT	SITE	65	67	HEPARAN SULFATE (POTENTIAL).
FT	SITE	71	73	HEPARAN SULFATE (POTENTIAL).
FT	SITE	76	78	HEPARAN SULFATE (POTENTIAL).
FT	SITE	3615	3617	MEDIATES MOTOR NEURON ATTACHMENT (POTENTIAL).
FT	DISULFID	199	212	BY SIMILARITY.
FT	DISULFID	206	225	BY SIMILARITY.
FT	DISULFID	219	234	BY SIMILARITY.
FT	DISULFID	285	297	BY SIMILARITY.
FT	DISULFID	292	310	BY SIMILARITY.
FT	DISULFID	304	319	BY SIMILARITY.
FT	DISULFID	325	337	BY SIMILARITY.
FT	DISULFID	332	350	BY SIMILARITY.
FT	DISULFID	344	359	BY SIMILARITY.
FT	DISULFID	368	381	BY SIMILARITY.
FT	DISULFID	375	394	BY SIMILARITY.
FT	DISULFID	388	403	BY SIMILARITY.
FT	DISULFID	428	479	BY SIMILARITY.
FT	DISULFID	764	773	BY SIMILARITY.
FT	DISULFID	766	780	BY SIMILARITY.
FT	DISULFID	783	792	BY SIMILARITY.
FT	DISULFID	795	811	BY SIMILARITY.
FT	DISULFID	814	829	BY SIMILARITY.
FT	DISULFID	816	839	BY SIMILARITY.
FT	DISULFID	842	851	BY SIMILARITY.
FT	DISULFID	854	869	BY SIMILARITY.
FT	DISULFID	1159	1168	BY SIMILARITY.
FT	DISULFID	1161	1175	BY SIMILARITY.
FT	DISULFID	1178	1187	BY SIMILARITY.

DISULFID	1190	1206	BY SIMILARITY.
DISULFID	1209	1224	BY SIMILARITY.
DISULFID	1211	1234	BY SIMILARITY.
DISULFID	1237	1246	BY SIMILARITY.
DISULFID	1249	1263	BY SIMILARITY.
DISULFID	1275	1287	BY SIMILARITY.
DISULFID	1277	1293	BY SIMILARITY.
DISULFID	1295	1304	BY SIMILARITY.
DISULFID	1307	1322	BY SIMILARITY.
DISULFID	1563	1572	BY SIMILARITY.
DISULFID	1565	1579	BY SIMILARITY.
DISULFID	1582	1591	BY SIMILARITY.
DISULFID	1594	1610	BY SIMILARITY.
DISULFID	1613	1628	BY SIMILARITY.
DISULFID	1615	1638	BY SIMILARITY.
DISULFID	1641	1650	BY SIMILARITY.
DISULFID	1653	1668	BY SIMILARITY.
DISULFID	1792	1839	BY SIMILARITY.
DISULFID	1886	1932	BY SIMILARITY.
DISULFID	1976	2021	BY SIMILARITY.
DISULFID	2073	2118	BY SIMILARITY.
DISULFID	2170	2215	BY SIMILARITY.
DISULFID	2268	2313	BY SIMILARITY.
DISULFID	2365	2413	BY SIMILARITY.
DISULFID	2456	2506	BY SIMILARITY.
DISULFID	2554	2599	BY SIMILARITY.
DISULFID	2641	2686	BY SIMILARITY.
DISULFID	2831	2876	BY SIMILARITY.

Query Match  
Best Local Similarity 2.98; Score 103.5; DB 1; Length 3707;  
Matches 87; Conservative 44; Mismatches 167; Indels 127; Gaps 19;

26	EPQDTRARCSIG-LSCHW--DGDVLCPLGSLQ-----APGVLVPTROTETELVLR----	73
326	ERNRFA-CENGKCALKMLRCDDPDCEDRTDANGSVKPGEGCGPHFCVSTNRCTPA	384
74	---SPQRTDCAIRVVVHLAVHGMARPEAKSDSELOESNNASLOAQVLSFQAVPI	130
385	SFHCDESDCPDR-----SDEGCMRPQVYTPPQOSIQ-----	418
131	ARCALLEVQVPAIDLVPGQSGVSAVDFCEPSLSLAEVQIWTSTKPKRYKELNTQOLPDG	190
419	-----SRGQVY--TFTCVANGVPTPIIMWRLMWHGHPAPRVTMTSEGG	460
191	DNVLTLDVSEEDDFSL-----YLRVPDAKSLMYKMLTGQON--TILNHTDLVP	241
461	RGTLLTRDYKADQAGATTCAMNSRGVAFGIPDGVLELVPQRGPCDGHFYLEDSASCLP	520
242	CACIQWASLEPDERVEFCFREDPGAHRLNHLIARLVISFGVMOIDAPCCLPG-KVTL	300
521	CCFCGVTNVCQSSLR-----FRD-----QIRL-----SFDQPNDRKGVAVTM	557
301	CMAQAPQSPQPLVPPVPPQKATVNEP-QDFOLVAGHPNLCQVSTWEXYQLOACSMADS	359
558	-----PSQPPVPPPLSTQLOIDPQLDPEFQVLDLSRFLVHADFMALPKQFLGNKVD	609
360	LCPPKDDMLLVKKTGNTNVSVALP-----SCTPL-PSMASTRAA	401
610	YCGFLAKRYKRYELARCM-----LEPVQKPDVILVAGGYRLHSRGHTPTNPGLNOROV	662
402	RLGEE 406	
663	OLSEE 667	

RESULT 6  
NAL2\_HUMAN STANDARD: PRT: 1062 AA.  
O9NWX02: O9BNVNS: O9HG66: O9HAY9: O9NMK3;  
16-OCT-2001 (Rel. 40, Created)  
16-OCT-2001 (Rel. 40, Last sequence update)  
01-MAR-2002 (Rel. 41, Last annotation update)

DE NACHT-, LRR- and PYD-containing protein 2 (Nucleotide-binding site  
DE protein 1);  
GN NALP2 OR NBS1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_Taxid=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM 2).  
RX MEDLINE-21169419; PubMed-11270363;  
RA Berlin J., Distefano P.S.;  
RT "The pyrin domain: a novel motif found in apoptosis and inflammation  
RT proteins.";  
RL Cell Death Differ. 7:1273-1274(2000).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RX MEDLINE-21148093; PubMed-11250163;  
RA Martinon F., Hofmann K., Tschopp J.;  
RT "The pyrin domain: a possible member of the death domain-fold family  
RT implicated in apoptosis and inflammation.";  
RL Curr. Biol. 11:R118-R120(2001).  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RC TISSUE-Kidney epithelium, and Colon;  
RA Matanabe K., Kumagai A., Itakura S., Yamazaki M., Tashiro H., Ota T.,  
RA Suzuki Y., Ohayashi M., Nishi T., Shibahara T., Tanaka T.,  
RA Nakamura Y., Isegal T., Sugano S.;  
RT "NEDO human cDNA sequencing project.";  
RL Submitted (FEB-2000) to the EMBL/Genbank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RC TISSUE-Lung, and Placenta;  
RA Strausberg R.;  
RL Submitted (FEB-2001) to the EMBL/Genbank/DBJ databases.  
CC -1- FUNCTION: May be implicated in apoptosis (By similarity).  
CC -1- COFACTOR: Binds ATP (By similarity).  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are  
CC produced by alternative splicing.  
CC -1- SIMILARITY: CONTAINS 1 DAPIN DOMAIN.  
CC -1- SIMILARITY: CONTAINS 9 LECICINE-RICH REPEATS (LRR).  
CC -1- SIMILARITY: CONTAINS 9 LECICINE-RICH REPEATS (LRR).  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
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CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
CC  
DR EMBL: AF298547; AAC15253.1; ALT\_INIT.  
DR EMBL: AF310106; AAG30289.1; -  
DR EMBL: AK000517; BAA91223.1; -  
DR EMBL: AK025952; BAB15293.1; -  
DR EMBL: AK000784; BAA91377.1; ALT\_INIT.  
DR EMBL: BC003592; AAH03592.1; -  
DR EMBL: BC001039; AAH01039.1; -  
DR InterPro: IPR000767; Disease\_resist.  
DR InterPro: IPR003592; LRR\_out.  
DR InterPro: IPR004020; PAAD\_DAPIN.  
DR PRINTS: PRO0364; DISEASEREST.  
DR SMART: SM00370; LRR\_7.  
DR PROSITE: PS50824; DAPIN\_1.  
DR PROSITE: PS50837; NACHT\_1.  
KW Apoptosis; ATP-binding; Leucine-rich repeat; Repeat;  
KW Alternative splicing.  
FT DOMAIN 1 94 DAPIN.  
FT DOMAIN 207 526 NACHT.  
FT REPEAT 467 491 LRR 1.  
FT REPEAT 622 645 LRR 2.  
FT REPEAT 754 777 LRR 3.  
FT REPEAT 810 832 LRR 4.

Query Match	2.88;	Score 100.5;	DB 1;	Length 1062;
Best Local Similarity	22.3%;	Pred. No. 4.2;		
Matches 126;	Conservative 62;	Mismatches 177;	Indels 199;	Gaps 34

SELF	7
2 HUMAN	
DCC_HUMAN	STANDARD; PRT; 1447 AA.
P43146;	
01-NOV-1995 (Rel. 32, Created)	
01-NOV-1995 (Rel. 32, Last sequence update)	
01-MAR-2002 (Rel. 41, Last annotation update)	
Tumor suppressor protein DCC precursor (Colorectal cancer suppressor)	
DCC.	
Homo sapiens (Human).	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	

CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95011532; PubMed=7926722;  
RA Hedrick L.; Cho K.R., Fearon E.R., Wu T.-C., Kinzler K.W.,  
RA Vogelstein B.;  
RT "The DCC gene product in cellular differentiation and colorectal  
tumorigenesis.";  
RL Genes Dev. 8:1174-1183(1994).  
RN [2]  
RP SEQUENCE OF 1-750 FROM N.A.  
RX MEDLINE=90100559; PubMed=2294591;  
RA Fearon E.R., Cho K.R., Nigro J.M., Kern S.E., Simons J.W.,  
RA Ruppert J.M., Hamilton S.R., Preisinger A.C., Thomas G., Kinzler K.W.,  
RA Vogelstein B.;  
RT "Identification of a chromosome 18q gene that is altered in  
colorectal cancers.";  
RL Science 247:49-56(1990).  
RN [3]  
RP SEQUENCE OF 107-472 FROM N.A. (SCRAMBLED EXONS).  
RX MEDLINE=91121517; PubMed=1991322;  
RA Nigro J.M., Cho K.R., Fearon E.R., Kern S.E., Ruppert J.M.,  
RA Oliner J.D., Kinzler K.W., Vogelstein B.;  
RT "Scrambled exons.";  
RL Cell 64:607-613(1991).  
RN [4]  
RP GENE STRUCTURE, AND VARIANTS CARCINOMA HIS-1375.  
RX MEDLINE=94245241; PubMed=8188295;  
RA Cho K.R., Oliner J.D., Simons J.W., Hedrick L., Fearon E.R.,  
RA Preisinger A.C., Hedge P., Silverman G.A., Vogelstein B.;  
RT "The DCC gene: structural analysis and mutations in colorectal  
carcinomas.";  
RL Genomics 19:525-531(1994).  
RN [5]  
RP VARIANT CARCINOMA THR-168, AND VARIANT GLY-201.  
RX MEDLINE=94243823; PubMed=8187090;  
RA Miyake S., Nagai K., Yoshino K., Oto M., Endo M., Yuasa Y.;  
RT "Point mutations and allelic deletion of tumor suppressor gene DCC in  
human esophageal squamous cell carcinomas and their relation to  
metastasis.";  
RL Cancer Res. 54:3007-3010(1994).  
RN [6]  
RP FUNCTION: IDENTIFIED AS A TUMOR SUPPRESSOR GENE.  
RX [6]  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -1- TISSUE SPECIFICITY: FOUND IN AXONS OF THE CENTRAL AND PERIPHERAL  
CC NERVOUS SYSTEM AND IN DIFFERENTIATED CELL TYPES OF THE INTESTINE.  
CC -1- DISEASE: COLORECTAL TUMORS THAT LOST THEIR CAPACITY TO  
CC DIFFERENTIATE INTO MUCUS PRODUCING CELLS UNIFORMLY LACK DCC  
CC EXPRESSION. INACTIVATION OF DCC DUE TO ALLELIC DELETION AND/OR  
CC POINT MUTATIONS MAY CAUSE BOTH LYMPHATIC AND HEMATOGENOUS  
CC METASTASIS OF ESOPHAGEAL SQUAMOUS CELL CARCINOMAS.  
CC -1- SIMILARITY: BELONGS TO THE IMMUGLOBULIN SUPERFAMILY. DCC  
CC SUBFAMILY.  
CC -1- SIMILARITY: CONTAINS 4 IMMUGLOBULIN-LIKE C2-TYPE DOMAINS.  
CC -1- SIMILARITY: CONTAINS 6 FIBRONECTIN TYPE III-LIKE DOMAINS.  
CC [7]  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC [8]  
CC -----  
DR EMBL, X76132; CAA53735.1; -  
DR EMBL, M32292; AAA35751.1; -  
DR EMBL, M32286; AAA52174.1; -  
DR EMBL, M32288; AAA52175.1; ALT\_SEQ.  
DR EMBL, M32390; AAA52176.1; -  
DR EMBL, M63696; AAA52177.1; -  
DR EMBL, M63700; AAA52178.1; -  
DR EMBL, M63702; AAA52179.1; -  
DR EMBL, M63718; AAA52180.1; -

Db	188	RVVLEFGALQISRLAPGDIGIYRCSSARNPASSRFGNEAEVRLDSPGLHRLQYLFQIRPS	247
Oy	276	-----	275
Db	248	NYVAIEGKDAVLECCVSGYPPPSFTWLNGEEVIQLRSKRYSLIGSGNLLISNVTDDSGM	3078
Oy	276	-----ARLRVLPSPGWMADAPCCLEPGKVTLCMQADP-QSPCQPLVPVP-	318
Db	308	YVCVYVYTKNNENISASAEFLVLP-PWELNHSNL-----YAESNDIEFECTYSGKRPPT	361
Oy	319	---QKNATVNEPQDFOLVAGHPNLGVQSTWEKYLQACSMADSLGPFKDD---MLVYE	371
Db	362	VNMKRGDVPVIPSDFEIVGGSNLRI-----LGVKSDGEGFYGVAAE	403
Oy	372	MKTGLNLTSGCALPSSCTP-----LPSMASTRARLGEELLQDRSHQCOL	419
Db	404	NEGNATQTSQQLVPRKPAITSSSVLPSPAPRDVVPVAVLSREFVRLS-----	448
Oy	420	MNDNNGSLMACPMCKYHRRWVLTWLTCLLAALFEFLILKKDKRKAARGS-RTALLL	478
Db	449	-----WRPFAE-----AKNGIQFTYF	465
Oy	479	HSADGAGYERLVQALASALSQMPLR-----VAVDLSRRELSAHGALANFHNO	526
Db	466	FREGRGNREALNTTQPGSLQLTGVNLKPEAMTYFERVVAAYNMCGEES-----	514
Oy	527	RRRIQEGGVILFSPAAYAOCCOMLO-----LGVVEPGPHALAMLSGVLPDPLQ	579
Db	515	-----QPIKA-TOPELQVPPVENVLQAVSTSPSILITWEP---PAYAN	555
Oy	580	GR-----ATGRYGVYEDGL	594
Db	556	GPVQGYRLCTEVTSGTEKQNIENVDL	581

RESULT 8

ABP2\_HUMAN

ID ABP2\_HUMAN

AC P21333;

DT 01-MAY-1991 (Rel. 18, Created)

DT 01-MAY-1991 (Rel. 18, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Endothelial actin-binding protein (ABP-280) (Nonmuscle filamin)

DE (Filamin 1) (Alpha-filamin).

GN FLN1 OR FLN.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI\_TaxId=9606;

STANDARD;

PRT; 2647 AA.

SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RX MEDLINE-90361737; PubMed-2391361;

RA Gollin J.B., Yamini R., Egan S., Stewart M., Stossel T.P., Kwiatkowski D.J., Hartwig J.H.;

RT "Human endothelial actin-binding protein (ABP-280, nonmuscle filamin): a molecular leaf spring."

RT J. Cell Biol. 111:1089-1105(1990).

SEQUENCE FROM N.A.

RX MEDLINE-96311563; PubMed-8733135;

RA Chen E.Y., Zollo M., Mazzarella R.A., Ciccodicola A., Chen C.-N., D'Urso M., Heiner C., Burrough F.W., Ripetto M., Schlessinger D.,

RT "Long-range sequence analysis in Xq28: thirteen known and six candidate genes in 219.4 kb of high GC DNA between the RCP/GCP and GGD loci."

RT Hum. Mol. Genet. 5:659-668(1996).

Tomliolo D.: Mapping of two genes encoding isoforms of the actin binding protein Abp-280, a dystrophin like protein, to Xq28 and to chromosome 7. Hum. Mol. Genet. 2:761-766(1993).

- FUNCTION: PROMOTES ORTHOGONAL BRANCHING OF ACTIN FILAMENTS AND LINKS ACTIN FILAMENTS TO MEMBRANE GLYCOPROTEINS.

- SUBUNIT: HOMODIMER. INTERACTS WITH CYPSP.

- TISSUE SPECIFICITY: PERIPHERAL CYTOPLASM.

- PTM: PHOSPHORYLATION EXTENT CHANGES IN RESPONSE TO CELL ACTIVATION.

- SIMILARITY: THE ACTIN-BINDING DOMAIN IS OF A TYPE FOUND IN MANY ACTIN-BINDING PROTEINS (SUCH AS ACTININ, DYSTROPHIN, FIBRIN, ABP-120, ABP-180, OR BETA-FODRIN).

- SIMILARITY: CONTAINS 2 CALPONIN-HOMOLOGY (CH) DOMAINS.

- SIMILARITY: CONTAINS 24 FILAMIN REPEATS.

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EMBL; X53416; CAA37495.1; -  
EMBL; L44140; AA92644.1; -  
EMBL; X70082; CAA49687.1; -  
EMBL; X70085; CAA49690.1; -  
PIR; A37098; A37098.  
HSSP; P13466; 1KSR.  
MIM; 300017; -  
InterPro; IPR001589; Actinin\_act\_bind.  
InterPro; IPR001715; Calponin\_hom.  
InterPro; IPR001298; Filamin.  
Pfam; PF00307; CH; 2.  
Pfam; PF00630; Filamin; 24.  
SMART; SMO0033; CH; 2.  
PROSITE; PS00019; ACTININ\_1; 1.  
PROSITE; PS00020; ACTININ\_2; 1.  
PROSITE; PS00021; CH; 2.  
PROSITE; PS50194; FILAMIN\_REPEAT; 24.  
Actin-binding; Phosphorylation; Repeat.  
DOMAIN 1 274  
DOMAIN 2 149  
DOMAIN 3 266  
DOMAIN 4 374  
DOMAIN 5 474  
DOMAIN 6 570  
DOMAIN 7 663  
DOMAIN 8 763  
DOMAIN 9 866  
DOMAIN 10 965  
DOMAIN 11 1061  
DOMAIN 12 1154  
DOMAIN 13 1249  
DOMAIN 14 1349  
DOMAIN 15 1442  
DOMAIN 16 1539  
DOMAIN 17 1636  
DOMAIN 18 1740  
DOMAIN 19 1779  
DOMAIN 20 1860  
DOMAIN 21 1950  
DOMAIN 22 2039  
DOMAIN 23 2131  
DOMAIN 24 2230  
DOMAIN 25 2335  
DOMAIN 26 2420  
DOMAIN 27 2516  
DOMAIN 28 2551  
DOMAIN 29 2646  
DOMAIN 30 2647

FT	SITE	1761	1762	CLEAVAGE (BY CALPAIN).
FT	MOD_RES	1	1	BLOCKED.
FT	CONFLICT	1772	1772	A -> G (IN REF. 3).
FT	CONFLICT	2634	2634	H -> D (IN REF. 2).
SO	SEQUENCE	2647 AA;	280759 MM;	6C1A07041DFA3D42 CRC64;
Query Match				
Best Local Similarity 2.88; Score 99.5; DB 1; Length 2647;				
Matches 145; Conservative 76; Mismatches 197; Indels 285; Gaps 42;				
QY	122	VLSFOAVPIARCALLLEVQVADLVOP	-----GOSVGSANFDCFEASLGAE-----	VOIMSY 172
DB	537	VYGEFFYPM	-----VPGYITVITWGQONIGRSP	--FEVVGTECGNOKVRAMG- 583
QY	173	TKPRYQKELMTQOOLPDGDVNLTLTLDVSEODESFLLYLRVPDAKSLMYKNLTGPONI	232	
DB	584	-PGLGCV	-----VGKSAF-----	VEAIGDVGITGLF-SVEGSOA 619
QY	233	TLNHTDVLPLC-IQWSLEP	-----DSERVEFCPPREDPGAHRIIMHARLVLS	282
DB	620	KICDDKGDGSCDVRYPQEGEYAVHYLCN	SEDIRLSFPMADIRAPDPHPRVARG	679
QY	283	PGWQIADAPCLP	-----GKVTLCWQAPDQSPQ	-----PLVPPV 317
DB	680	PGLKTVAVANKRAEFTYDANKHGRAPLRVQVODNEGCEVEALVKDNGNGTSCSYPRK	739	
QY	318	PORNAV	-----NEPODFOLVAG--HPNLGVQVSTWEKVLQACSNADSLGPFKDDM	367
DB	740	PKHTANVSGVSIPIPSFRVNVGASHPN	-----KXV-----	YGP-----777
QY	368	LIVEMKGLNFTSVCALEPS	-----GCTPLPSMASTRARLGEELLQDF	411
DB	778	-----GVAKTGLKAHEPTYFTVDCAEAGGDVSIIGIKCAPGVGAPADIDFDIIR	828	
QY	412	RSHOCQMLNDNDNMGSLMACPMDKTIHRRWLVWLACLLAALEFFLLKDR	-----	465
DB	829	-----NDNFTV-----	KYPR	-----GAGSTYIMVLFADQATPTSP 861
QY	466	-----RKAARG-----	SRTALL	--H--SADGAGYEEL-----489
DB	862	IRKVEPSHDASKYKAGDPGLSRTGVLELKRPTHNTVNAKAAGKGLDVOFSGLTGDAVR	921	
QY	490	-----	VGALAS	-----ALSONPLRVAV---DLMSRRELTAHG 518
DB	922	DVDIIDHNDNTYVKKYTPVOOGSPGVNVTYGGDPIPKSPFSAVSPSLD--SKIKVSGIG	980	
QY	519	ALA	-----	WPHHRRRILOEGGVILLFSFA--AVAOQOQLQLOTYPERGPHDALAAWLS 571
DB	981	EKYDVGDDEFYVSKAGAGQGVASKTIVGSGAIVPCK	-----	VEPG-----LGADNS 1029
QY	572	CV--LPDFLQGRATGRY-VGVYFDGLHPDSVSPFR--VAPLFSLEPTOLPAFLDALOGGC	627	
DB	1030	VYAFEL	-----	REEGYEVEVYTDGVVPDS--PPRLLEAVN--TKPSKVKAFGPGLOGS- 1080
QY	628	STISAGRPADREVERVTOALRSALDSCITSSSEAPGCCCEMDLGPC	670	
DB	1081	--SAGSPA	-----	RFTIDTKGAGTGGLGTF--GPC 1108
RESULT 9				
W70T_MOUSE STANDARD; PRT; 922 AA.				
AC	Q9DZV7;			
DT	01-MAR-2002 (Rel. 41, Created)			
DT	01-MAR-2002 (Rel. 41, Last sequence update)			
DT	01-MAR-2002 (Rel. 41, Last annotation update)			
DE	70 kDa WD-repeat tumor rejection antigen homolog.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxId=10090;			
RN	[1]			



RESULT	10	NOTCH_BARE	STANDARD;	PRT;	2437 AA.
ID	NOTCH_BARE				
AC	P46530;				
DT	01-NOV-1995	(Rel. 32, Created)			
DT	01-NOV-1995	(Rel. 32, Last sequence update)			
DT	01-MAR-2002	(Rel. 41, Last annotation update)			
DE	Neurogenic locus notch homolog protein precursor.				
GN	NOTCH OR NOTCH1A.				
OS	Brachydanio rerio (zebrafish) (zebra danio).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Actinopterygii; Neopterygii; Telostei; Euteleostei; Ostariophysi;				
OC	Cypriniformes; Cyprinidae; Danio.				
OX	NCBI_Taxid=7955;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Embryo;				
RX	MEDLINE=94128602; PubMed=82977791;				
RA	Bierkamp C.; Campos-Ortega J.A.;				
RT	"A zebrafish homologue of the Drosophila neurogenic gene Notch and				
RL	its pattern of transcription during early embryogenesis.";				
CC	Mech. Dev. 43:87-100(1993).				
CC	-1- FEMORO: IMPLICATED IN CELL FATE SPECIFICATIONS DURING				
CC	EMBRO DEVELOPMENT. MAY BE INVOLVED IN THE FORMATION OF THE				
CC	NEURAL PLATE, NOTOCHORD AND BRAIN VESICLES.				
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein.				
CC	-1- DEVELOPMENTAL STAGE: EXPRESSED IN ALL CELLS IN PREGASTRULATION				
CC	STAGES. DURING GASTRULATION IS DIFFERENTIALLY EXPRESSED,				
CC	ACCUMULATING PREDOMINANTLY IN THE PRECHORDAL MESODERM AND				
CC	NOTOCHORD. AT THE END OF GASTRULATION, EXPRESSED ALONG THE				
CC	ANTERIOR-POSTERIOR AXIS INCLUDING THE DEVELOPING NEURAL PLATE				
CC	AND DIFFERENTIATING MESODERM. ALSO PRESENT IN THE DEVELOPING				
CC	BRAIN AND HEAD REGIONS.				
CC	-1- SIMILARITY: HIGH, WITH OTHER NOTCH-TYPE PROTEINS.				
CC	-1- SIMILARITY: CONTAINS 36 EGF-LIKE DOMAINS.				
CC	-1- SIMILARITY: CONTAINS 3 LIN/NOTCH REPEATS.				
CC	-1- SIMILARITY: CONTAINS 6 ANK REPEATS.				
CC	-----				
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CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> .				
CC	-----				

[illegible]

Query Match	Best Local Similarity	2.7%	Score 98.5	DB 1	Length 1447
Matches 97	Conservative 61	Mismatches 176	Indels 125	Gaps 21	
20 SLERLMEPDTRARCSLGLSCHLMDGDVLCPLGSLQSPAPVLPTRLRQTEVLV-----R 73					

[illegible]

Lung tumors  
Oncogene 10:2179-2183(1995).  
[2]  
REVIEWS.  
Gray D.A.;  
Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.  
[3]  
SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.  
MEDLINE-98124180; PubMed-9464533;  
Frederick A., Rolfe M., Chiu M.I.;  
The human UBP locus at 3p21.31 encodes two tissue-selective,  
cytoplasmic isoforms with dualubiquitinating activity that have reduced  
expression in small cell lung carcinoma cell lines.  
Oncogene 16:153-165(1998).  
-1- CATALYTIC ACTIVITY: Ubiquitin C-terminal thiolester + H(2)O =  
ubiquitin + a thiol.  
-1- SUBCELLULAR LOCATION: Cytoplasmic.  
-1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; UNPBL (SHOWN HERE) AND UNPES;  
ARE PRODUCED BY ALTERNATIVE SPLICING.  
-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C19; ALSO KNOWN AS  
FAMILY 2 OF UBIQUITIN CARBOXYL-TERMINAL HYDROLASES.  
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or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
EMBL: U20657; AAB72237.1;  
EMBL: AF017305; AAC27355.1;  
EMBL: AF017306; AAC27356.1;  
MEROPS: C19.010;  
MIM: 603486;  
InterPro: IPR001394; UCH-2.  
Pfam: PF00442; UCH-1; 1.  
Pfam: PF00443; UCH-2; 1.  
PROSITE: PS00972; UCH\_2\_1; 1.  
PROSITE: PS00973; UCH\_2\_2; 1.  
PROSITE: PS00235; UCH\_2\_3; 1.  
Ubiquitin conjugation; Hydrolase; Thiol protease; Multigene family;  
Proto-oncogene; Alternative splicing.  
ACT\_SITE 311  
ACT\_SITE 873 873  
ACT\_SITE 881 881  
VARSELIC 232 279  
BY SIMILARITY.  
KSTRAPSRNFTTSPKSSASPSYSSASLIANGDSTSTCGMH  
SSGVSRG -> N (IN ISOFORM UNPES).  
C->A: LOSS OF ACTIVITY.  
S -> R (IN REF. 3).  
R -> S (IN REF. 3).  
MUTAGEN 311 311  
CONFLICT 373 373  
CONFLICT 744 744  
SEQUENCE 963 AA; 108564 MW; 1B62B752P9410CD7 CRC64;  
Query Match 2.7%; Score 97; DB 1; Length 963;  
Best Local Similarity 20.1%; Pred. No. 7.1;  
Matches 107; Conservative 66; Mismatches 189; Indels 170; Gaps 26;  
3 VSMFLSLALGRNVVSLERMEQDTRARCSLGSCHLMGDVCLPSGLQSPGVL- 61  
133 VEYVLLLELKCEN-----SDPTN-----LSCHFSKADPTI--AVTEKMRKLFN 174  
62 VPRRLQTELVLRCPKT-----DCAL-----RVRVYVLAHVGHAPEEAGSD 106  
175 IPAPERERLRNKNKTSNTYEQSLKNDNTVQDACLTOGQVAVTEQNEGTV--PROTLQSK 232  
107 SELQESRN-----ASLQAVVLSFQAYPIARCALLEVOV----- 140  
233 SSTAPSRNFTTSPKSSASPSYSSASLIANGDS--TSTCGMHSSGVSRSRGSGFSASYNCQ 290  
141 --PADLVQPOQ-SVGSANVFQDFEASLGLAEVQIWSYTKP-----RYQELNLTQQLPD 189  
291 EPPSSHQPGSLGSLGNLGNCTF--MNSALQCLSTWAPLPLDYFLKDEYEAEIN----- 340

QY 190 GDNVL-LTLVSEEDQDFSLTLRPPVDAKLSM-----YKNLNG---PONTTL 234  
Db 341 RDNPLGKMGELAE-----AYAEILKQWMSGRDAHVAPSMFTQVGRFAPQFSGY 389  
QY 235 NHTDLVPCLCIQVMSLEPDSERVEPCF-----REDGARNHNLHIALRYLS--- 282  
Db 390 QOQSOELLAEFLDLHEDLNVRKKPYLELDKANGRPDAVVAKEAMENHRNDSDYVD 449  
QY 283 --PEVMQDAPCCLEPGKTYLCAQADQSPQPLVPPYPOKNATYNE-----POD----- 329  
Db 450 TEHGLFSTLYVCECAKSVTF-----DPCYLLTLP.LPKKDRMEVELVPADHCRPTQ 504  
QY 330 ----FOLVAGHPNLGVOSTWEKVOLQACSMADSLG--PFKDDMLVEMKGLNNT----- 379  
Db 505 YRVVPLPLGANSVDLCALSRSLGIAENNVADVYNHRFK--TFQMDCLNIMPDD 561  
QY 380 ----SVC--ALEPSCGCTPL-----PSMASTRARLGEELLODFRSHQ 415  
Db 562 IFVEYECSTVDSGSECYTLPPYFRERKSRPSSASALYGGPILLSVPKHK 613  
RESULT 14  
ID RYR3\_HUMAN STANDARD: PRT: 4870 AA.  
AC 015413; 015412; 015175;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Ryanodine receptor 3 (brain-type ryanodine receptor) (RYR3) (RYR-3)  
GN DE (Brain ryanodine receptor-calcium release channel).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND VARIANTS.  
RC TISSUE-Petal brain;  
RX MEDLINE-98175492; PubMed-9515741;  
RA Leeb T., Brienly B.;  
RT cDNA cloning and sequencing of the human ryanodine receptor type 3  
RT (RYR3) reveals a novel alternative splice site in the RYR3 gene.;  
RN FEBS Lett. 423:367-370(1998).  
[2]  
RN SEQUENCE FROM N.A. (ISOFORM 2), AND TISSUE SPECIFICITY.  
RC TISSUE-Brain;  
RX MEDLINE-98055474; PubMed-9395096;  
RA Nakashima Y., Nishimura S., Maeda A., Barsoumian E.L., Hakamata Y.,  
RA Nakai J., Allen P.D., Imoto K., Kita T.;  
RT Molecular cloning and characterization of a human brain ryanodine  
RT receptor.;  
RN FEBS Lett. 417:157-162(1997).  
[3]  
RN SEQUENCE OF 520-660 FROM N.A., AND TISSUE SPECIFICITY.  
RC TISSUE-Skeletal muscle;  
RX MEDLINE-98268728; PubMed-9607712;  
RA Martin C., Chapman K.E., Seckl J.R., Aschley R.H.;  
RT Partial cloning and differential expression of ryanodine  
RT receptor/calcium-release channel genes in human tissues including the  
RL hippocampus and cerebellum.;  
RN Neuroscience 85:205-216(1998).  
[4]  
RN SEQUENCE OF 3943-4870 FROM N.A.  
RC TISSUE-T-cell;  
RX MEDLINE-95010709; PubMed-7523185;  
RA Hakamata Y., Nishimura S., Nakai J., Nakashima Y., Kita T., Imoto K.;  
RT Involvement of the brain type of ryanodine receptor in T-cell  
RT proliferation.;  
RN FEBS Lett. 352:206-210(1994).  
[5]  
RN SEQUENCE OF 4644-4842 FROM N.A.  
RC TISSUE-Cervical carcinoma, and Hepatoma;



```

1017 PRLVYVYALDE---FKKSNRSLREAVRTFVG-YGYNIER-----SDQELADSAVERKVS 1067
0Y AOVVLSF---QAVPIARCAL---LEVOVPADLVOPGOSVGSVAFDCE--EASIGAEVOIMS 171
1068 IDKIRFERERSAVASGKMYEFEEVYTGDM-----RVGNARPCRDVEYEGADQAFV 1122
0Y 172 YTKPRYOK-----ELNLQQLPDGDNVLLTLDVSEODFSFLYLKRPVPALKSIMYKN 225
1123 FEGNNGORWHOSGSGYFGRTWQPDGVVCGMINLD-----DASMIFF-----T 1162
0Y 226 LTGPONITLNTDLDL-----VPCLCIOV-----WSLEPDSERVEF---C----- 260
1163 LNELLLITTKGSELAFADYEIENGFPICCLIGLSQIRMINIGTASTKFTYMCLOEGE 1222
0Y 261 -PFRDPCGHRNLM-----HIAIRVLSPCGWOLDAPCCJPGKYT----- 299
1223 EPEFVNMNRDVAMWFSKRLPTFVNVKRDHIEKMRIDG-----TWDSPCL--KYTHKTF 1276
0Y 300 -----LCWQAPDQSPCQPLVPPVPQKATVNEPQDFOLVAGHPNLCV 341
1277 GTONSNADMIYCRLSMPVECHSFSHSPC--LDSEAFQKRQME-----ILSHTTQCY 1329
0Y 342 QVSTWEKVQLOACSNADSLGPRFDDMLVEMKGTGLNNTSCALBPSGCTPLPSMASTRAA 401
1330 YAIRFACQDPCVWGVWVTP--DYHLXSEKEDLN-----KNCTVTVTLDDER-G 1376
0Y 402 RUGELLDQDFRSHQCMQNLNMDNMGSLMACPMKXIIHRWVLYVLACLL-LAAALFFELL 460
1377 RVHESV-----KSNCTYMWGGLVVS-----SORSNRSVNDLEIGCLVDLAMEGLSF-- 1424
0Y 461 LKQRRKARQSR-----TALLHSADAGYERLYGALASALSOMPLRAYV 506
1425 -----SANGKELCTCYOYENPTKYFPAVFLQPTSTSLFOELGKILKNA--MPLSAI 1474
0Y 507 DLMSRRELHANGALMFMHQRRIIDEGGVILLFSPAAYVACQOQMLQLOVEP 560
1475 -----FSEKKN-----PVQCPRLDVQTIOP 1497
RESULT 15
12ML MOUSE STANDARD: PRT: 1476 AA.
P28665;
01-DEC-1992 (Rel. 24, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Moringlobulin 1 precursor (MUG1).
MUG1 OR MUG-1.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A., AND SEQUENCE OF 28-57.
TISSUE=Liver;
MEDLINE=91358495; PubMed=1840592;
Overbergh L., Torrekens S., van Leuven F., van den Bergh H.;
Molecular characterization of the murinoglobulins.;
J. Biol. Chem. 266:16903-16910(1991).
J. FUNCTION: A PROTEINASE ACTIVATES THE INHIBITOR BY SPECIFIC
PROTEOLYSIS IN THE BAIT REGION, WHICH, BY AN UNKNOWN MECHANISM
LEADS TO REACTION AT THE CYSTEINYL-GLUTAMYL INTERNAL THIOLESTER
SITE AND TO A CONFORMATIONAL CHANGE, WHEREBY THE PROTEINASE IS
TRAPPED AND/OR COVALENTLY BOUND TO THE INHIBITOR. WHILE IN THE
TETRAMERIC PROTEINASE INHIBITORS STERIC INHIBITION IS SUFFICIENTLY
STRONG, MONOMERIC FORMS NEED A COVALENT LINKAGE BETWEEN THE
ACTIVATED GLUTAMYL RESIDUE OF THE ORIGINAL THIOLESTER AND A
TERMINAL AMINO GROUP OF A LYSINE OR ANOTHER NUCLEOPHILIC GROUP ON
THE PROTEINASE, FOR INHIBITION TO BE EFFECTIVE.
SUBUNIT: MONOMER.
TISSUE SPECIFICITY: PLASMA.
SIMILARITY: TO OTHER PROTEINS OF THE ALPHA-MACROGLOBULIN FAMILY,
INCLUDING COMPLEMENT COMPONENTS C3, C4, AND C5.

```

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CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
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CC -----
DR EMBL; M65736; AAA73048.1;
DR PIR; A41185; A41185.
DR HSSP; P01023; 1BV8.
DR MGD; MGI:99837; Mugi.
DR InterPro; IPR002890; A2M_N.
DR InterPro; IPR001599; Alpha_2_macroglbln.
DR Pfam; PF00207; A2M_1.
DR Pfam; PF01835; A2M_N.1.
DR PROSITE; PS00477; ALPHA_2_MACROGLOBULIN; 1.
KW Serine protease inhibitor; glycoprotein; plasma; bait region; signal;
KW Multigene family.
FT SIGNAL 1 27
FT CHAIN 28 1476 MORINGLOBULIN 1.
FT DOMAIN 677 734 BAIT REGION (APPROXIMATELY).
FT DISULFID 48 86 BY SIMILARITY.
FT DISULFID 251 276 BY SIMILARITY.
FT DISULFID 269 288 BY SIMILARITY.
FT DISULFID 461 555 BY SIMILARITY.
FT DISULFID 587 773 BY SIMILARITY.
FT DISULFID 634 680 BY SIMILARITY.
FT DISULFID 849 885 BY SIMILARITY.
FT DISULFID 923 1323 BY SIMILARITY.
FT DISULFID 1081 1129 BY SIMILARITY.
FT DISULFID 1354 1469 BY SIMILARITY.
FT THIOLEST 974 977 BY SIMILARITY.
FT CARBOHYD 55 55 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 294 294 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 313 313 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 500 500 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 749 749 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 776 776 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 871 871 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 993 993 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1142 1142 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1180 1180 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1426 1426 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 1476 AA; 165139 MW; D145D325B2DDDEAB CRC64;
Query Match 2.7%; Score 96.5; DB 1; Length 1476;
Best Local Similarity 20.5%; Pred. No. 14;
Matches 76; Conservative 47; Mismatches 161; Indels 87; Gaps 17;
0Y 67 QTELVRCPQ-----KTDCALRVVVVLAV-----HGWAEPEEA--- 102
DB 454 ETSILPNCQNIHTVOAHFILKGDGLVLRKELIFVLYMAGOSITOTGHTHOVEGEAPVK 513
0Y 103 GKSSLEOESRNASLOAOVLSFOAVPIARCALLEVOVPADLVOPGOSVGSVAFDCEAS 162
DB 514 GK-----FALEIPVEFSWVPKMKMLYTLPLDDEVIL-ADSVNEIRKCLRNK 559
0Y 163 LGAEVOIWSYTKPRQKELNLQQLPDGDNVLLTLDVSEODFSFLYLKRPVPALKSIM 222
DB 560 VDLRFST-SQSLPSSQTRLOVTA--POSTLGLAAVQOS-----VLLLRPESE-LEPSW 609
0Y 223 YKNLTGPONITLNTDLDL-----CLCIOV-----SLEPDSERVEFCPFREDP 266
DB 610 IYNLPQMG-----QNKFPVSSRLSDQEDCILYSSWLAKEHNLVHGHTKEDYRIVYEDM 664
0Y 267 G--AHRNLMHARLVLSPCWQOLDAPCC--LPKVTYLCWQAPDQSPCQPLVPPVPQKN 321
DB 665 GLTAFTNLMIRLPIYCFDGVNVPISAPRVEFDIAFTPEISWSIKRTLSKRPREP--PRKD 722
0Y 322 ATVNEPQDFOLVAGHPNLCVQVSTWEKVQLOACSNM-----DSLGRFDDMLLVEMKT 374

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Db	723	PSSNDPLETIRKYPETWV---	MDIVVNSIGLAEVENTVPDITLWKAGALCISNDT	778
Oy	375	GLNNTSYCALB	385	
Db	779	GLGLSSVPLQ	789	

Search completed: September 28, 2002, 19:43:34  
Job time: 282 sec



GenCore version 4.5  
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3M protein - protein search, using sw model

Run on: September 28, 2002, 17:59:47 ; Search time 43.34 Seconds  
(Without alignments)  
1494.329 Million cell updates/sec

Title: US-09-899-471-2  
Perfect score: 3605  
Sequence: 1 MPVSWFLSLALGRNPVVS.....SSEAPGCCBEMDLGPTTLE 674

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: PIR.71: \*  
1: PIR1: \*  
2: PIR2: \*  
3: PIR3: \*  
4: PIR4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	116	3.2	267	2 A38442	probable tumor sup
2	114.5	3.2	1013	2 B70841	probable helz prot
3	110	3.1	2910	2 T42214	otogelin - mouse
4	108.5	3.0	361	2 T39784	hypothetical prote
5	106.5	3.0	478	2 D75564	hypothetical prote
6	105.5	2.9	698	2 A62593	hypothetical prote
7	105.5	2.9	1451	2 B41185	alpha-2 macroglobu
8	105	2.9	1615	2 B49502	protein-tyrosine-p
9	105	2.9	1767	2 A49502	heparan sulfate pr
10	103.5	2.9	3707	2 S18252	hypothetical prote
11	103	2.9	851	2 T31520	probable transcrip
12	103	2.9	906	2 G83156	protein-tyrosine-p
13	102.5	2.8	1711	1 A55148	alpha-2 macroglobu
14	101.5	2.8	1476	2 A41185	tumor suppressor p
15	100	2.8	1447	2 A54100	gelation factor AB
16	99.5	2.8	2647	2 A31098	complement C4 - ch
17	99	2.7	1617	2 T28153	transmembrane prot
18	99	2.7	3014	1 JCS620	genome polyploid
19	99	2.7	3014	1 JCS620	probable transcrip
20	98.5	2.7	824	2 H90647	ATP-dependent heli
21	98	2.7	824	2 H90647	helicase, ATP-depe
22	98	2.7	824	2 H90647	nestin - human
23	97.5	2.7	1618	2 S21424	protein-tyrosine-p
24	97.5	2.7	1763	2 T17465	telomerase-associa
25	97.5	2.7	1894	2 C54689	conserved hypochet
26	97.5	2.7	2629	2 T30987	ubiquitin thiolest
27	97	2.7	604	2 G83091	ATP-dependent heli
28	97	2.7	963	2 T09478	
29	96.5	2.7	813	2 AF0526	

30	96.5	2.7	1187	2 JF0347	hypothetical prote
31	96.5	2.7	1691	1 D54689	protein-tyrosine-p
32	96.5	2.7	2535	2 T04824	hypothetical prote
33	96	2.7	564	2 D96017	probable peptidase
34	95	2.6	1573	2 S01845	DNA (cytosine-5')-
35	95	2.6	10223	2 T30225	polyketide synthas
36	94.5	2.6	445	2 E70854	probable membrane
37	94.5	2.6	837	2 A34898	granulocyte colony
38	94.5	2.6	6260	2 T30228	polyketide synthas
39	94	2.6	509	2 JC5288	SHP substrate-1 pr
40	94	2.6	513	2 JC5289	transcription fact
41	93.5	2.6	927	2 A48085	hypothetical prote
42	93.5	2.6	1513	2 T23681	protein unc-22 (lm
43	93.5	2.6	6831	2 A88852	twitchin (stimlari
44	93.5	2.6	6839	2 S57242	hypothetical prote
45	93.5	2.6	7160	2 T27935	

ALIGNMENTS

RESULT 1  
A38442  
probable tumor suppressor - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 18-Oct-1991 #sequence\_revision 18-Oct-1991 #text\_change 16-Feb-1997  
C:Accession: A38442  
R:Nigro, J.M.; Cho, K.R.; Fearon, E.R.; Kern, S.E.; Ruppert, J.M.; Oliner, J.D.; Kinz  
Cell 64, 607-613, 1991  
A:Title: Scrambled exons.  
A:Reference number: A38442; MUID:91121517  
A:Accession: A38442  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-267 <NIG>  
A:Cross-references: GB:M63696; GB:M63700; GB:M63702; GB:M63718; GB:M63698  
C:Keywords: transmembrane protein

Query Match	3.2%	Score 116:	DB 2:	Length 267;				
Best Local Similarity	25.6%	Pred. No. 0.13;						
Matches	72;	Conservative 31;	Mismatches 100;	Indels 78; Gaps 16;				
QY 155	VEDCFEASLGA	VOIWSYTKPRYQKELNITQOLPD	-----GDNVLLTL	DVSEEDFSFL 209				
DB 8	LYOC-EASL	GGSGIISRYAKAVAPLRLSOTESYTA	FMGDTVLKCEVIGE	-----59				
QY 210	YLRFVPPAL	KSLWKYNLGPONITLHND	-----LVPCLC	QVWSLEPDSER	VEFCPPRED 265			
DB 60	---PMPT	---HMQRN	---QODL	PIPGDSRVVLP	SGALQISRLD	GDIGITRCSAR-N 109		
QY 266	PGARNLMLH	RLRYLSPGVOLDAPCCIPGRKVTLC	QWAPD	---OSP	COPLVPVP	-----OK 320		
DB 110	PASRT	---GNEAEV	RLTSP	---PFLN	HPSNL	-----YKES	NDIEFCVSGK	PFTVMMK 162
QY 321	NATYNEPO	DFOLVAGHPNL	CVQVSTWEK	VQLOAC	SNADISGPK	DD	---ML	LVEMKTGL 376
DB 163	NGDVVPS	DFQIVGSGSMRI	-----	SG	---LG	VVKSDEG	FQVCAV	ENEGN 204
QY 377	NNTSV	CALEPSCGTP	PLPS	-----	MASTRARL	403		
DB 205	AQTS	AOILVFK	---PI	SSSVLP	SPARPDV	VPVPLVSS	RFVRL 242	
RESULT 2								
B70841								
C:Species: Mycobacterium tuberculosis								
C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998								
C:Accession: B70841								
R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon								
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holtroyd,								
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skellton, S.; Squares, S.								

Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 17-Mar-2000

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D0      59 KVVHTEKLOLKR-----TVLHRAI-SHCS-----ACAGSKEVLOTWDLAANTTY 102

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Db 303 ASGGVAFAPQTPAECLLAARRSLGRLEPLLGRRSPAQVA-----HEAQVQA 347

Oy 570 LSCVLEDFELOGRATGRVGVYFDGLHPDSVSPSPRVA---PLEST---PTQLPA---FL 620

Db 348 ALTHLP-----HYAAQVOQAAERNAASAEPREAAATDPLVGREAGPVLATGHEI 399

Oy 621 DALGGCSTSGACRPADPRAVERVYQALRSAL 649

Db 400 VEPGSPDPLEVRLPGDRLLTLRPDYRAEL 428

RESULT 6

AB82593

hypothetical protein XP\_2169 (imported) - Xylella fastidiosa (strain 9a5c)

C:Species: Xylella fastidiosa

C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000

C:Accession: AB82593

R:Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq

Nature 406, 151-157, 2000

At:Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A:Reference number: AB82515; MUID:20365717

A:Note: for a complete list of authors see reference number A59328 below

A:Accession: AB82593

A:Status: preliminary

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-698 <SIN>

A:Cross-references: GB:AE004030; GB:AE003849; NID:g9107292; PIDN:AF84968.1; GSPDB:GN

A:Experimental source: strain 9a5c

R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.

R:Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carre

as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.

submitted to Genbank, June 2000

A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La

chado, M.A.; Madeira, A.M.F.; Martins, H.M.F.; Marino, C.L.; Marques, M.V.; Martins

A:Authors: Mattheis, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.

, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmiter,

A:Authors: V. Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawa

A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silv

M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.

A:Reference number: A59328

C:\Genetics:						
A:Gene: KF2169						
Query Match	2.9%;	Score 105.5;	DB 2;	Length 698;		
Best Local Similarity	20.4%;	Pred. No. 3;				
Matches 142;	Conservative	84;	Mismatches 257;	Indels 213;	Gaps 34;	
QY	9 SLAIGRPVVVVSLERLME-----PDTA-RCSLGSLCHMDVDVLCPGSQA--PCPV 60	: : :   :	:   :   :	:	:	
Dd	150 TIALRRGVDDALMTLSQAVELLPEEPAYLFESLGA-VLKQHIAFAERFQRITELNPH 208	:	:	:	:	:
OY	61 LVPRRLDTLVLRCKTKTICALRV-RVYVHL-----AVGHWAERE-EAGKSDSELOES 112	: :   :	:   :   :	:	:	
Dd	209 VTPFRALLIQAORGRILDALARILEBALSPEDGYPAHRTTGFEFLLAGHPDRALTTL 268	:	:	:	:	:
OY	113 RNASIAQQVTVSFQAVPIARCALLEVOVPADLVQGSGSVSAVFDFCFEASLGAEVOLWTSY 172	: :   :	:   :   :	:	:	
Dd	269 R-----QVLTWPDPDPRLLLEALLTKAKOLDMDDDRATFTDALD----- 307	:	:	:	:	:
OY	173 TKPRYKEELNTQQLPDCGNVILTTDY----SEBDSFFLYLIRVPDAKLKSIMYKNLTG 228	: :   :	:   :   :	:	:	
Dd	308 IKRP-----NHDLMLARLVAAPVGSDEARIVTERILSNMREHLPAL--ETLMS 353	:	:	:	:	:
OY	229 PONTLNHTDLVPLCLCIQVWSLEP----DSERVEFCFPREDPGAHRNLMHIARLVLSPG 284	: :   :	:   :   :	:	:	
Dd	354 LHMID-NNPFAETAJARQIVAIEGRISGEORIYEALLQOREPT----- 396	:	:	:	:	:
OY	285 WMODAPCCCELGKVTLQMADPOSSCOPLVPPVFOKNATVNPR---OD-----FOLVAG 335	: :   :	:   :   :	:	:	
Dd	397 -----ATAACL-----QQLIESVEHEHTILRPMGLGVODRAGOFE--- 431	:	:	:	:	:



[illegible]

A:Residues: 13707 <NO>  
A:Cross-references: EMBL:M77114; NID:g200295; PIDD:AAA39911.1; PID:g200296  
R: Noonan, D.M.; Horigan, E.A.; Ledbetter, S.R.; Vogeli, G.; Sasaki, M.; Yamada, Y.; H  
J. BIOL. Chem. 263, 16379-16387, 1988  
A:Title: Identification of cDNA clones encoding different domains of the basement mem  
A:Reference number: A92680; MWID:89034110  
A:Accession: A31917  
A:Molecule type: mRNA  
A:Residues: 940;1601 <NO2>  
A:Cross-references: GB:J04054; NID:g200252; PIDD:AAA39899.1; PID:g200253  
A:Accession: B31917  
A:Molecule type: mRNA  
A:Residues: 1870-2600 <NO3>  
A:Cross-references: GB:J04055; NID:g200300; PIDD:AAA39912.1; PID:g200301  
R: Schulze, B.; Mann, K.; Battistutta, R.; Wiedemann, H.; Timpl, R.  
Eur. J. Biochem. 231, 551-556, 1995  
A:Title: Structural properties of recombinant domain III-3 of perlecan containing a g  
A:Reference number: S66460; MWID:95377282  
A:Accession: S66460  
A:Molecule type: protein  
A:Residues: 1272-1274, 'X', 1276, 'X', 1278-1279 <SCH>  
C:Superfamily: LDL receptor ligand-binding repeat homology; laminin G r  
C:Keywords: glycoprotein  
F:199-234/Domain: LDL receptor ligand-binding repeat homology <LDL1>  
F:285-319/Domain: LDL receptor ligand-binding repeat homology <LDL2>  
F:325-359/Domain: LDL receptor ligand-binding repeat homology <LDL3>  
F:368-403/Domain: LDL receptor ligand-binding repeat homology <LDL4>  
F:764-811/Domain: laminin-type EGF-like homology <LEG>  
F:1159-1206/Domain: laminin-type EGF-like homology <LEG7>  
F:1563-1610/Domain: laminin-type EGF-like homology <EG7>  
F:1613-1668/Domain: laminin-type EGF-like homology <LEG8>  
F:3163-3198/Domain: EGF homology <EGF>  
F:3270-3423/Domain: laminin G repeat homology <LG2>  
F:3464-3492/Domain: EGF homology <EGF7>  
F:126, 1891, 2336, 2394, 2427/Binding site: carbohydrate (Asn) (covalent) #status predic

	Query Match	2.9%	Score 103.5;	DB 2;	Length 3707;	
	Best Local Similarity	20.5%;	Pred. No. 36;			
	Matches 87;	Conservative 44;	Mismatches 167;	Indels 127;	Gaps 19;	
OY	EPQPLARSLG-LSCHTW--DGDVLCRLGSLOS-----APGVLYPTRQLTELYLR-----	73				
Db	EPNEPA-CENGHCALKLWRCDDEDFCEDRTIDANCYSVKQPGVEGCPTHHQCVSTNRCIPA	384				
OY	74 ---CPOKTDCAILRVVVVHLAVHGMAREPEEAKGSDSELOSRNASIQAQVYLSPQAYPI	130				
Db	385 SFHDSESDCDR-----SDEGCMPROYVTTPROSIDA-----	418				
OY	131 ARCALLEYQPADVLQPGQSOGSAVEDCFEASISAEVOIMSYTKERYOKELNLTOOLPDG	190				
Db	419 -----SRQGTV---TFTCVANGVPRIINMRLNMGHIPAHPRVMTSSEG	460				
OY	191 DNVLITLDVSEODESFLL-----YLRPYPDALSKLMTKKYLTERPN--ITLNHTDLVP	241				
Db	461 RGTLLIRQVKADGAGALYCCEAMNSRGMTFGIPDGYLELVPPQSGPCPDGHFYLEDASCIP	520				
OY	242 CICIOWNISLEPDSEREVERCEPFREDGGAFNRMLNHISGLVLSFGVMQDLAPCLLP-KTYL	300				
Db	521 CFEGCGVINVCSSLR-----FRD-----QIRLU-----SFDPANDKFVNNTY	557				
OY	301 CWQAPDPSPCQPLVPVPVQKNATVNER-QDEFOLVAGHNLCZOVSTWEKVQLOACSMADS	359				
Db	558 -----PSQGPVPLPSSTOQLDIRPALQDEROYVDSLRFVLVDHAFMLPKQFLGNKYDS	609				
OY	360 LGPRKDMILEAKTGLNNTSVCALEP-----SGCTPL-PSMASTRAA	401				
Db	610 YGGELARKKVRLETARGM-----LEPVOKEDVILVGAGYRLHSRGHPRHGTGLNQGV	662				
OY	402 RLGEF 406					
Db	663 QLSFE 667					



Accession: A41185

70 LVLRCPOKTCALRV-----RVVHLAVHGMAPEEFAGKSDSELOESRNASLQAOVLSF 125





GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 28, 2002, 19:39:44 : Search time 62.3 Seconds

(without alignments)  
1244.454 Million cell updates/sec

Title: US-09-899-471.5  
Perfect score: 3741  
Sequence: 1 MPVSWFLSLALGRNPVVS.....SSEAPCCCEMDLPCTTLE 698

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

A\_Geneseq\_032802:\*

- 1: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:\*
- 2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:\*
- 3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:\*
- 4: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:\*
- 5: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:\*
- 6: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:\*
- 7: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:\*
- 8: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:\*
- 9: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:\*
- 10: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:\*
- 11: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:\*
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- 14: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:\*
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- 19: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:\*
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- 21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:\*
- 22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2389.5	63.9	692	AAB61880	Human cytokine rec
2	2376	63.5	705	AAU29322	Human PRO polypept
3	2376	63.5	705	AAU04956	Human Interleukin
4	2376	63.5	705	AAB87606	Human PRO20040. H
5	2376	63.5	705	AAB61884	Chimeric Zcytor14
6	2314	61.9	675	AAB61885	Chimeric Zcytor14
7	2300.5	61.5	688	AAB61883	Chimeric Zcytor14
8	1888.5	50.5	575	AAB61881	Human variant Zcyt
9	1088.5	29.1	309	AAV76143	Human secreted pro
10	971.5	26.0	332	AAW25864	Human protein sequ
11	875.5	23.4	267	AAB88448	Human membrane or

12	591.5	15.8	204	AAE10920	Human gene 12 enco
13	312	8.3	617	AAV76048	Murine skin cell p
14	312	8.3	617	AAE55987	Skin cell protein,
15	310.5	8.3	667	AAU04957	Human Interleukin
16	177	4.7	864	AAW04184	Murine Interleukin
17	177	4.7	864	AAW61271	Mouse Interleukin
18	177	4.7	864	AAW92408	Murine IL-17R prot
19	177	4.7	864	AAV99935	Murine IL-17R prot
20	177	4.7	864	AAV97130	Murine Interleukin
21	177	4.7	864	AAV97180	Murine Interleukin
22	177	4.7	864	AAV97180	Murine Interleukin
23	177	4.7	864	AAV97180	Murine Interleukin
24	177	4.7	864	AAV97180	Murine IL-17R poly
25	150.5	4.0	330	AAV72748	Murine skin cell s
26	150.5	4.0	330	AAV72748	Skin cell protein,
27	147.5	3.9	866	AAW55886	Human Interleukin
28	147.5	3.9	866	AAW61272	Human Interleukin
29	147.5	3.9	866	AAW92409	Human IL-17R prote
30	147.5	3.9	866	AAV99941	Human IL-17R prote
31	147.5	3.9	866	AAV97131	Human Interleukin
32	147.5	3.9	866	AAV97181	Human Interleukin
33	147.5	3.9	866	AAW03807	Human Interleukin
34	147.5	3.9	866	AAW62066	Human IL-17R (hCTL
35	147.5	3.9	866	AAV72754	Human Interleukin
36	130	3.5	1042	ABG26706	Human Interleukin
37	119.5	3.2	1013	AAW81163	Novel human diagno
38	112	3.0	1447	AAW8553	Mycobacterium tube
39	112	3.0	1447	AAW33498	Deleted in colorec
40	112	3.0	1447	AAW50693	Human DCC protein.
41	112	3.0	1728	AAW13144	Human UNC-40 prote
42	111.5	3.0	877	AAW28379	Deleted in Colorec
43	111	3.0	2969	AAW56442	Novel human diagno
44	108	2.9	997	ABG08088	Fragment HGJ1737 o
45	107.5	2.9	1433	ABG08373	Novel human diagno

#### ALIGNMENTS

RESULT 1	
AA61880	standard: Protein; 692 AA.
AA61880;	
AC	
XX	
DT	08-MAY-2001 (first entry)
XX	
DE	Human cytokine receptor Zcytor14.
XX	
KW	Cytokine receptor; Zcytor14; human; inflammation; rheumatoid arthritis;
KW	antiflammatory; gene therapy; vaccine.
XX	
OS	Homo sapiens.
XX	
PN	W0200104304-A1.
XX	
PD	18-JAN-2001.
XX	
PF	30-JUN-2000; 2000WO-US18383.
XX	
PR	07-JUL-1999; 99US-0348854.
XX	
PA	(ZYMO ) ZYMOGENETICS INC.
XX	
PI	Presnell SR, Burkhead SK, Powderder SL;
XX	
DR	WPI; 2001-112618/12.
DR	N-PSDB; AAC85027.
XX	
PT	New polypeptide encoding a human cytokine receptor Zcytor14, for
PT	treating inflammation e.g. rheumatoid arthritis -
XX	
PS	Claim 2; Page 2; 112pp; English.

The invention provides a new human cytokine receptor designated zcytor14. zcytor14 can be expressed by standard recombinant methodology. The encoding nucleic acid is useful for detecting the expression of a zcytor14 gene in a biological sample. Anti-zcytor14 antibodies can be used to screen biological samples in vitro for the presence of zcytor14 proteins, polypeptides and peptides having zcytor14 activity can be administered to a subject who lacks an adequate amount of this polypeptide, for treating inflammation and conditions such as rheumatoid arthritis. In contrast, zcytor14 antagonists (e.g. anti-zcytor14 antibodies) can be used to treat a subject who produces an excess of zcytor14. zcytor14 nucleotide sequences can also be used to provide zcytor14 to a subject. The present sequence represents the human cytokine receptor zcytor14.

Sequence 692 AA:

Query Match 63.9%; Score 2389.5; DB 22; Length 692;  
Best Local Similarity 67.0%; Pred. No. 5.4e-218;  
Matches 464; Conservative 66; Mismatches 138; Indels 25; Gaps 5;

```

1 MPVSWELSLALGNFVSVLERLMEPDTARCSLGLSCHLMDGVLCPLGSLQASAPGV 60
1 mvpwflslalgnfvsvlerlmeptdarcsllglschlmddvllcplgslqasapgv 60
1 lpprflqltelvrlrcpqrtdcalrvrvvhlavhghmaeppe---AGKSDSELQESRNAS 116
1 lpprflqltelvrlrcpqrtdcalrvrvvhlavhghmaeppe---AGKSDSELQESRNAS 116
61 laptlhlqetelvirckqetcdclclraavhlahvhwpeedeekfgsaadsgveepnas 120
61 laptlhlqetelvirckqetcdclclraavhlahvhwpeedeekfgsaadsgveepnas 120
117 LQAGVVLSPQAFVIRACALLEVVPADLVQPGOSVGSVAFECFASLGAEOIWTSTKR 176
117 lqagvvlspqafviracallevvpadvlqpgosvgsvafecfaslgaioiwtstkr 176
121 lqagvvlspqafviracallevvpadvlqpgosvgsvafecfaslgaioiwtstkr 180
121 lqagvvlspqafviracallevvpadvlqpgosvgsvafecfaslgaioiwtstkr 180
177 YQKELINLQOQLPDCRGLLEVNDSTQSCVNLFWLNTSTGDNVLTLDVSEEDQFSLTYLR 236
177 yqkelinlqoqlpdcrglleevndstqscvnlfwlntstgdnvltldvseedqfsltylr 236
181 yekelnhqqlp-----alpwlnvsadgdnvhlvlnveeqhffgslslym 225
181 yekelnhqqlp-----alpwlnvsadgdnvhlvlnveeqhffgslslym 225
237 PVPDAKLKLYNLTNGPQNTLNTLNTLNTLNTLNTLNTLNTLNTLNTLNTLNTLNTLNTL 296
237 pvpdaklklynltnpqnltlntlntlntlntlntlntlntlntlntlntlntlntlntl 296
226 qvqgppkprwhnltlqplltlntclvpcclqgvvlpdpvstnltclpfredprahqnl 285
226 qvqgppkprwhnltlqplltlntclvpcclqgvvlpdpvstnltclpfredprahqnl 285
297 WHIARLVLSFGWQMDAPCCLPBGKVTLCQAPDQSPQPLVPPVPOKNATYNEQDFOL 356
297 whiarlvlsfgwqmdapccllpbgkvtlclqapdqspqplvppvpoknatyneqdfol 356
286 wgaarllrltlqswllldpcslpaeealclwraqgdcqplvpplswenlvdkylefpl 345
286 wgaarllrltlqswllldpcslpaeealclwraqgdcqplvpplswenlvdkylefpl 345
357 VAGHPNLCVOVSTWKEVQLOQASWADSLGPFKDDMLVEMKTLGNTSVCALPESGCPPL 416
357 vaghpnlcvoovstwkevqloqaswadslgpfkddmlvemktlgntsvcalpescgcppl 416
346 lkgpnlclvqynsskclqclqecclwadsipklkdvllletlqpgdnzslcalpsqctsl 405
346 lkgpnlclvqynsskclqclqecclwadsipklkdvllletlqpgdnzslcalpsqctsl 405
417 PSMASTRARLGEELLQDFRSQCMQMLMNDNGSLMACPMKXYIHRWVVLWTLACLTLA 476
417 psmastrarlgellqdfrrsqcmqlmndngslmacpmkxyihrwvvlwtlaccltla 476
406 pskastreaarlgelyllqdlqsgcqlw-dddlgalacpmkylhkrwvvlwtlaccllfa 464
406 pskastreaarlgelyllqdlqsgcqlw-dddlgalacpmkylhkrwvvlwtlaccllfa 464
477 AALFFELLKTRDRRAKRSRTRALLHSHADAGYERLVGALASLSQMLRVAVDLMKSR 536
477 aalffellktrdrarakrsrtrallhshadagyerlvgalaslsqmlrvavdlnksr 536
465 aalsllllllkxkhaaaagaaagaaalllysaddsgferlvgalasclqplrvavdlwstr 524
465 aalsllllllkxkhaaaagaaagaaalllysaddsgferlvgalasclqplrvavdlwstr 524
537 ELAHHGALAMFHHORRRILOEGGVVILFSPAIVAOQOMLOQLTVER---GPHALAM 593
537 elahhgalamfhhorrriloeggvvillfspaivaoqomloqltver---gphalam 593
525 elsaqgppavfhaqtrqclqeggvvllflspgavalcsewldqdvsgpghaphafas 584
525 elsaqgppavfhaqtrqclqeggvvllflspgavalcsewldqdvsgpghaphafas 584
594 LSCVLPDFLOGRATRGVGVVFDGLHPDPSFPRVAPLFLPTOLPAFLDALOGGCT 653
594 lscvlpdflogratrgvgvvfdglhpdpsfprvaplflptolpafldaloggct 653
585 lscvlpdflogratrgvgvgacdrllhpdavpalftvryftlpsqldpfldgalqgprap 644
585 lscvlpdflogratrgvgvgacdrllhpdavpalftvryftlpsqldpfldgalqgprap 644
654 SAGRPADREVERVQALRSALDSC--TSSSEAPG 684
654 sagrpadrevervqalrsaldsc--tssseapg 684
645 rsgrlgeraegvralpaldsyfhnppgtpapg 677
645 rsgrlgeraegvralpaldsyfhnppgtpapg 677

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ID AAU29322 standard; Protein; 705 AA.
XX
XX
AC AAU29322;
XX
XX 18-DEC-2001 (first entry)
DT
XX
XX Human PRO polypeptide sequence #299.
DE
XX
KW PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;
KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200168848-A2.
XX
PD 20-SEP-2001.
XX
PF 28-FEB-2001; 2001WO-US06520.
XX
XX 01-MAR-2000; 2000WO-US05601.
XX 02-MAR-2000; 2000WO-US05841.
XX 03-MAR-2000; 2000US-187202P.
XX 06-MAR-2000; 2000US-186968P.
XX 14-MAR-2000; 2000US-189320P.
XX 14-MAR-2000; 2000US-189328P.
XX 15-MAR-2000; 2000WO-US06884.
XX 21-MAR-2000; 2000US-190828P.
XX 21-MAR-2000; 2000US-191007P.
XX 21-MAR-2000; 2000US-191048P.
XX 21-MAR-2000; 2000US-191314P.
XX 28-MAR-2000; 2000US-192655P.
XX 29-MAR-2000; 2000US-193032P.
XX 29-MAR-2000; 2000US-193053P.
XX 30-MAR-2000; 2000WO-US08439.
XX 04-APR-2000; 2000US-194449P.
XX 04-APR-2000; 2000US-194477P.
XX 11-APR-2000; 2000US-195975P.
XX 11-APR-2000; 2000US-196000P.
XX 11-APR-2000; 2000US-196187P.
XX 11-APR-2000; 2000US-196590P.
XX 11-APR-2000; 2000US-196820P.
XX 18-APR-2000; 2000US-198121P.
XX 18-APR-2000; 2000US-198585P.
XX 25-APR-2000; 2000US-199397P.
XX 25-APR-2000; 2000US-199550P.
XX 25-APR-2000; 2000US-199654P.
XX 03-MAY-2000; 2000US-201516P.
XX 17-MAY-2000; 2000WO-US13705.
XX 22-MAY-2000; 2000WO-US14042.
XX 30-MAY-2000; 2000WO-US14941.
XX 02-JUN-2000; 2000WO-US15264.
XX 05-JUN-2000; 2000US-209832P.
XX 28-JUL-2000; 2000WO-US20710P.
XX 22-AUG-2000; 2000US-0644848.
XX 24-AUG-2000; 2000WO-US23328.
XX 08-NOV-2000; 2000WO-US30952.
XX 01-DEC-2000; 2000WO-US32678.
XX 20-DEC-2000; 2000WO-US34956.
XX
XX (GETH ) GENENTECH INC.
XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
XX Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
XX MPI: 2001-602746/68.
XX N-PSDB; AAs46223.
XX
XX Novel nucleic acids encoding PRO polypeptides, used to diagnose the
XX presence of tumours, such as prostate and breast tumours, in mammals and
XX to screen for modulators of the compounds -

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PS Claim 11; Fig 598; 774pp; English.

CC Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.  
 CC The PRO polypeptides and their associated nucleic acids can be used to  
 CC detect the presence of a tumour in a mammal by comparing the level of  
 CC expression of a PRO polypeptide in a test sample of cells from the animal  
 CC and a control sample of normal cells, whereby a higher level of  
 CC expression in the test sample indicates the presence of a tumour in the  
 CC mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats  
 CC and rabbits but are preferably human. The polypeptides can be used to  
 CC stimulate tumour necrosis factor (TNF) alpha release from human blood,  
 CC when contacted with it. A specific polypeptide can be used to stimulate  
 CC the proliferation or differentiation of chondrocyte cells. The PRO  
 CC proteins can be used to determine the presence of tumours and also  
 CC susceptibility to tumour development, particularly adrenal, lung, colon,  
 CC breast, prostate, rectal, cervical, or liver tumours, in mammalian  
 CC subjects. The oligonucleotide probes specific for the PRO nucleic acids  
 CC can be used for genetic analysis of individuals with genetic disorders.

SO Sequence 705 AA:

Query Match 63.5%; Score 2376; DB 22; Length 705;  
 Best Local Similarity 65.9%; Pred. No. 1,1e-216;  
 Matches 466; Conservative 66; Mismatches 135; Indels 40; Gaps 7;

QY 1 MPVSWFLSLALGRNPVVSLERLMEPDOTAKCSLGLSCLMDVDVLCPLPSLQSGAPPV 60  
 DB 1 mpvswflslalgrnpvvsleerlmepdotakcsrlsclmdvdvclplpslqsgapppv 60  
 QY 61 LVPRLQTELVKRCPOKTPCALRVRYVHLAVGHMAEPPE---AKGSDSELOESRNAS 116  
 DB 61 lvprlqtelevkrcpoktpcalrvryvhlavghmaeppe---akgsdselesrnas 120  
 QY 117 LQAQVLSFGQVPIARCALLEVOVPADLVOPGSGVSAVDFCEASGAEVQINSGYRPR 176  
 DB 117 lqaqvlsfgyqvtarcllevqvpalvgfsgsvsvydfcefaagserirysytpcr 180  
 QY 177 YQKRLNLTQQLPDCGLEVRDSTIQSCWVLPMLNVSIDGDNVLLTLIDVSEEDFSLYLIR 236  
 DB 181 yekrlntlqqlpdcglevrdsstioscwvlpmlnvsidgdnvhlvlnvseeqhfjslywm 225  
 QY 237 PVPAKLSLWKNTLGPONITLHNTDLPVPCICQVMSLEPDSERVECFREDGARNRL 296  
 DB 226 qvqgppkprwhnlqppqlllnhdclvpclclqvwplepdsrvtnclptfedprahnl 285  
 QY 297 WHIARLNVLSFGVWOLDAPCCLPKGVTLQMOAPDOSFCPLVPPVPOKNATVNEPDQPL 356  
 DB 286 wgaarllrltqswltdapcspaaealcwrrapgdpcplvppiswenvtvdvyleppl 345  
 QY 357 VAGHPNLCVOVSTWKEVQLOACSMADSLGPFKDDMLLEVKKTGILNNTSVCLAEPSGCTPL 416  
 DB 346 lkgpnlcvqvnsekllqgeclwadsllgplkddvllltergpdnrlcalcpsgctsl 405  
 QY 417 PSMASTRAARAGEELLQDFRSHQOMLNDNMSGIMACMDKTYIHRRWLVYLACLILA 476  
 DB 406 pskastraarageyllqdlqsgcqlw-dddgalwacmdkyihrrwlvvylacllla 464  
 QY 477 AALFFLLKDKRRK-----AARGSRFALLSHASDAGCYERLVGALASALS 522  
 DB 465 aalsllllllkkdhakgylrltlkdvrrsgaary-raallllysdaddsfellvglaasalc 523  
 QY 523 QMPLRVAVDLMSRRRLSHAGLAWFHHRRIILQEGGVILLFSPAAYAOQOMLQQTIV 582  
 DB 524 qlplrvaavdlmsrrrlshaglawfhhrrililqeggvvllfspaayalcsewllqdgvs 583  
 QY 583 EP---GPHDALAAMLSVLPDPLQGRATRGVGVYFDGLLHPSVSPFRNAPLFSLPTQ 639  
 DB 584 gphaghdalraalscvlpdflqgratrgvsvygaacfdallhpadpalftlvpfvlpsq 643  
 QY 640 LPAFLDALQGGCSTSGAPRADVERVYTOALRSALDSC--TSSEAPG 684  
 DB 644 lpdfllgalqgrpraprsrqlgeraaqvralqpaldsyflnppgcpag 650

RESULT	3	AAU04956	standard; Protein; 705 AA.
ID	AAU04956	standard; Protein; 705 AA.	
XX	AAU04956;		
AC	24-OCr-2001 (first entry)		
XX	Human Interleukin 17 receptor, IL-17RH2.		
DE	Human Interleukin 17 receptor, IL-17RH2.		
XX	Human; Interleukin-17 receptor; IL-17RH2; agonist; antagonist;		
KW	PRO20040; DNA 164625-2890; systemic lupus erythematosus;		
KW	rheumatoid arthritis; osteoarthritis; diabetes mellitus;		
KW	allergic disease; asthma; demyelinating disease;		
KW	degenerative cartilaginous disorder; transplantation associated disease.		
XX			
OS	Homo sapiens.		
XX			
FH	Key	Location/Qualifiers	
FT	Peptide	1..20	
FT	Protein	/label- Signal_peptide	
FT	Region	21..705	
FT	Modified-site	/label- Mature_IL_17RH2	
FT	Region	107..112	
FT	Modified-site	/note- "N-myristoylation site"	
FT	Region	118..121	
FT	Modified-site	/note- "Asn is N-glycosylated"	
FT	Region	152..157	
FT	Modified-site	/note- "N-myristoylation site"	
FT	Region	186..189	
FT	Modified-site	/note- "Asn is N-glycosylated"	
FT	Region	198..201	
FT	Modified-site	/note- "Asn is N-glycosylated"	
FT	Region	211..214	
FT	Modified-site	/note- "Asn is N-glycosylated"	
FT	Region	238..241	
FT	Modified-site	/note- "Asn is N-glycosylated"	
FT	Region	248..251	
FT	Modified-site	/note- "Asn is N-glycosylated"	
FT	Region	319..324	
FT	Modified-site	/note- "N-myristoylation site"	
FT	Region	334..337	
FT	Modified-site	/note- "Asn is N-glycosylated"	
FT	Region	357..360	
FT	Modified-site	/note- "Asn is N-glycosylated"	
FT	Region	391..394	
FT	Modified-site	/note- "Asn is N-glycosylated"	
FT	Region	438..443	
FT	Modified-site	/note- "N-myristoylation site"	
FT	Region	453..473	
FT	Modified-site	/note- "N-myristoylation site"	
FT	Region	516..521	
FT	Modified-site	/note- "N-myristoylation site"	
FT	Region	552..555	
FT	Modified-site	/note- "CAMP/GMP-dependent protein kinase phosphorylation site"	
FT	Region	583..586	
FT	Modified-site	/note- "Glycosaminoglycan attachment site"	
FT	Region	612..617	
FT	Modified-site	/note- "N-myristoylation site"	
FT	Region	692..697	
FT	Modified-site	/note- "N-myristoylation site"	
FT	Region	696..701	
FT	Modified-site	/note- "N-myristoylation site"	
FT	Region	700..705	
FT	Modified-site	/note- "N-myristoylation site"	
XX			
PD	MO200146420-A2.		
XX	28-JUN-2001.		



DR N-PSDB: AAF92138.  
 XX Eighty four nucleic acids encoding PRO polypeptides, useful in  
 PT molecular biology, including use as hybridization probes, and in  
 PT chromosome and gene mapping.  
 PS  
 PS Claim 12; Fig 162; 278pp: English.  
 CC The present sequence is a human PRO polypeptide (secreted and  
 CC transmembrane). The PRO protein, and PRO agonists, PRO antagonists or  
 CC anti-PRO antibodies are useful for preparation of a medicament useful in  
 CC the treatment of a condition which is responsive to the PRO protein.  
 CC agonists, antagonists of anti-PRO antibodies. The PRO protein may also be  
 CC employed as molecular weight markers for protein electrophoresis. The PRO  
 CC coding sequence has applications in molecular biology, including use as  
 CC hybridisation probes, and in chromosome and gene mapping.  
 CC  
 XX Sequence 705 AA:  
 SQ  
 Query Match 63.5%; Score 2376; DB 22; Length 705;  
 Best Local Similarity 65.9%; Pred. No. 1.1e-216;  
 Matches 466; Conservative 66; Mismatches 135; Indels 40; Gaps 7;  
 QY 1 MPVSWFLSLALGRNVVVSLEERIMEPQDARCSLGLSCHIMDGVLCIPGSLQASPGV 60  
 DB 1 MPVSWFLSLALGRNVVVSLEERIMEPQDARCSLGLSCHIMDGVLCIPGSLQASPGV 60  
 QY 61 LVPTRQLQELVLRCPQKTDALRVVVVHLAVHGHMAEPPEE-----AGKSDSELQESRNAS 116  
 DB 61 LVPTRQLQELVLRCPQKTDALRVVVVHLAVHGHMAEPPEE-----AGKSDSELQESRNAS 116  
 QY 117 LQAOVLSFOAPVIRACALLEVOVPADLVOPGOSVGSVAVEPCFEASLGAEOIWSYTKPR 176  
 DB 117 LQAOVLSFOAPVIRACALLEVOVPADLVOPGOSVGSVAVEPCFEASLGAEOIWSYTKPR 176  
 QY 121 LQAOVLSFOAPVIRACALLEVOVPADLVOPGOSVGSVAVEPCFEASLGAEOIWSYTKPR 180  
 DB 121 LQAOVLSFOAPVIRACALLEVOVPADLVOPGOSVGSVAVEPCFEASLGAEOIWSYTKPR 180  
 QY 177 YQKELNLQOQLPDCRGLERVDSIOSCWVLPWLNSTGDNVLTLDVSEEDFSLTYR 236  
 DB 177 YQKELNLQOQLPDCRGLERVDSIOSCWVLPWLNSTGDNVLTLDVSEEDFSLTYR 236  
 QY 181 YQKELNLQOQLPDCRGLERVDSIOSCWVLPWLNSTGDNVLTLDVSEEDFSLTYR 225  
 DB 181 YQKELNLQOQLPDCRGLERVDSIOSCWVLPWLNSTGDNVLTLDVSEEDFSLTYR 225  
 QY 237 PVPDALKSLWYKNTLGPONTITLNTHTDLPVLCIQVWSLEPDSERVEPCFREDPGAHNTL 296  
 DB 237 PVPDALKSLWYKNTLGPONTITLNTHTDLPVLCIQVWSLEPDSERVEPCFREDPGAHNTL 296  
 QY 226 YQVGPQKPRWKNLTGPGITLTHTDLPVLCIQVWSLEPDSERVEPCFREDPGAHNTL 285  
 DB 226 YQVGPQKPRWKNLTGPGITLTHTDLPVLCIQVWSLEPDSERVEPCFREDPGAHNTL 285  
 QY 297 WHIALRLVSPGVWOLDARCCLEGGKVTLCQAPQOSPCQPLVPVPOKNAVNEPQDFOL 356  
 DB 297 WHIALRLVSPGVWOLDARCCLEGGKVTLCQAPQOSPCQPLVPVPOKNAVNEPQDFOL 356  
 QY 286 WQAALIRILLTGLSWILDAPCSIPAAALCWRAPGSDCPGLVPLSWENVTDKVLEFPL 345  
 DB 286 WQAALIRILLTGLSWILDAPCSIPAAALCWRAPGSDCPGLVPLSWENVTDKVLEFPL 345  
 QY 357 VAGHFNLCYOVSTWKEVVOLOACSWADSLGPFKDMILVEMKTGUNTGVCALEPSCGTPFL 416  
 DB 357 VAGHFNLCYOVSTWKEVVOLOACSWADSLGPFKDMILVEMKTGUNTGVCALEPSCGTPFL 416  
 QY 346 LKGNHNLGVNVSSEKIQIGECIWDASLIPKDVILLTRGPQDNZSCALEPSCGTS1 405  
 DB 346 LKGNHNLGVNVSSEKIQIGECIWDASLIPKDVILLTRGPQDNZSCALEPSCGTS1 405  
 QY 417 PSMASRAARLGEELQDRSHOCQMOIMNDNMGLWACPMKXTHRRVWLWACLILA 476  
 DB 417 PSMASRAARLGEELQDRSHOCQMOIMNDNMGLWACPMKXTHRRVWLWACLILA 476  
 QY 406 PKASTRAARLGEELQDRSHOCQMOIMNDNMGLWACPMKXTHRRVWLWACLILA 464  
 DB 406 PKASTRAARLGEELQDRSHOCQMOIMNDNMGLWACPMKXTHRRVWLWACLILA 464  
 QY 477 AALFFLLKTRRRK-----AARSGRTALLSHADGAGYERLVGALASALS 522  
 DB 477 AALFFLLKTRRRK-----AARSGRTALLSHADGAGYERLVGALASALS 522  
 QY 465 AALFFLLKTRRRK-----AARSGRTALLSHADGAGYERLVGALASALS 523  
 DB 465 AALFFLLKTRRRK-----AARSGRTALLSHADGAGYERLVGALASALS 523  
 QY 523 OMPLEVAVDLMSRRELISANGALAMFHNRRIIOEGGVILLFSPAVALCOQMOLOLQV 582  
 DB 523 OMPLEVAVDLMSRRELISANGALAMFHNRRIIOEGGVILLFSPAVALCOQMOLOLQV 582  
 QY 583 BP---GPHDALAMLSCLVLPDFLQGRATGRVGVFPDGLLPDSVSPFRVAPLPSLQPV 639  
 DB 583 BP---GPHDALAMLSCLVLPDFLQGRATGRVGVFPDGLLPDSVSPFRVAPLPSLQPV 639  
 QY 584 GPGAGHPHAFASISCVLPDFLQGRATGRVGVFPDGLLPDSVSPFRVAPLPSLQPV 643  
 DB 584 GPGAGHPHAFASISCVLPDFLQGRATGRVGVFPDGLLPDSVSPFRVAPLPSLQPV 643  
 QY 640 LPAFLDALOGGCGTSAGRAPDRVERVYQALRSALDSC--TSSSEAPG 684  
 DB 640 LPAFLDALOGGCGTSAGRAPDRVERVYQALRSALDSC--TSSSEAPG 684  
 QY 644 LPDFLQGRATGRVGVFPDGLLPDSVSPFRVAPLPSLQPV 690  
 DB 644 LPDFLQGRATGRVGVFPDGLLPDSVSPFRVAPLPSLQPV 690

RESULT 5  
 AAB61884  
 ID AAB61884 standard; Protein; 705 AA.  
 XX  
 AC AAB61884;  
 XX  
 DT 08-MAY-2001 (first entry)  
 XX  
 DE Chimeric zcytor14 protein #2.  
 XX  
 KW Cytokine receptor; zcytor14; human; inflammation; rheumatoid arthritis;  
 KW antiinflammatory; gene therapy; vaccine.  
 OS Homo sapiens.  
 PN WO200104304-A1.  
 XX  
 PD 18-JAN-2001.  
 XX  
 PF 30-JUN-2000; 2000MO-US18383.  
 XX  
 PR 07-JUL-1999; 99US-0348854.  
 XX  
 PA (ZYMO) ZYMOGENETICS INC.  
 XX  
 PI Presnell SR, Burkhead SK, Pownder SL;  
 XX  
 DR WPI; 2001-112618/12.  
 XX  
 PT New polypeptide encoding a human cytokine receptor zcytor14, for  
 PT treating inflammation e.g. rheumatoid arthritis -  
 XX  
 PS Claim 2; Page 105-107; 112pp: English.  
 XX  
 CC The invention provides a new human cytokine receptor designated zcytor14.  
 CC zcytor14 can be expressed by standard recombinant methodology. The  
 CC encoding nucleic acid is useful for detecting the expression of a  
 CC zcytor14 gene in a biological sample. Anti-zcytor14 antibodies can be  
 CC used to screen biological samples in vitro for the presence of zcytor14.  
 CC Proteins, polypeptides and peptides having zcytor14 activity can be  
 CC administered to a subject who lacks an adequate amount of this  
 CC polypeptide, for treating inflammation and conditions such as rheumatoid  
 CC arthritis. In contrast, zcytor14 antagonists (e.g. anti-zcytor14  
 CC antibodies) can be used to treat a subject who produces an excess of  
 CC zcytor14. zcytor14 nucleotide sequences can also be used to provide  
 CC zcytor14 to a subject. The present sequence represents a chimeric  
 CC zcytor14 protein.  
 CC  
 XX  
 SQ Sequence 705 AA:  
 Query Match 63.5%; Score 2376; DB 22; Length 705;  
 Best Local Similarity 65.9%; Pred. No. 1.1e-216;  
 Matches 466; Conservative 66; Mismatches 135; Indels 40; Gaps 7;  
 QY 1 MPVSWFLSLALGRNVVVSLEERIMEPQDARCSLGLSCHIMDGVLCIPGSLQASPGV 60  
 DB 1 MPVSWFLSLALGRNVVVSLEERIMEPQDARCSLGLSCHIMDGVLCIPGSLQASPGV 60  
 QY 61 LVPTRQLQELVLRCPQKTDALRVVVVHLAVHGHMAEPPEE-----AGKSDSELQESRNAS 116  
 DB 61 LVPTRQLQELVLRCPQKTDALRVVVVHLAVHGHMAEPPEE-----AGKSDSELQESRNAS 116  
 QY 117 LQAOVLSFOAPVIRACALLEVOVPADLVOPGOSVGSVAVEPCFEASLGAEOIWSYTKPR 176  
 DB 117 LQAOVLSFOAPVIRACALLEVOVPADLVOPGOSVGSVAVEPCFEASLGAEOIWSYTKPR 176  
 QY 121 LQAOVLSFOAPVIRACALLEVOVPADLVOPGOSVGSVAVEPCFEASLGAEOIWSYTKPR 180  
 DB 121 LQAOVLSFOAPVIRACALLEVOVPADLVOPGOSVGSVAVEPCFEASLGAEOIWSYTKPR 180  
 QY 177 YQKELNLQOQLPDCRGLERVDSIOSCWVLPWLNSTGDNVLTLDVSEEDFSLTYR 236  
 DB 177 YQKELNLQOQLPDCRGLERVDSIOSCWVLPWLNSTGDNVLTLDVSEEDFSLTYR 236  
 QY 181 YQKELNLQOQLPDCRGLERVDSIOSCWVLPWLNSTGDNVLTLDVSEEDFSLTYR 225  
 DB 181 YQKELNLQOQLPDCRGLERVDSIOSCWVLPWLNSTGDNVLTLDVSEEDFSLTYR 225  
 QY 237 PVPDALKSLWYKNTLGPONTITLNTHTDLPVLCIQVWSLEPDSERVEPCFREDPGAHNTL 296  
 DB 237 PVPDALKSLWYKNTLGPONTITLNTHTDLPVLCIQVWSLEPDSERVEPCFREDPGAHNTL 296

226 qvqgppkprwhknltpqifitlnhtclvpcldiqvwplepdsrvtnicpfredprahnl 285  
 297 WHIARLRLVLSFGVWQDAPCCPLPGKVTLCQWAPDQSPQPLVPEVPQKNATVNEPQDQL 356  
 286 wgaarlrlltqlswlldapcsipaeealcwarpagpdcqplvpplswenvtvdvlefpj 345  
 357 VAGHPNLCVOYSTWEKVOLOACSNMADSLGPFKDMILVEMKGTGLNNTSVCALEPSCGTP 416  
 346 lkgpnltcvynsskqlqecclwadsipklkdvlllettrgpdnrlcalpescstl 405  
 417 PSMASTRARARLGEELIDFRSHQCQGLMNDNMGSIMACPMKXIIHRRWTVWLACILLA 476  
 406 pskastraarlgeylldgtqsgcqlw-dddlglawacpmkxyihkrrvalwlacllla 464  
 477 ALFFFLKKDRRK-----AARGSTRALLSHSADGAGYERLVGALASALS 522  
 465 aalslillllkkhkgwlrllkqdvtrsgaarg-raallllysdsgsfertlvgalasalc 523  
 523 QMPRLAVNDLMSRRRLSARGLAMFHHORRRLIQEGGVILLFSPAAYAOCCQWLOLQTV 582  
 524 qlrlrvavdlvstrrelsqgprwafhaqrtrqlqeggvvllfsgavalcsewldqdv 583  
 583 EP---GPHDALAAMLSCVLPDFLOGRATGRVYGVFDGLLHPSVSPFRVAPLFSLP 639  
 584 gpgahghdtrraaslscvlpdflgrrapgsyvgacfdarllhpdavpalftvrvflpsq 643  
 640 LPAFLDALOGGCGSTSGRPRADREVRVTOALRSALDSC--TSSSEAPG 684  
 644 lpfllgalqgrraprgrlqeraeqvralqpaldeyfhnpptpapg 690  
 ESURT 6  
 AB61885 standard; Protein: 675 AA.  
 AAB61885;  
 08-MAY-2001 (first entry)  
 Chimeric Zcytor14 protein #3.  
 Cytokine receptor: Zcytor14; human; inflammation; rheumatoid arthritis;  
 antinflammatory; gene therapy; vaccine.  
 Homo sapiens.  
 WO200104304-A1.  
 18-JAN-2001.  
 30-JUN-2000; 2000MO-US18383.  
 07-JUL-1999; 99US-0348854.  
 (ZYMO) ZYMOGENETICS INC.  
 Presnell SR, Burkhead SK, Powder SL;  
 WPI; 2001-112618/12.  
 New polypeptide encoding a human cytokine receptor Zcytor14, for  
 treating inflammation e.g. rheumatoid arthritis -  
 Claim 2; Page 107-109; 112pp; English.

CC arthritis. In contrast, Zcytor14 antagonists (e.g. anti-Zcytor14  
 CC antibodies) can be used to treat a subject who produces an excess of  
 CC Zcytor14. Zcytor14 nucleotide sequences can also be used to provide  
 CC Zcytor14 to a subject. The present sequence represents a chimeric  
 CC Zcytor14 protein.  
 XX  
 SQ Sequence 675 AA;  
 Query Match 61.9%; Score 2314; DB 22; Length 675;  
 Best Local Similarity 65.5%; Pred. No. 7.9e-211;  
 Matches 454; Conservative 63; Mismatches 134; Indels 42; Gaps 6;  
 1 MPVSMFLSLAGRPVYVSLERLMEPOPTARCSGLSLHMGDVLCGLGSLQASAGPV 60  
 1 mpywflslalgrpsvslsterlvpgqdaclncspjlsclwdsdlclpgdivpapg 60  
 61 LVPTRLQTELVLRCEPKTDICALRVRVVVALAVGHMAEPD---AGKSDSELOESRNAS 116  
 61 laphlqltelvllrqketcdclrvavhlavhghwepeedeekfsgaadsyveepnas 120  
 117 LQAVVLSFOAIPYARCALLLEQVPADLVQPCQSVGSAVDFCEASLGAETQIMSTYKPR 176  
 121 lqavvlstfgayptarcvlllevqpaaivqfgsvgsyvdydcfaaalgsevirwlytqpr 180  
 177 YQKELNTQOLPDORGLEVRBSIQSCWVLPWLVNSFDGNVLLTLVSEPDQDSFLYLXR 236  
 181 yekelntqqlp-----alpwlvnsadgdnvhlvlnvseeqhglslvyn 225  
 237 PVDPALSKLWYKNLTGPONITLNTHTDLVPCLCIQWVSLPDSREVECFREDPGAHRL 296  
 226 qvqgppkprwhknltpqifitlnhtclvpcldiqvwplepdsrvtnicpfredprahnl 285  
 297 WHIARLRLVLSFGVWQDAPCCPLPGKVTLCQWAPDQSPQPLVPEVPQKNATVNEPQDQL 356  
 286 wgaarlrlltqlswlldapcsipaeealcwarpagpdcqplvpplswenvtvdvlefpj 338  
 357 VAGHPNLCVOYSTWEKVOLOACSNMADSLGPFKDMILVEMKGTGLNNTSVCALEPSCGTP 416  
 339 -----vnsekqlqecclwadsipklkdvlllettrgpdnrlcalpescstl 388  
 417 PSMASTRARARLGEELIDFRSHQCQGLMNDNMGSIMACPMKXIIHRRWTVWLACILLA 476  
 389 pskastraarlgeylldgtqsgcqlw-dddlglawacpmkxyihkrrvalwlacllla 447  
 477 ALFFFLKKDRRKRAARGSTRALLSHSADGAGYERLVGALASALSQMPRLAVNDLMSRR 536  
 448 aalslillllkkhakaargraailllysdsgsfertlvgalasalcqlrlrvavdlwstr 507  
 537 ELSAHGALAMFHHORRRLIQEGGVVILLFSPAAYAOCCQWLOLQTV---GPHDALAM 593  
 508 elsaqgprwafhaqrtrqlqeggvvllfsgavalcsewldqvgvsgpghphdflras 567  
 594 LSCVLPDFLOGRATGRVYGVFDGLLHPSVSPFRVAPLFSLPLOLPAFLDALOGGCGST 653  
 568 lscvlpdflgrrapgsyvgacfdarllhpdavpalftvrvflpsqpldflgalqgrrap 627  
 654 SAGRPADREVRVTOALRSALDSC--TSSSEAPG 684  
 628 rsgrlqeraeqvralqpaldeyfhnpptpapg 660  
 RESULT 7  
 AAB61883 standard; Protein: 688 AA.  
 AAB61883;  
 08-MAY-2001 (first entry)  
 Chimeric Zcytor14 protein #1.  
 Cytokine receptor: Zcytor14; human; inflammation; rheumatoid arthritis;

KM antiinflammatory; gene therapy; vaccine.  
 XX  
 OS Homo sapiens.  
 XX  
 PM WO200104304-A1.  
 XX  
 PD 18-JAN-2001.  
 XX  
 PF 30-JUN-2000; 2000MO-US18983;  
 XX  
 PR 07-JUL-1999; 9905-0348854;  
 XX  
 PA (ZYMO ) ZYMOGENETICS INC.  
 XX  
 PI Presnell SR, Burkhead SK, Powder SL;  
 XX  
 DR WPI: 2001-112618/12.  
 XX  
 PT New polypeptide encoding a human cytokine receptor zcytor14, for  
 PT treating inflammation e.g. rheumatoid arthritis -  
 XX  
 PS Claim 2: Page 102-104; 112pp: English.  
 XX  
 CC The invention provides a new human cytokine receptor designated zcytor14.  
 CC zcytor14 can be expressed by standard recombinant methodology. The  
 CC encoding nucleic acid is useful for detecting the expression of a  
 CC zcytor14 gene in a biological sample. Anti-zcytor14 antibodies can be  
 CC used to screen biological samples in vitro for the presence of zcytor14.  
 CC proteins, polypeptides and peptides having zcytor14 activity can be  
 CC administered to a subject who lacks an adequate amount of this  
 CC polypeptide, for treating inflammation and conditions such as rheumatoid  
 CC arthritis. In contrast, zcytor14 antagonists (e.g. anti-zcytor14  
 CC antibodies) can be used to treat a subject who produces an excess of  
 CC zcytor14. zcytor14 nucleotide sequences can also be used to provide  
 CC zcytor14 to a subject. The present sequence represents a chimeric  
 CC zcytor14 protein.  
 CC  
 SQ Sequence 688 AA:  
 Query Match 61.5%; Score 2300.5; DB 22; Length 688;  
 Best Local Similarity 64.5%; Pred. No. 1.6e-209;  
 Matches 456; Conservative 63; Mismatches 131; Indels 57; Gaps 8;  
 QY 1 MPVSWFLSLALGRNPVYVLERLMEPODTRARCSGLSCHLMDGDLCLPGSLQASGPV 60  
 DB 1 mpvswflslalgrnpvylervgpdalchspglscrlwdsdlclpgdlvppgqv 60  
 QY 1 IVPTRLOTETVLRCPQKTDALRYRVVYHLAVHGMAREE-----AGKDSLEQESRMAS 116  
 DB 1 i v p t r l o t e t v l r c p k t d a l r y r v v y h l a v h g m a r e e ----- a g k d s l e q e s r m a s 116  
 QY 61 laptlgtetvltcqtetcdclrtvavhahgmweepedeekfgyaadsqveepnas 120  
 DB 61 laptlgtetvltcqtetcdclrtvavhahgmweepedeekfgyaadsqveepnas 120  
 QY 117 LQAQVVLSEFQAYPIARCALLLEVOPADLVOPGOSGSAVFDFEASLGAEOVMSTYKPR 176  
 DB 121 lqayvvlsefqaypiarcalllevopadlvopgogsvavfddfeslgaevomstykpr 180  
 QY 177 YQKELNLTQQLPDCRGLERVDSIOSCVLFWLNVSTGDNVLLTLDVSEEDPSFLLYLR 236  
 DB 181 yekelnltqqlp-----alpwlnvsadgnvhlvlnvseeqhgflgslwlm 225  
 QY 237 PVPDALKSLMYKNLGTGPONTLNTHTDLPVCLCIQVMSLEPDSEREFCEFPREDPGAHRL 296  
 DB 226 pvpdalkslmyknltgtpontlnthtdlvpclciqvmslepdserfefcfpredpgahrnl 285  
 QY 297 WHIARLVLSPGVWQADAPCLPGKVTLCMOAPDOSPCOPLVPVPYOKNATVNEPQDFOL 356  
 DB 286 whiarlvlspgvwqadapclpgkvtlcmoapdospcoplvpvpynknatvnepqdfol 348  
 QY 357 VAGHPMLCVQVSTWVEVQAOCSMADSIGPEKDDMLLVEMKTLGNNTSVCALEPSCGCTPL 416  
 DB 339 v a g h p m l c v q v s t w v e v q a o c s m a d s i g p e k d d m l l v e m k t l g n n t s v c a l e p s c g c t p l 416  
 QY 417 PSMASRAARLAGEELLQDFRSHQCMQMDNDMGSLSVACPDKXTHRRVYLVWLACLLLA 476

DB 389 pskasttraarigeYllqdlgsqgcqlw-dddlgalwaacpmdkylnkxwlvwlacllfa 447  
 QY 477 AALFFFLTKKDRRK-----AARGSRFALLHSADGAGYERLVGALASALS 522  
 DB 448 aalsllllkkdkhkyrlrlkqdvrsaaarg-raalllysaddsgferllygalaalac 506  
 QY 523 QMPLRAVADLMSRRRLSAGALAMPFHQRRILOEGGVILLFFSPAAYAOCCQMLQOTV 582  
 DB 507 qlplravadtwsrrelseagpavavfhagrtqltqsgyvvllfspgavalcsewldqys 566  
 QY 583 EP---GPHDALAAMLSCVLPDFLOGRATGRVGYTFDGLHPDSVSPFRVADLSFPTQ 639  
 DB 567 gpgahpghdfafraalscvlpdflqgragsygaefdrllhpdavpalfitvpvflpsq 626  
 QY 640 LPALFDLGGCGSTRAGRPADRVERTQALRSALDSC--TSSEARG 684  
 DB 627 lpdflgdlqgrprprsrgrlgeraeqvsralpaldsfyfppltpapq 673  
 RESULT 8  
 ID AAB61881  
 XX AAB61881 standard; Protein: 575 AA.  
 AC AAB61881;  
 XX  
 XX 08-MAY-2001 (first entry)  
 DE Human variant zcytor14 protein zcytor14-1.  
 XX  
 KM Cytokine receptor; zcytor14; human; inflammation; rheumatoid arthritis;  
 KM antiinflammatory; gene therapy; vaccine; variant; zcytor14-1.  
 OS Homo sapiens.  
 XX  
 PN WO200104304-A1.  
 XX  
 PD 18-JAN-2001.  
 XX  
 PF 30-JUN-2000; 2000MO-US18383.  
 XX  
 PR 07-JUL-1999; 9905-0348854.  
 XX  
 PA (ZYMO ) ZYMOGENETICS INC.  
 XX  
 PI Presnell SR, Burkhead SK, Powder SL;  
 DR WPI: 2001-112618/12.  
 DR N-PSDB; AAC85029.  
 PT New polypeptide encoding a human cytokine receptor zcytor14, for  
 PT treating inflammation e.g. rheumatoid arthritis -  
 XX  
 PS Disclosure: Page 2-3; 112pp: English.  
 XX  
 CC The invention provides a new human cytokine receptor designated zcytor14.  
 CC zcytor14 can be expressed by standard recombinant methodology. The  
 CC encoding nucleic acid is useful for detecting the expression of a  
 CC zcytor14 gene in a biological sample. Anti-zcytor14 antibodies can be  
 CC used to screen biological samples in vitro for the presence of zcytor14.  
 CC proteins, polypeptides and peptides having zcytor14 activity can be  
 CC administered to a subject who lacks an adequate amount of this  
 CC polypeptide, for treating inflammation and conditions such as rheumatoid  
 CC arthritis. In contrast, zcytor14 antagonists (e.g. anti-zcytor14  
 CC antibodies) can be used to treat a subject who produces an excess of  
 CC zcytor14. zcytor14 nucleotide sequences can also be used to provide  
 CC zcytor14 to a subject. The present sequence represents a variant of  
 CC the human cytokine receptor zcytor14, designated zcytor14-1. This  
 CC variant is a truncated form of the receptor polypeptide and lacks  
 CC amino acid residues 1-113 of zcytor14.  
 XX  
 SQ Sequence 575 AA:

[illegible]

PR	12-MAY-1998:	98US-0085109.
PR	12-MAY-1998:	98US-0085105.
PR	18-MAY-1998:	98US-0085180.
PR	18-MAY-1998:	98US-0085906.
PR	18-MAY-1998:	98US-0085920.
PR	18-MAY-1998:	98US-0085921.
PR	18-MAY-1998:	98US-0085922.
PR	18-MAY-1998:	98US-0085923.
PR	18-MAY-1998:	98US-0085924.
PR	18-MAY-1998:	98US-0085925.
PR	18-MAY-1998:	98US-0085927.
XX	(HUMA-) HUMAN GENOME SCI INC.	
PI	Ruben SM; Florence K, Ni J, Rosen CA, Carter KC, Moore PA;	
PI	Olsen HS; Shi Y, Young PE, Wei F, Brewer LA, Soppet DR;	
PI	Lafleur DW, Endress GA, Ebner R;	
DR	WPI: 2000-062296/05.	
DR	N-PSTDB: AAZ65269.	
PS	New isolated human genes and the secreted polypeptides they encode,	
PS	useful for diagnosis and treatment of e.g. cancers, neurological	
PS	disorders, immune diseases, inflammation or blood disorders	
XX	Claim 11: Page 372-373; 475pp; English.	
XX	AZ65250 to AZ65350 represent 97 isolated human secreted protein genes.	
CC	AAI76124 to AAI76223 are the secreted proteins encoded by the 97 human	
CC	genes. The gene encoding this protein was found to be on chromosome 3.	
CC	The genes and their corresponding secreted polypeptides are	
CC	useful for preventing, treating or ameliorating medical conditions, also	
CC	e.g. by protein or gene therapy. Also pathological conditions can be	
CC	diagnosed by determining the amount of the new polypeptides in a sample	
CC	or by determining the presence of mutations in the new genes. Specific	
CC	uses are described for each of the 97 genes, based on which tissues they	
CC	are most highly expressed in, and include developing products for the	
CC	diagnosis or treatment of cancer, tumours, developmental abnormalities,	
CC	and foetal deficiencies, blood disorders, diseases of the immune system,	
CC	autoimmune diseases, inflammation, allergies, Alzheimer's and cognitive	
CC	disorders, schizophrenia, arthritis, asthma, psoriasis, sepsis, skin	
CC	disorders, atherosclerosis, diabetes, cardiovascular disorders, kidney	
CC	disorders, digestive/endocrine disorders, infections and AIDS. The	
CC	polypeptides are also useful for identifying their binding partners.	
CC	The sequences shown in AAI76224 to AAI76424 represent fragments of the	
XX	secreted proteins.	
SQ	Sequence 309 AA:	
Query Match	29.1%: Score 1088.5; DB 21: Length 309;	
Best Local Similarity	71.0%: Pred. No. 9.3e-95;	
Matches 211: Conservative 21: Mismatches 60: Indels 5: Gaps 2:		
Yy	1 MPVSMFLSLALGNPVVLSLERLMEPOTACSLISCHLMGDDVCCLPESLQAPGV 60	
Dd	1 mpyvflslalgrspvvlslertlvpgdatctspglscldwddllcpdlpapapgv 60	
Yy	61 LVEFTLOTELVLNCPKTDLCALRRVVVAHLAVGHAAEPEE---AGKSDELQESNRAS 116	
Dd	61 lapthtqtelvrlrcqketdcclrtvxhlavghwpeedeekfggaadlgyeeprnas 120	
Yy	117 LQAQNVLSFPAATPARCALLEVQVPADLVQPQOSVASAFVDCFEASLGAETQINSTRKR 176	
Dd	121 lqqqvaylsfqaypatcavllevqpaaavgfigsvsvvyddcfcaalgsevrllsyqtpr 180	
Yy	177 YQEELNLITQQLPDGRGLEVRDSICSWLPMTLVNSFDGDVNLTLTLDVSEEDDFSLILYLR 236	
Dd	181 ykeexnhtgtqlpdcrqglevrnsipscvalpwlnvasdgdnvhlylviseeghfjstlywm 240	
Yy	237 PVPDAKLSTMYKNLTGPONITLNHTDLVPCLCIQWLSLESDSERVFECPRFEDGCAH 293	



Db 241 qvqgpkprwhknltpqtlclnhtclvpcldqvwpdpdsvrtrsapgrtp-ah 296

# RESULT 10

AAAM25864 standard; Protein: 332 AA.

AAAM25864;

16-OCT-2001 (first entry)

Human protein sequence SEQ ID:1379.

Human; cancer; ulcer; HIV infection; human immunodeficiency virus; anti-inflammatory; antirheumatic; antiarthritic; immunosuppressive; antibacterial; endocrine; cardiac; central nervous system; vitruide; anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia; antiaggregant; haemostatic; vulnary; antilucer; osteopathic; eczema; dermatological; antiallergic; antiasomatic; antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic; antiparkinsonian; infection; immunostimulant; gene therapy; antisense therapy; vaccine; inflammation; antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis; cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmune; genetic disease; haematopoietic disorder; platelet disorder; asthma; thrombocytopaenia; osteoporosis; severe combined immunodeficiency; allergic rhinitis; diabetes; multiple sclerosis; depression; Alzheimer's disease; Parkinson's disease; neurodegenerative disorder; neurological disorder.

Homo sapiens.

MO200153455-A2.

26-JUL-2001.

22-DEC-2000; 2000MO-US35017.

23-DEC-1999; 99US-0471275.

21-JAN-2000; 2000US-0488725.

25-APR-2000; 2000US-0552317.

(HYSE-) HYSEQ INC.

Tang YT, Liu C, Drmanac RT;

WPI: 2001-457603/49.

N-PSDB: AAH99805.

Isolated human polynucleotides encoding polypeptides, useful for the treatment and diagnosis of e.g. cancer, ulcers and HIV infection -

Claim 20; Page 283; 1217PP; English.

AAH99166 to AAH99904 encode the human proteins given in AAAM25225 to AAAM25963. The proteins can have activities based on the tissues and cells they are expressed in, such as: antitumour; antirheumatic; antiallergic; immunosuppressive; antibacterial; endocrine; cardiac; central nervous system; vitruide; anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; antiaggregant; haemostatic; vulnary; antilucer; osteopathic; dermatological; antiallergic; antiasomatic; antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic; antiparkinsonian; and immunostimulant. The proteins and polynucleotides encoding them can be used in gene therapy, antisense therapy and vaccine production. The proteins and polynucleotides are useful for screening for agonists or antagonists of a protein and for the treatment and diagnosis of disorders associated with the activity of a protein e.g. inflammation, rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction, neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal infections, autoimmunity, genetic diseases, haematopoietic disorders, anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers, osteoporosis, severe combined immunodeficiency, eczema, allergic rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression, Alzheimer's disease, Parkinson's disease, neurodegenerative and

CC neurological disorders.

XX Sequence 332 AA;

Query Match 26.0%; Score 971.5; DB 22; Length 332;  
Best Local Similarity 69.1%; Pred. No. 1.4e-83;  
Matches 188; Conservative 23; Mismatches 56; Indels 5; Gaps 2;

QY 1 MPVSMFLSLALGRNPVSVLERLMEPODTARCSGLSCMLMDGVLCPLGSLQSAAPV 60  
DB 2 MPVSMFLSLALGRNPVSVLERLMEPODTARCSGLSCMLMDGVLCPLGSLQSAAPV 61  
QY 61 LVPTRIOTELVLRCPQKTDCAIRRVVHLAVGHMAEPDE---AGKSDSELSQESRNAS 116  
DB 62 LAPTHTQTELVLRCPQKTDCAIRRVVHLAVGHMAEPDEDEKFGGAADSYVEEPNRS 121  
QY 117 LQAGVYVSPQAPYFARCALLLEVOPADIVOPQSGSANVDFCFEASLGAELVQIWTSTKPR 176  
DB 122 LQAGVYVSPQAPYFARCALLLEVOPADIVOPQSGSANVDFCFEASLGAELVQIWTSTKPR 181  
QY 177 YQKELNLTQQLPDCRGLFVRDSIOSCVLPMVNSTDGNVLTLPDSEEDPSFLLYLR 236  
DB 182 YQKELNLTQQLPDCRGLFVRDSIOSCVLPMVNSTDGNVLTLPDSEEDPSFLLYLR 241  
QY 237 PVPDAKSLMYKNLTGPQNTLNTHTDLPVCLC 268  
DB 242 qvqgpkprwhknltpqtlclnhtclvpcldqvwpdpdsvrtrsapgrtp-ah 296

## RESULT 11

AAAB8448 standard; Protein: 267 AA.

AAAB8448;

23-MAY-2001 (first entry)

Human membrane or secretory protein clone PSEC0233.

Human; secretory protein; membrane protein; vaccine; gene therapy;

rheumatoid arthritis; diabetes.

Homo sapiens.

EP167182-A2.

10-JAN-2001.

07-JUL-2000; 2000EP-0114090.

08-JUL-1999; 99EP-0194179.

11-JAN-2000; 2000JP-0118775.

02-MAY-2000; 2000JP-0183766.

(HELI-) HELIX RES INST.

Ota T, Isegaki T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;

WPI: 2001-093869/11.

N-PSDB: AAF93875.

Nucleic acids encoding secretory proteins/membrane proteins, useful in gene therapy or as candidate target molecules in drug development -

Claim 1; SEQ ID 264; 609pp + CD ROM; English.

This invention relates to nucleic acid sequences AAF93744 - AAF93916 which encode human secretory or membrane proteins represented by AAAB8448 - AAAB8449. Included in the invention are primers AAF93917 - AAF94295 and AAF62232 - AAF62235 which are used to isolate the cDNA sequences of the invention. The invention also includes methods for the production of antibodies directed against the proteins, and cDNA

sequences, which can be used in vaccines. The polynucleotide sequences can be used in gene therapy. The polynucleotide sequences and the proteins they encode may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate secretion of protein/membrane protein expression. The nucleic acids and complementary sequences may also be used as DNA probes in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect and quantitate the presence of similar nucleic acid sequences in samples. They may also be used to study the expression and function of secretory proteins/membrane polypeptides and their role in metabolism. The polypeptides may be used as antigens in the production of antibodies against them and in assays to identify modulators (agonists and antagonists) of expression and activity. The antibodies (agonists and antagonists) may also be used as therapeutic agents to down regulate expression and activity. The antibodies may also be used as diagnostic agents for detecting the presence of the polypeptides in samples (e.g. by enzyme linked immunosorbent assay (ELISA)). Examples of diseases which may be treated include rheumatoid arthritis and diabetes.

Sequence 267 AA:

Query Match 23.4%; Score 875.5; DB 22; Length 267;  
Best Local Similarity 60.7%; Pred. No. 1.4e-74;  
Matches 179; Conservative 25; Mismatches 58; Indels 33; Gaps 5;

1 MPVSWFLSLALGRPPVVSLELMEPODFARCSLGLSCHLMDGVLCPLPSLQAPGPV 60  
1 MPVWFLSLALGRPPVVSLELMEPODFARCSLGLSCHLMDGVLCPLPSLQAPGPV 60  
61 LVPRLOTLELVKRCQKDFKCALRRVRYVLAHVGHWAEPEE---AGKSPSELOESRRAS 116  
61 LVPRLOTLELVKRCQKDFKCALRRVRYVLAHVGHWAEPEE---AGKSPSELOESRRAS 116  
61 LVPRLOTLELVKRCQKDFKCALRRVRYVLAHVGHWAEPEE---AGKSPSELOESRRAS 116  
61 LVPRLOTLELVKRCQKDFKCALRRVRYVLAHVGHWAEPEE---AGKSPSELOESRRAS 116  
117 LQAVLSFQAFPIARCKALLEVQPADLVQPSQSVSAVDFCEASIGAEVQVSYTKPR 176  
121 LQAVLSFQAFPIARCKALLEVQPADLVQPSQSVSAVDFCEASIGAEVQVSYTKPR 176  
121 LQAVLSFQAFPIARCKALLEVQPADLVQPSQSVSAVDFCEASIGAEVQVSYTKPR 176  
177 YKRLNTQQLPDCRGLEVRBSIQSCWVLPWLVNSTDGNYLTLDVSEODESFLYLRL 236  
181 YKRLNTQQLPDCRGLEVRBSIQSCWVLPWLVNSTDGNYLTLDVSEODESFLYLRL 236  
237 PVPDAKSLWTKNLTGPNITLY-NHTDLVPCLCIQWLSLEPDSERVEFCFEREDP 290  
226 qvqgppkprwhknlvrppsqvshncrmpv-----grtq-chlredp 267

RESULT 12

AAE10920 standard; Protein: 204 AA.

AAE10920:

18-DEC-2001 (first entry)

Human gene 12 encoded immune system-related protein HADEX14.

Human: immune system-related protein; allergy; rheumatoid arthritis; cancer; Gaucher's disease; viral hepatitis; gene therapy; cytostatic; diabetes mellitus; arrhythmia; wound healing; ischemic lesion; AIDS; Acquired Immune Deficiency Syndrome; vitruicide; hepatocytic; vasotrophic; autoimmune disorder; inflammation; cardiovascular disorder; hair loss; wound healing; cell proliferation; skin aging; endocrine disorder; food preservative.

Homo sapiens.

Key Location/Qualifiers  
Domain 50..55

Domain /label= Immunogenic\_epitope  
Domain /label= Immunogenic\_epitope

PN WO20016722-A1.  
XX 13-SEP-2001.  
XX 07-MAR-2001; 2001WO-US07260.  
XX 08-MAR-2000; 2000US-187873P.  
XX 11-AUG-2000; 2000US-224367P.  
XX (HUMA-) HUMAN GENOME SCI INC.  
PI NI J, Hilbert D, Kenny J, Moore PA, Choi GH, Soppet DR, Ebner R;  
PI Gruber JR, Endress GA, Ruben SM;  
DR N-PSDB; AAD18278.  
PT Novel isolated immune system-related polypeptide useful for treating  
PT rheumatoid arthritis, AIDS, allergy, cancer, Gaucher's disease,  
PT diabetes mellitus, arrhythmia, wound healing, ischemic lesions and  
PT viral hepatitis

Claim 11, Page 312-313; 315pp; English.

The invention relates to human immune system-related protein and their DNA. Human immune system related protein and DNA are useful for preventing, treating or ameliorating a medical condition in a mammalian subject, for diagnosing, preventing or treating immune system-associated disorders, autoimmune disorders (rheumatoid arthritis), inflammatory disorders (allergies), infectious diseases (e.g., viral hepatitis), complement activation disorders, immune complex diseases, neoplastic disorders (cancer), hyperproliferative disorders (Gaucher's disease), disorders associated with neovascularisation, diseases at the cellular level, cardiovascular disorders (arrhythmias), wound healing and epithelial cell proliferation, endocrine disorders (diabetes mellitus) and neurological disorders (ischemic lesions). Immune-system related protein or DNA is useful for preventing hair loss, skin aging due to sunburn, to maintain organs before transplantation, to treat weight disorders, to modulate mammalian characteristics, to change a mammal's mental or physical state, or as a food additive or preservative. Immune-system related DNA is useful in gene therapy, for chromosome identification, radiation hybrid mapping, long range restriction mapping and in forensic biology. The present sequence represents a human immune-system related protein of the invention.

Sequence 204 AA:

Query Match 15.8%; Score 591.5; DB 22; Length 204;  
Best Local Similarity 64.6%; Pred. No. 9.5e-48;  
Matches 122; Conservative 21; Mismatches 41; Indels 5; Gaps 2;

QY 501 LHSADGAGTERLVGALASLSQMPRLRYAVDLSRRRLSANGALMFHQRRRLLEGV 560  
Db 1 LHSADGAGTERLVGALASLSQMPRLRYAVDLSRRRLSANGALMFHQRRRLLEGV 560  
QY 561 VILLFSPAAYACQOQWLOQVER---GPHDALMLSCVLPDFLOGRATGRVGYFDG 617  
Db 61 VILLFSPAAYACQOQWLOQVER---GPHDALMLSCVLPDFLOGRATGRVGYFDG 617  
QY 618 LHPDVSPPSPFRVAPLPSLPQALPAFLALOGGCSAGRPADRYRYQALRSALDSC- 676  
Db 121 LHPDVSPPSPFRVAPLPSLPQALPAFLALOGGCSAGRPADRYRYQALRSALDSC- 676  
QY 677 -TSSSEAPG 684  
Db 181 hppgtpapg 189

RESULT 13

AAV76048 standard; Protein: 617 AA.

XX AAY76048;  
 AC XX  
 DT 27-MAR-2000 (first entry)  
 XX XX  
 DE Murine skin cell protein, SEQ ID NO:303.  
 XX XX  
 KM Skin; dermal papilla; keratinocyte; neonatal foreskin fibroblast;  
 KM embryonic skin cell; keratinocyte stem cell; transit amplifying cell;  
 KM secreted; transmembrane; inflammation; cancer; neurological disease;  
 KM angiogenesis; tumour vascularisation; growth disorder;  
 KM developmental disorder; skin wound; hair follicle disorder;  
 KM anti-inflammatory; cytostatic; neuroprotective; vulnery.  
 XX Mus sp.  
 OS XX  
 PN W09955865.A1.  
 PD 04-NOV-1999.  
 XX XX  
 PF 29-APR-1999; 99WO-N200051.  
 XX XX  
 PR 29-APR-1998; 98US-0069726.  
 PR 09-NOV-1998; 98US-0188930.  
 XX XX  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 XX XX  
 PI Strachan L, Sleeman M, Watson JD, Onrust R, Kumble A, Murison JG;  
 XX XX  
 DR WPI; 2000-072177/06.  
 DR N-PSDB; AAZ61753.  
 XX XX  
 PT Novel polynucleotides useful for the treatment of various conditions  
 including wounds and cancer.  
 XX XX  
 PS Claim 4; Page 179-180; 235pp; English.  
 XX XX  
 CC The invention relates to novel nucleic acid sequences derived from rat  
 CC dermal papilla, human keratinocytes and neonatal foreskin fibroblasts,  
 CC and mouse embryonic skin, keratinocyte stem cells and transit amplifying  
 CC cells. Polypeptides of the invention may be used to treat inflammation,  
 CC cancer and neurological diseases. The proteins may be used to stimulate  
 CC the growth and motility of keratinocytes, to inhibit the growth of  
 CC cancer cells, to modulate angiogenesis and tumour vascularisation, to  
 CC modulate skin inflammation, to modulate epithelial cell growth and to  
 CC inhibit binding of HIV-1 to leukocytes. The invention may also be used  
 CC to treat growth and developmental defects, skin wounds and hair follicle  
 CC disorders. Sequences AAY75942-Y76123 represent polypeptides encoded  
 CC by cDNA sequences derived from several mouse, rat or human skin cell  
 CC types. Sequences AAY75942-Y75947, AAY76020-Y76021, AAY76094-Y76104 and  
 CC AAY76119 are proteins with an N-terminal signal sequence, indicating  
 CC that they are secreted. Sequences AAY75986-Y75989, AAY76061-Y76071,  
 CC AAY76106-Y76109 and AAY76121-Y76122 are proteins with one or more  
 CC putative transmembrane domains.  
 CC XX  
 SO Sequence 617 AA;

Query Match 8.3%; Score 312; DB 21; Length 617;  
 Best Local Similarity 23.9%; Pred. NO. 2, 1e-20;  
 Matches 134; Conservative 66; Mismatches 224; Indels 136; Gaps 21;

QY 175 PRXQKELNLOOLPDCRLEV-----RDSIOSC--WVLPMLNVSDGDNVLLTLVDVSEE 226  
 DB 137 pelsfdl-----lpevqavrtllpaggkavrtlyqwaledcedlsspfdt----- 181  
 QY 227 QDPSFLLYLPVPDALKSLMYKNLTGPNITLNHNDVLPICICLOWMSLEPDSERVERCFP 286  
 DB 182 -----gkivsghtvdipyeellipcmcleasylgedtyrkkcpf 221  
 QY 287 RENDPGAH-RNIMHTARLRVLSPG---WQLDAPCCLLGKVTTLQWQAPDQPCQPLVPPVP 342  
 DB 222 qswpeaygsdfwgsifrfcdysqhnqvmaltlirpklleaslowrwdplpccetl----- 276

QY 343 OKNATVNEPQDFQVAG---HPNLCVQVSTWEKVQLQAC-----SMADSLGPFKDDM 391  
 DB 277 -pnatagesegwyllenvdlhnpqlcfkfs--fenshvecpbgsgslpwtvsmtdt-gaqg 333  
 QY 392 LLYEAKTGTNNTSVCLERSGC---TPLEMASTRARALGELLQD-----FRSHQCMQL 443  
 DB 334 ltlhfsrtlyafsaasdpjlgpdpmpvysisqgsvpvtldllpflrgencllv 393  
 QY 444 WNDWMGSLMACPMOKYIHRRWLV-----WACLILAAALFFLLKKDRRAAGS 496  
 DB 394 wrsd-----vlfawhvlcpddapylgtlll-----rslsgqrt 427  
 QY 497 RTALLHSADGAGYERLVGALASALSOM---PLRAVADLMSRRELSAHGALAMFHORR 553  
 DB 428 rpylllhaadseaqrllvgaleellrtalggydvtvdlwegthvarlplwaater 487  
 QY 554 ILOEGGVILLFSPAIVAOCCQMLQVYEPGPHDALAAMLSCVLPFLQGRATGRYGV 613  
 DB 488 varegvtvlllwnccags-----tacsqdpqaaslrtllcaaprl-----lla 531  
 QY 614 YFDGLHPDSVSPFRVAVLFSLPQLPAFLDALQGCSTSA-----GRADRERYTQ 667  
 DB 532 yfslcaqgdiprlalprylrldlprllraldaqpataaswshlgakrciknrleg 591  
 QY 668 A---LRSALDSCSTSSSEAP 683  
 DB 592 chlleaakddygstnsp 611

## RESULT 14

AAB55987 standard; Protein; 617 AA.

AAB55987;

08-MAR-2001 (first entry)

Skin cell protein, SEQ ID NO: 303.

Mouse; skin cell; cytostatic; antiinflammatory; anti-HIV;

keratinocyte growth stimulation; vulnery; immunomodulatory; vaccine;

inflammation; neurological disease.

Mus sp.

W020006984-A2.

23-NOV-2000.

15-MAY-2000; 2000WO-N200075.

14-MAY-1999; 99US-0312283.

(GENE-) GENESIS RES & DEV CORP LTD.

Watson JD, Strachan L, Onrust R, Sleeman M, Kumble KD, Murison JG;

WPI; 2001-007495/01.

N-PSDB; AAC99686.

New isolated polynucleotide used in the identification of genetic

disorders and encoding polypeptides used for treating inflammatory

disease, cancer and neurological diseases

Claim 4; Page 244-245; 352pp; English.

The present sequence is a polypeptide which is expressed in

mammalian skin cells. The polypeptide is useful for stimulating

keratinocyte growth and motility, inhibiting the growth of cancer cells,

modulating angiogenesis, inhibiting angiogenesis and vascularisation of

tumours, modulating skin inflammation, stimulating the growth of

epithelial cells, inhibiting the binding of human immunodeficiency virus (HIV)-1 to leukocytes, and treating inflammatory disease, cancer and neurological diseases. The polynucleotide can be used as a marker, in the identification of genetic disorders, and for the design of oligonucleotides for examining expression patterns.

Sequence 617 AA:

Query Match 8.38; Score 312; DB 22; Length 617;  
Best Local Similarity 23.98; P-Val. No. 2.1e-20;  
Matches 134; Conservative 66; Mismatches 224; Indels 136; Gaps 21;

175 PROKELNLTQQLDRCRLV-----RDSIOSC--WVLPMLNVTSGDGNVLTLDVSEE 226  
137 pelsdl-----lpevavrvtlpgpkasvrlcygwalecedlsspfdt----- 181  
227 QDSFLLYLRVPDALKSLMKNLGPNITLHNDVPCICIGVMSLEPDSERVERCPF 286  
182 -----qkivsgntvdlpyefllipcmcleasyldedlvtrkkcpi 221  
287 REDPGAH-RNLMTARLRKLVSPG---VMQLDAPCCLPKGVTLQWAPDQSPCPVPPVP 342  
222 qswpeaygsdfwgsirftcdysqhmqwmaltlrcplkleaslcwqddpltpceti----- 276  
343 QKNATVNEPDQFQVAG---HPNLGVYSTWVKVLOAC-----SNADSLGPFKDDM 391  
277 -palatagesegwylleuvdlhpqclfkts--fensshvechphsgslpsvltvsmtdt-qaq 333  
392 LAVEMKRTGLNNTSYCALEPSSG---TPLPSMASTRARLGEELDD-----FRSHOCMO 443  
334 ltlhfsrtyatfsaasdgplgdpitpmpvysiqtgsvptcldlilpflrqmcilv 393  
444 WNDNMGSLMACPMKXIHRRWLV-----WILCLLAAALFFFLKRRKKAARG 496  
394 wrsd-----vhfawkhvlcpddapyqlil-----tslsgqrc 427  
497 RTLLILHSADGAGERYLVGALASLSOM---PLRAVDLMSRRELISAHGALANFHHRORR 553  
428 rpylllhaadseagrrtlrvalaelrltalgggrdyldwlegtharipglplwaarer 487  
554 ILQEGGVILFSPAAVACCOMLQLOLVEPGRHDLAAMSCVLPDFQGRATGRVGV 613  
488 vareggtvlllmcagps-----taesgdpqgaaslrcllcaaprl-----lla 531  
614 YEDGLHPDSVPSPFRVAPLESPTOLPAFLDALOGGCSSTA-----GRPADRVERVQ 667  
532 yferlcakgdlprlprlpryllrlrdlrrlraldaqpattlasswhlqakrclknrlq 591  
668 A-----LRSAIDSCSSSEAP 683  
592 chlleaakddygstncsp 611

RESULT 15

AA04957  
AA04957 standard; Protein: 667 AA.

AA04957;

24-OCT-2001 (first entry)

Human Interleukin 17 receptor, IL-17RH3.

Human; Interleukin-17 receptor, IL-17RH3; agonist; antagonist;  
PRO8877; DNA 119502-2789; systemic lupus erythematosus;  
rheumatoid arthritis; osteoarthritis; diabetes mellitus;  
allergic disease; asthma; demyelinating disease;  
degenerative cartilaginous disorder; transplantation associated disease.

Homo sapiens.

Key Location/Qualifiers

Key Location/Qualifiers

FT Peptide 1..23  
FT /label= signal\_peptide  
FT Protein 24..667  
FT /label= Mature\_IL\_17RH3  
FT Region 90..96  
FT /note= "N-myristoylation site"  
FT Region 104..108  
FT /note= "CAMP/GMP-dependent protein kinase phosphorylation site"  
FT Modified-site 318..322  
FT /note= "Asn is N-glycosylated"  
FT Region 322..329  
FT /note= "tyrosine kinase phosphorylation site"  
FT Modified-site 347..351  
FT /note= "Asn is N-glycosylated"  
FT Region 358..364  
FT /note= "N-myristoylation site"  
FT Modified-site 364..368  
FT /note= "Asn is N-glycosylated"  
FT Region 453..462  
FT /note= "Eukaryotic cobalamin-binding protein motif"  
FT Domain 455..472  
FT /note= "transmembrane domain"  
FT Region 470..476  
FT /note= "N-myristoylation site"  
FT Region 482..486  
FT /note= "Glycosaminoglycan attachment site"  
FT Region 645..649  
FT /note= "CAMP/GMP-dependent protein kinase phosphorylation site"  
WO200146420-A2.  
28-JUN-2001.  
20-DEC-2000; 2000MO-US34956.  
23-DEC-1999; 9905-0172096.  
30-DEC-1999; 99MO-US31274.  
PR 11-JAN-2000; 2000US-0175481.  
PR 18-FEB-2000; 2000MO-US04341.  
PR 02-MAR-2000; 2000MO-US05841.  
PR 21-MAR-2000; 2000US-0191007.  
PR 02-JUN-2000; 2000MO-US15264.  
PR 22-JUN-2000; 2000US-0213087.  
PR 22-AUG-2000; 2000US-0644488.  
PR 24-AUG-2000; 2000MO-US23328.  
PR 24-OCT-2000; 2000US-0242837.  
PR 10-NOV-2000; 2000MO-US30873.  
PR 28-NOV-2000; 2000US-0253646.  
PR 01-DEC-2000; 2000MO-US32678.  
(GETH ) GENENTECH INC.  
Chen J, Filvaroff E, Fong S, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Li H, Hillan KJ, Tumas D, Van Lookeren M, Vandlen RL, Matanabe CK, Williams PM, Wood WI, Yansura DG;  
WPI: 2001-451708/48.  
DR N-PSDB; AAS09516.  
XX Novel PRO polypeptides homologous to interleukin-17, useful for the diagnosis and treatment of immune related disease e.g. rheumatoid arthritis and diabetes -  
XX Claim 10; Fig 16; 188pp; English.  
XX The sequence is PRO8877 which is the human interleukin 17 receptor, IL-17RH3, encoded by DNA 119502-2789. A composition containing ant/agonists to the PRO polypeptides or individual components are useful for treating a mammal with an immune related disease., e.g. systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 28, 2002, 19:42:54 ; Search time 72.7 Seconds

(without alignments)  
1660.942 Million cell updates/sec

Title: US-09-899-471-5  
Perfect score: 3741  
Sequence: 1 MPVSFLLSLALGRNPVVS.....SSAPGCCCEMDLGPCTTLE 698

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%  
Listing first 45 summaries

Database :

SPTREMBL\_19:\*  
1: sp.archaea:\*  
2: sp.bacteria:\*  
3: sp.fungi:\*  
4: sp.human:\*  
5: sp.invertebrate:\*  
6: sp.mammal:\*  
7: sp.mhc:\*  
8: sp.organelle:\*  
9: sp.phage:\*  
10: sp.plant:\*  
11: sp rodent:\*  
12: sp.virus:\*  
13: sp.vertebrate:\*  
14: sp.unclassified:\*  
15: sp.virus:\*  
16: sp.bacteriap:\*  
17: sp.archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2629	70.3	567	11	099J43 mus musculu
2	1786.5	47.8	538	4	09BR97 O9br97 homo sapien
3	177	4.7	864	11	060943 mus musculu
4	147.5	3.9	866	4	043844 homo sapien
5	147.5	3.9	866	4	096R46 homo sapien
6	119.5	3.2	1013	16	053499 mycobacteri
7	114	3.0	3021	12	068870 hepatitis c
8	112	3.0	1445	11	063155 rattus norv
9	111.5	3.0	2012	4	09BR84 O9br84 homo sapien
10	111.5	3.0	2910	11	055225 mus musculu
11	111	3.0	2873	12	093070 hepatitis g
12	108	2.9	3021	12	081495 hepatitis c
13	107.5	2.9	634	4	096Q25 homo sapien
14	107.5	2.9	680	4	09BVM0 O9bvm0 homo sapien
15	107.5	2.9	689	4	09BSA7 O9bsa7 homo sapien
16	107.5	2.9	733	4	096IS8 O96is8 homo sapien

17	107.5	2.9	746	4	096926 O969r6 homo sapien
18	107.5	2.9	1187	4	094812 O948r2 homo sapien
19	106.5	2.8	478	16	09R789 O9r789 deinococcus
20	106.5	2.8	1152	4	09URK1 O9urk1 homo sapien
21	106.5	2.8	1186	4	094839 O948r3 homo sapien
22	106.5	2.8	1187	4	096R23 O96r23 homo sapien
23	106	2.8	581	10	094BR5 O94br5 cinamomum
24	106	2.8	1030	10	09BR59 O9br59 homo sapien
25	105.5	2.8	549	10	09FV22 O9fv22 cinamomum
26	104	2.8	1002	11	091VB4 O91vb4 mus musculu
27	103.5	2.8	758	4	09NKR9 O9nkr9 homo sapien
28	103.5	2.8	1160	10	09FHR8 O9fhr8 arabidopsis
29	103.5	2.8	3021	12	081258 O81258 hepatitis c
30	103	2.8	906	16	09HX92 O9hx92 pseudomonas
31	103	2.8	946	10	022015 O22015 cyllindrothe
32	102.5	2.7	1248	4	09UJ61 O9uj61 homo sapien
33	102	2.7	1767	5	09W4F5 O9w4f5 drosophila
34	102	2.7	1767	5	024495 O24495 drosophila
35	102	2.7	4848	2	007944 O07944 streptomyce
36	101.5	2.7	698	16	09PH5 O9ph5 xylella.fas
37	101.5	2.7	1274	10	09S287 O9s287 arabidopsis
38	101	2.7	2873	12	093069 O93069 hepatitis g
39	100.5	2.7	454	5	09UA07 O9ua07 caenorhabdi
40	100.5	2.7	462	5	09Y198 O9y198 caenorhabdi
41	100.5	2.7	475	5	09U343 O9u343 caenorhabdi
42	100.5	2.7	634	5	09U9Y8 O9u9y8 caenorhabdi
43	100.5	2.7	647	5	062395 O62395 caenorhabdi
44	100.5	2.7	864	4	043297 O43297 homo sapien
45	100.5	2.7	936	13	098ST1 O98st1 gallus gall

#### ALIGNMENTS

RESULT 1  
ID 099J43 PRELIMINARY; PRT; 567 AA.  
AC 099J43;  
DR 01-JUN-2001 (TREMBLrel. 17, Created)  
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
DI 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE HYPOTHETICAL 62.8 KDA PROTEIN.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_Taxid=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Strusberg R.;  
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL, BC004759; AAH04759.1;  
KM Hypothetical protein.  
SQ SEQUENCE 567 AA; 62798 MW; C1AAB79E2006BID CRC64;

Query Match	Score	Length	ID	Description
Best Local Similarity	70.3%;	567	11	099J43 mus musculu
Matches 487; Conservative	99.6%;	Pred. No. 2.6e-230;		
Mismatches 2; Indels 0; Gaps 0;				
OY 1 MPVSFLLSLALGRNPVVSLERLMEPODARCSLGSCHLMDGVLCIPGSLQSAAPGV 60				
DB 1 MPVSFLLSLALGRNPVVSLERLMEPODARCSLGSCHLMDGVLCIPGSLQSAAPGV 60				
OY 61 LPVTRQTELVLCRPOKTDALRYRVVHLAVHGMMEPERAGKSDSELRNSLQAO 120				
DB 61 LPVTRQTELVLCRPOKTDALRYRVVHLAVHGMMEPERAGKSDSELRNSLQAO 120				
OY 121 VVLSFOAYPIARCALLEVQPADLVOPGOSVSAVFDFEASLGAEOIWSYTKRYORE 180				
DB 121 VVLSFOAYPIARCALLEVQPADLVOPGOSVSAVFDFEASLGAEOIWSYTKRYORE 180				
OY 181 LNEVQQLPDCRGLEVRDSISCSWVLPMLNVSTDDDNVLLITDVSEQDFSLIYLRPYPD 240				
DB 181 LNEVQQLPDCRGLEVRDSISCSWVLPMLNVSTDDDNVLLITDVSEQDFSLIYLRPYPD 240				

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Db 181 LNTLQOLPDCRGLFVDSIOSCWVLPWLVNSTDGDNVLLTLDVSEEDFSLLYLRPVD 240
QY 241 ALKSLMYKNLTPGPNITLNTHTDLPVLCICIQVMSLEPDEREFCFPREDPGAHRLMHTA 300
Db 241 ALKSLMYKNLTPGPNITLNTHTDLPVLCICIQVMSLEPDEREFCFPREDPGAHRLMHTA 300
QY 301 RLRLVSPGWOLDAPCCLEKRYTLCAWAPQSPQPLVPVPYPOKNAVNEPODFOLVACH 360
Db 301 RLRLVSPGWOLDAPCCLEKRYTLCAWAPQSPQPLVPVPYPOKNAVNEPODFOLVACH 360
QY 361 PNLQVSTWMEVQLOACSWADSLGPFKDDMLVEMKTGLNNTSVCALEPSCGTPPSMA 420
Db 361 PNLQVSTWMEVQLOACSWADSLGPFKDDMLVEMKTGLNNTSVCALEPSCGTPPSMA 420
QY 421 STRAARLCEBELLQDFRSHOCQMOLMNDNMGSLWACPMDKYTHRRVYLVWLACLLAALF 480
Db 421 STRAARLCEBELLQDFRSHOCQMOLMNDNMGSLWACPMDKYTHRRVYLVWLACLLAALF 480
QY 481 FELLKKDR 489
Db 481 FELLKKDR 489

```

RESULT 2

Q9BR97 PRELIMINARY: PRT: 538 AA.

QY 01-JUN-2001 (TREMBlrel. 17, Created)

DT 01-JUN-2001 (TREMBlrel. 17, last sequence update)

DE 01-DEC-2001 (TREMBlrel. 19, last annotation update)

DE HYPOTHEICAL 59.1 KDA PROTEIN.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI\_Taxid=9606;

RP SEQUENCE FROM N.A.

RC TRISSUE-ENDOMETRIAL ADENOCARCINOMA;

KL Strausberg R.;

KL Submitted (Apr-2001) to the EMBL/Genbank/DBJ databases.

DR EMBL: BC006411; AAH06411.1; -

KW Hypothetical protein.

SEQUENCE 538 AA: 59127 MW: 65E6344DA6A5AFD2 CRC64;

Query Match 47.8%; Score 1786.5; DB 4; Length 538;  
 Best Local Similarity 64.7%; Pred. No. 9.7e-154;  
 Matches 346; Conservative 51; Mismatches 109; Indels 29; Gaps 5;

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QY 1 MPVSWFLSLALGRNPVVSLERLNEPDDTARCSLGLSCHLMQGVLCPLGSLQSAAPGV 60
Db 1 MPVSWFLSLALGRNPVVSLERLNEPDDTARCSLGLSCHLMQGVLCPLGSLQSAAPGV 60
QY 61 LVPRLDTLRLRCQKQKDCALRVVAVLAHGHNAPEPE---AGKSDSELOESRNAS 116
Db 61 LVPRLDTLRLRCQKQKDCALRVVAVLAHGHNAPEPE---AGKSDSELOESRNAS 116
QY 117 LQAQVVSFOAYPIARCTALEVQVADLVQPOGOSVSAVDECEASIGAVQISYTKPR 176
Db 117 LQAQVVSFOAYPIARCTALEVQVADLVQPOGOSVSAVDECEASIGAVQISYTKPR 176
QY 121 LQAQVVSFOAYPIARCTALEVQVADLVQPOGOSVSAVDECEASIGAVQISYTKPR 180
Db 121 LQAQVVSFOAYPIARCTALEVQVADLVQPOGOSVSAVDECEASIGAVQISYTKPR 180
QY 177 YQELNLTQQLPDCRGLFVDSIOSCWVLPWLVNSTDGDNVLLTLDVSEEDFSLLYLR 236
Db 177 YQELNLTQQLPDCRGLFVDSIOSCWVLPWLVNSTDGDNVLLTLDVSEEDFSLLYLR 236
QY 181 YKELNLTQQLPDCRGLFVDSIOSCWVLPWLVNSTDGDNVLLTLDVSEEDFSLLYLR 225
Db 181 YKELNLTQQLPDCRGLFVDSIOSCWVLPWLVNSTDGDNVLLTLDVSEEDFSLLYLR 225
QY 237 PYVDALSLMTKNTLTPGPNITLNTHTDLPVLCICIQVMSLEPDEREFCFPREDPGAHRL 296
Db 237 PYVDALSLMTKNTLTPGPNITLNTHTDLPVLCICIQVMSLEPDEREFCFPREDPGAHRL 296
QY 226 QVQGPFRPMHKNLTGPOITLNTHTDLPVLCICIQVMSLEPDEREFCFPREDPGAHRL 285
Db 226 QVQGPFRPMHKNLTGPOITLNTHTDLPVLCICIQVMSLEPDEREFCFPREDPGAHRL 285
QY 297 WHIARLRLVLSFGVQWOLDAPCCLEKRYTLCAWAPQSPQPLVPVPYPOKNAVNEPODFOL 356
Db 297 WHIARLRLVLSFGVQWOLDAPCCLEKRYTLCAWAPQSPQPLVPVPYPOKNAVNEPODFOL 356
QY 286 WQARLRLVLSFGVQWOLDAPCCLEKRYTLCAWAPQSPQPLVPVPYPOKNAVNEPODFOL 345
Db 286 WQARLRLVLSFGVQWOLDAPCCLEKRYTLCAWAPQSPQPLVPVPYPOKNAVNEPODFOL 345

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QY 357 VAGHNLQVQVSTWMEVQLOACSWADSLGPFKDDMLVEMKTGLNNTSVCALEPSCGTP 416
Db 357 VAGHNLQVQVSTWMEVQLOACSWADSLGPFKDDMLVEMKTGLNNTSVCALEPSCGTP 416
QY 346 LKGNHNLQVQVSTWMEVQLOACSWADSLGPFKDDMLVEMKTGLNNTSVCALEPSCGTP 405
Db 346 LKGNHNLQVQVSTWMEVQLOACSWADSLGPFKDDMLVEMKTGLNNTSVCALEPSCGTP 405
QY 417 PSMASTRAARLCEBELLQDFRSHOCQMOLMNDNMGSLWACPMDKYTHRRVYLVWLACLLA 476
Db 417 PSMASTRAARLCEBELLQDFRSHOCQMOLMNDNMGSLWACPMDKYTHRRVYLVWLACLLA 476
QY 406 PSKASTRAARLCEBELLQDFRSHOCQMOLMNDNMGSLWACPMDKYTHRRVYLVWLACLLA 464
Db 406 PSKASTRAARLCEBELLQDFRSHOCQMOLMNDNMGSLWACPMDKYTHRRVYLVWLACLLA 464
QY 477 AALFEFLKKDRRRRAARCSRTALLSHADGACERYL-----GALASALSNP 525
Db 477 AALFEFLKKDRRRRAARCSRTALLSHADGACERYL-----GALASALSNP 525
QY 465 AALSLILLKKDRH---AKGWLRLKODVRSNGEMEQALGGPPGSOACASSPLP 516
Db 465 AALSLILLKKDRH---AKGWLRLKODVRSNGEMEQALGGPPGSOACASSPLP 516

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RESULT 3

Q60943 PRELIMINARY: PRT: 864 AA.

QY 060943

AC 060943

DT 01-NOV-1996 (TREMBlrel. 01, Created)

DT 01-NOV-1996 (TREMBlrel. 01, last sequence update)

DE 01-DEC-2001 (TREMBlrel. 19, last annotation update)

DE INTERLEUKIN 17 RECEPTOR.

GN IL17R.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI\_Taxid=10090;

RP SEQUENCE FROM N.A.

RC TRISSUE-THYMOMA EL4;

RX MEDLINE-96111968; PubMed-8777726;

RA Yao Z., Fanslow W.C., Seldin M.F., Rousseau A.M., Painter S.L.,

RT Comeau M.R., Cohen J.I., Spriggs M.K.;

RT Herpesvirus Saimiri encodes a new cytokine, IL-17, which binds to a

novel cytokine receptor.;

RT Immunity 3:811-821(1995).

DR EMBL: U01993; AAC52357.1; -

DR MGI:107399; 1117r.

KW Receptor.

SEQUENCE 864 AA: 97807 MW: 343FD51AA687DA31 CRC64;

Query Match 4.7%; Score 177; DB 11; Length 864;  
 Best Local Similarity 20.5%; Pred. No. 4e-07;  
 Matches 121; Conservative 65; Mismatches 189; Indels 216; Gaps 29;

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QY 198 SIQSCW-----VLPWLVNSTDGDNVLLTLDVSEEDFSLLYLRPVP----- 239
Db 198 SIQSCW-----VLPWLVNSTDGDNVLLTLDVSEEDFSLLYLRPVP----- 239
QY 240 DALKSLWY--KNLT--GPQNTLN-----HTDLYPLCICIQVMSLEPD----- 277
Db 240 DALKSLWY--KNLT--GPQNTLN-----HTDLYPLCICIQVMSLEPD----- 277
QY 53 KNTCLDSDSHPRNLTLPSSPKNTYINLSVSTQGEELVPLAVE--WTLOTFDASITYLEG 111
Db 53 KNTCLDSDSHPRNLTLPSSPKNTYINLSVSTQGEELVPLAVE--WTLOTFDASITYLEG 111
QY 278 -----SER--VEFCFPREDPGAHRLMHTAHLR--VLSPG-----VQOLDAPCC 318
Db 278 -----SER--VEFCFPREDPGAHRLMHTAHLR--VLSPG-----VQOLDAPCC 318
QY 112 AELSVQDLNNTNERLCYVE--QLSMQHLHRRKRRFSFHHVDPQGEYTVHHLKPR-- 167
Db 112 AELSVQDLNNTNERLCYVE--QLSMQHLHRRKRRFSFHHVDPQGEYTVHHLKPR-- 167
QY 319 PGKRYTLCAWAPQSPQPLVPVPYPOKNAVNEPODFOLVAGHNLQVQVSTWMEVQ 374
Db 319 PGKRYTLCAWAPQSPQPLVPVPYPOKNAVNEPODFOLVAGHNLQVQVSTWMEVQ 374
QY 168 -----IPDGPQNHKSKILFVDPDCDSKMKMTSCVSSSIMPONITVELLDQHLR 218
Db 168 -----IPDGPQNHKSKILFVDPDCDSKMKMTSCVSSSIMPONITVELLDQHLR 218
QY 375 LQAQVVSFOAYPIARCTALEVQVADLVQPOGOSVSAVDECEASIGAVQISYTKPR 405
Db 375 LQAQVVSFOAYPIARCTALEVQVADLVQPOGOSVSAVDECEASIGAVQISYTKPR 405
QY 219 VDFTLNNEST--PYQ--VLESFSDSEHNSCFDYYKQIFAPRQEEHOBANVTFLSKFH 274
Db 219 VDFTLNNEST--PYQ--VLESFSDSEHNSCFDYYKQIFAPRQEEHOBANVTFLSKFH 274
QY 406 -CA-----LEP--SGC-----PPLPSMASTRARLGBELLQDFRSHOCQMOLMND 447
Db 406 -CA-----LEP--SGC-----PPLPSMASTRARLGBELLQDFRSHOCQMOLMND 447
QY 275 WCHHHVQVQVFFSSCLNDCLRAHVVTPCVISNTVPR----- 313
Db 275 WCHHHVQVQVFFSSCLNDCLRAHVVTPCVISNTVPR----- 313
QY 448 NMGSWACPMDKYTHRRVYLVWLACLLAALFEFL-----LLKKDRRAARCS----- 496
Db 448 NMGSWACPMDKYTHRRVYLVWLACLLAALFEFL-----LLKKDRRAARCS----- 496
QY 314 -----PVADYI--PLWVYGLITLILILVGSVILILICMTWRLSGADQEKHGDSKIN 364
Db 314 -----PVADYI--PLWVYGLITLILILVGSVILILICMTWRLSGADQEKHGDSKIN 364

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QY 497 -----KALLHSADGAGYERLVGALASAL-SOMPLRAVADLMSRRELSA 540  
 DB 365 GILPVADLTPEPLRKRWITVYADHPLVEVYLFKFAOFLITACGEVADLLEEQVISE 424  
 QY 541 HGALAMHHORRRLLOEGVITLFS-----PAVAOCQOMLOQVTEPG 585  
 DB 425 VGVATWVSROKOEVENESKIIILCSRGTOAKMKAILGWAEPVQLRCDHM-----KPA 478  
 QY 586 PHALAMLSOVLDPLOGATGRVGVYFODLHPDPSPPRVAPLESL 636  
 DB 479 -GDLFTAAAMNLLDPFKRPACGTFNVCYFSGICSERDVPDLFNITSRYPL 528  
  
 RESULT 4  
 ID 043844 PRELIMINARY; PRT; 866 AA.  
 AC 043844;  
 DT 01-JUN-1998 (TREMblrel. 06, Created)  
 DT 01-JUN-1998 (TREMblrel. 06, Last sequence update)  
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
 DE IL-17 RECEPTOR.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98035683; PubMed=9367539;  
 RA Yao Z., Spriggs M.K., Derry J.M.J., Strockbine L., Park L.S.,  
 Vandenbos T., Zappon J., Painter S.L., Armitage R.J.;  
 RT "Molecular characterization of the human interleukin (IL)-17  
 receptor."  
 RL Cytokine 9:794-800(1997).  
 DR EMBL; U58917; AAB99730.1; --  
 KW Receptor.  
 SQ SEQUENCE 866 AA; 96122 MW; 88AF626A83F3FF70 CRC64;

Query Match 3.9%; Score 147.5; DB 4; Length 866;  
 Best Local Similarity 19.3%; Pred. No. 0.00019;  
 Matches 140; Conservative 78; Mismatches 239; Indels 269; Gaps 32;

QY 55 SAGP-----VLP-----TRLOTELVLRCPQKTDICALRVVYVHLAVGHNAERE 100  
 DB 10 AVPGPLIGLILLGLVLAIPGASLRILDRALVCSQP---GINCTYVKNSTCLDDSWIHPR 66  
 QY 101 EAGKSDSELOESRNASLOAVVLSF---QAVPIARCALLEVOVPADLVQPGOSVGSAYF 156  
 DB 67 -----NLTPSSPKDQIOIOLHFANTQOGDLEPVAN---IEWTLQTD----- 103  
 QY 157 DCFEASL---GAVOVWSTKPRYOKELNTQOLPDCRGLEVRDSIQ---SCWVLPWLN 209  
 DB 104 ---ASILYLEGAEVLSV---LOLNTNERL---CVREFELSKLRHHRMRFTFSH 148  
 QY 210 VSTDGDNVLLTLVDSEODFSFLYLRLRPVDALKSMTYKNLTGPNITLNTDVLVPCIC- 268  
 DB 149 FVVDPP-----QYEYTVVHLLPKPIPDGDPNHQSKNFLVPDCEHARMKVTPPCMS 199  
 QY 269 -----IOVMSLEPDSERVEFC-----PFREDPGAHRLMIHIAIRLVLS 306  
 DB 200 GSLMDENITVETLEAQLRVSTFLMNSTHYQIILTSFPHMNHSCFEHMH- 252  
 QY 307 PGWQDAPPCCLPGKVTYLCQAPDOSQOPLVPPVPQKNATVNEPODFO-----LVAGH 360  
 DB 253 -----IOVMSLEPDSERVEFC-----PFREDPGAHRLMIHIAIRLVLS 272  
 QY 361 PNLGVOSTWEKVYQLOACSWADSLGPFKDDMLVEMKTGLNNTSVCALEPSCGTPLPSPA 420  
 DB 273 LAGCCR---HOVOIQ-----PF-----FSSCLND---CLHNSATVSCPEMP 307  
 QY 421 STRAARLGEELLQDFRSHQCMQIMNDNMGSLMACPMDKYIHRRVYLVWVLAQILLAAALF 480  
 DB 308 DT-----PEPIDY-----MPLW-----VWFITGISTILVGSVI- 337

QY 481 FFLIAKKDRKRAAGS-----RTALLHSADGAGYERLVG 515  
 DB 338 -LIVCMTWRLAGSGSEKYSDDTKYTDGLPAADLIPPLPKRWITVYADHPLVYDVYL 396  
 QY 516 ALAS-ALSOMPLRAVADLMSRRELSAHGALAMHHORRRLLOEGVITLFSRAVAOCQ 574  
 DB 397 KFAOFLITACGTEVADLLEBOALS EAGVMTWVGROKOEVENESKIIYLCSRGTRAKWQ 456  
 QY 575 QWL-----OLQVTEPGP-HDALAMLSOVLDPLOGATGRVGVYFODLHPDVSPP 627  
 DB 457 ALLGRGAPVRLRCDHGRKVPQGLFTAAAMNLLDPFKRPACGTYVVCYFSEVSCDGDVPL 516  
 QY 628 FRYVAPLESLPTQLEPAF-----LDALOGCGSTSAGRPADRVERVTO-----A 668  
 DB 517 FGAPRPYPLMDRFEVEYFRIDLEWFOG-----RMRHVGLSGDNVTLRSPGRQ 566  
 QY 669 LRSAID 674  
 DB 567 LRAILD 572  
  
 RESULT 5  
 ID 096F46 PRELIMINARY; PRT; 866 AA.  
 AC 096F46;  
 DT 01-DEC-2001 (TREMblrel. 19, Created)  
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
 DE SIMILAR TO INTERLEUKIN 17 RECEPTOR.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX TISSUE=UTERUS, AND LEIOMYOSARCOMA;  
 RA Strausberg R.;  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC011624; AAH11624.1; --  
 KW Receptor.  
 SQ SEQUENCE 866 AA; 96131 MW; 28330BED2303B0C9 CRC64;

Query Match 3.9%; Score 147.5; DB 4; Length 866;  
 Best Local Similarity 19.3%; Pred. No. 0.00019;  
 Matches 140; Conservative 78; Mismatches 239; Indels 269; Gaps 32;

QY 55 SAGP-----VLP-----TRLOTELVLRCPQKTDICALRVVYVHLAVGHNAERE 100  
 DB 10 AVPGPLIGLILLGLVLAIPGASLRILDRALVCSQP---GINCTYVKNSTCLDDSWIHPR 66  
 QY 101 EAGKSDSELOESRNASLOAVVLSF---QAVPIARCALLEVOVPADLVQPGOSVGSAYF 156  
 DB 67 -----NLTPSSPKDQIOIOLHFANTQOGDLEPVAN---IEWTLQTD----- 103  
 QY 157 DCFEASL---GAVOVWSTKPRYOKELNTQOLPDCRGLEVRDSIQ---SCWVLPWLN 209  
 DB 104 ---ASILYLEGAEVLSV---LOLNTNERL---CVREFELSKLRHHRMRFTFSH 148  
 QY 210 VSTDGDNVLLTLVDSEODFSFLYLRLRPVDALKSMTYKNLTGPNITLNTDVLVPCIC- 268  
 DB 149 FVVDPP-----QYEYTVVHLLPKPIPDGDPNHQSKNFLVPDCEHARMKVTPPCMS 199  
 QY 269 -----IOVMSLEPDSERVEFC-----PFREDPGAHRLMIHIAIRLVLS 306  
 DB 200 GSLMDENITVETLEAQLRVSTFLMNSTHYQIILTSFPHMNHSCFEHMH- 252  
 QY 307 PGWQDAPPCCLPGKVTYLCQAPDOSQOPLVPPVPQKNATVNEPODFO-----LVAGH 360  
 DB 253 -----IOVMSLEPDSERVEFC-----PFREDPGAHRLMIHIAIRLVLS 272  
 QY 361 PNLGVOSTWEKVYQLOACSWADSLGPFKDDMLVEMKTGLNNTSVCALEPSCGTPLPSPA 420



Db 273 LKGCRR-----HOVOIO-----PF-----FSSCLND-----CIRHSATVSCPEMP 307  
 QY 421 STRAARIGEELLQDFRSHOCMOLMNDNMGSLWACPMCKYHRRMVLWLAICLLAALF 480  
 Db 308 DT-----PEPIPDY-----MPLM-----VWFITGISILVGSYV- 337  
 QY 481 FELLKRRKRRKARS-----RVALLLHSADGAGYERLVG 515  
 Db 338 -LLIYCMTWRLAGPSEKSYSDTKYDGLFVADLIPPLKPRKWIITYSADHPLTVYVL 396  
 QY 516 ALAS-ALSGMPLRVAVDLSRRELSTHIGALAMPHHRRRILOEGCVILLSPRAVACO 574  
 Db 397 KFAOFLTRACGTEVALDLEBOHISAGVMTWVGROKOEVENESKTIIVLCSRGTRAKQ 456  
 QY 575 OWL-----QLOTVBEPG-HDALAAWLSCVLPDLOGRATGRYGVYFDGLHPDSVSP 627  
 Db 457 ALLGSGAFVRLRCDHGKPGVGLFTTAMNMILPDKRACGTYVVCYFSEVSCGDVFDL 516  
 QY 628 PRVAPLESLPQLPAP-----LDALOGCSTSGAPRADVERVTO-----A 668  
 Db 517 FGAPRPRYELMDFEEVYRIDIEMFOPG-----RMHRYGELSGDNYLRSPPGRQ 566  
 QY 669 LRSALD 674  
 Db 567 LRAALD 572

RESULT 6  
 O53499 PRELIMINARY: PRT: 1013 AA.  
 AC O53499  
 DT 01-JUN-1998 (TREMBLrel. 06, Created)  
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE HELICASE.  
 GN HELZ OR RV2101 OR MW020.01.  
 OS Mycobacterium tuberculosis.  
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
 OC Actinomycetales; Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.  
 RX NCBI\_TaxID=1773;  
 RP  
 RC SEQUENCE FROM N.A.  
 RX STRAIN=H37RV;  
 RX MEDLINE=98295987; PubMed=9634230;  
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,  
 Gordon S.V., Eiglmier K., Gas S., Barry C.E. III, Tekala F.,  
 Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,  
 Davies R., Devlin K., Feltham D., Gentles S., Hamlin N., Holtroyd S.,  
 Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,  
 Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,  
 Rutter S., Seeger K., Skelton S., Squares S., Squares R.,  
 Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;  
 RA \*Deciphering the biology of Mycobacterium tuberculosis from the  
 RT complete genome sequence.\*  
 RL Nature 393:537-544(1998).  
 CC -1- SIMILARITY: TO HELICASE C-TERMINAL DOMAIN.  
 DR EMBL: AL021924; CAA17284.1;  
 DR Tuberculast; RV2101;  
 DR InterPro: IPR001410; DEAD.  
 DR InterPro: IPR001650; Helicase\_C.  
 DR InterPro: IPR00330; SNF2\_N.  
 DR Pfam: PF00271; Helicase\_C.1.  
 DR Pfam: PF00176; SNF2\_N.1.  
 DR SMART: SM00487; DEXDC.1.  
 DR SMART: SM00490; HELICC.1.  
 DR ATP-binding; Complete proteome; Helicase.  
 KM  
 QY SEQUENCE 1013 AA; 111629 MW; 601PFDLDB5CABEPI CRC64;

QY 90 LAVHGHMAEP--EAGKSDSELOESHNSLAQOVLSFOAYPIARCALLEVQPADL--- 144  
 Db 2 LVHGFMSNSGMRMAEDSLL-----VSPSALASARHPA-----APADLIAG 49  
 QY 145 VQPGQ-----SVGSAVDFCFE-----ASLGAEOIWSYTKRYKELNL- 184  
 Db 50 IHPKPRATAVLLPRLSRAPLSPDLIRLAPRAARDPMLAMTV--VVDLPTALA 107  
 QY 185 ---QQLPDCR-GLFY-----RDSIQSCVYLPMINVTG-----DNVL 218  
 Db 108 AFDDPAPRVRYGASVDYLAELAVFAREIVERGRVILQRLRDYTGAAACMPVLOGRVVA 167  
 QY 219 LTLVSEEDQDFSEFLYLRFV-----PDALSLWAKNLTGPNITLPHNDLV 264  
 Db 168 MT-----SLVSAMPVCAEYGGHDPHELATSLDAM-----VDAVRAALSPMDL 214  
 QY 265 PCLCTIQWSLEPDSRVECPREDPGAHNMHIAIRLRLVLSGVQOLDAPCCLPKVTLL 324  
 Db 215 P-----PRGRSKRHR-----AVEAW-LTALTCPDGRFDA 243  
 QY 325 CWAAPDQSPQPIVPPVQKNATVNEPQPOLVAGHPNLCVOYSTKEVQLOACSNADSL 384  
 Db 244 -----EPDELALA-----EALRPWDVGI-----GTV 266  
 QY 385 GFPRDMLVEMKGTGLNNTSVCALPESGCTPLPSMASTRARIGEELLQDFRSHQCM--- 441  
 Db 267 GPRAATPRLSEVETENET-----PAG-----SLMRL-ELLQSTQDPSLVA 309  
 QY 442 -QLMNDNMGSLMACPMCKYHRRV---LVWLACILLAALFELLKKDRKARGS 496  
 Db 310 EQANND--GSL-----RRLMDRPOELLFELGRASRIFFELY-----PALRTA 351  
 QY 497 RTALLHSADAGYERLYGALASALSQMDPLRAVVDLSRRELISAHQALMFHQRRITLO 556  
 Db 352 CPSGLELDADA--YRLSGTAAYVDEGFGVILPSM-----W--DRRKL- 393  
 QY 557 EGGVILLFSP--AAVACCOOMLQLOTV-----PGPHDALAAMLSCVLP----- 599  
 Db 394 --GLVLAATYVDGVGASKFRQQLVYFRRELAVAGDPLSEETALLETSPILRLR 451  
 QY 600 -----DFLOGRATGRYGVYFDGLL--HPDSVSPPRVAPLESLPQLPA 642  
 Db 452 GOWVALDTEQMRGLEFLERKPTGRTAELLALASHPDVDVTPLEVAV-----RADG 506  
 QY 643 FLDALOGCCSTAGRPADRVERTALASALDSCTS-----SSAPGCCBMDLGPCTTL 697  
 Db 507 WLDDLLAGAAASLQPLDPPDGFATRLRPOYORGIAWLAFLSLGIGSCLADMGLGKTV 566  
 QY 698 E 698  
 Db 567 Q 567

RESULT 7  
 O68870 PRELIMINARY: PRT: 3021 AA.  
 AC O68870  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE GENOME POLYPROTEIN [CONTAINS: ENVELOPE GLYCOPROTEIN E2 (GP68) (GP70)  
 DE (NS1)].  
 OS Hepatitis C virus.  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
 OC Hepacivirus.  
 OC NCBI\_TaxID=11103;  
 RX  
 RP SEQUENCE FROM N.A.  
 RA Seelig R., Weber P., Seeling H.P., Ledger N., Botner C., Renz M.;  
 RT Hepatitis C virus type V genome isolated from a patient in Germany.\*;  
 RL Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: TO HEPATITIS C VIRUS ENVELOPE GLYCOPROTEIN E1.

Query Match 3.2%; Score 119.5; DB 16; Length 1013;  
 Best Local Similarity 20.8%; Pred. No. 0.085;  
 Matches 150; Conservative 80; Mismatches 224; Indels 267; Gaps 38;

EMBL: X76918; CA54244.1; -  
 DR HSSP: P27958; 1A1V.  
 DR MEROPS; 529.001; -  
 DR InterPro: IPR001410; DEAD.  
 DR InterPro: IPR002522; HCV\_capsid.  
 DR InterPro: IPR002521; HCV\_core.  
 DR InterPro: IPR002519; HCV\_eav.  
 DR InterPro: IPR002531; HCV\_nsf.  
 DR InterPro: IPR002518; HCV\_nsf.  
 DR InterPro: IPR004109; HCV\_nsf.  
 DR InterPro: IPR000745; HCVNS4b.  
 DR InterPro: IPR001490; HCV\_NS4b.  
 DR InterPro: IPR002868; HCV\_NS5a.  
 DR InterPro: IPR002166; HCV\_RdRp.  
 DR InterPro: IPR001650; Helicase\_C.  
 DR Pfam: PF01543; HCV\_core; 1.  
 DR Pfam: PF01539; HCV\_nsf; 1.  
 DR Pfam: PF01560; HCV\_nsf; 1.  
 DR Pfam: PF01538; HCV\_NS1; 1.  
 DR Pfam: PF02907; HCV\_NS3; 1.  
 DR Pfam: PF01006; HCV\_NS4a; 1.  
 DR Pfam: PF01001; HCV\_NS4b; 1.  
 DR Pfam: PF01506; HCV\_NS5a; 1.  
 DR Pfam: PR00998; HCV\_RdRp; 1.  
 DR Pfam: PR00271; Helicase\_C; 1.  
 DR ProDom: PD186062; HCV\_NS1; 1.  
 DR ATP-binding; Coat protein; Envelope protein; Glycoprotein; Helicase;  
 KW Nonstructural protein; Polyprotein; RNA-directed RNA polymerase;  
 KW Transmembrane.  
 FT CHAIN 1 191 CORE PROTEIN.  
 FT CHAIN 192 383 ENVELOPE PROTEIN.  
 FT CHAIN 384 735 NS1 PROTEIN.  
 FT CHAIN 736 1012 NS2 PROTEIN.  
 FT CHAIN 1013 1663 NS3 PROTEIN.  
 FT CHAIN 1664 1717 NS4A PROTEIN.  
 FT CHAIN 1718 1978 NS4B PROTEIN.  
 FT CHAIN 1979 2430 NS5A PROTEIN.  
 FT CHAIN 2431 3021 NS5B PROTEIN.  
 SQ SEQUENCE 3021 AA; 329092 MW; BF2B499AA55A58CF CRC64;

Query Match 3.08; Score 114; DB 12; Length 3021;  
 Best Local Similarity 20.78; Pred. No. 1.2; Indels 218; Gaps 38;

Matches 147; Conservative 88; Mismatches 258; Indels 218; Gaps 38;  
 QY 6 FLSTALGRNVVVSLEKMEPQDARCSL---GLSCHLMDGVLCPLGSLQSGPYLY 62  
 DB 285 FLVGAATFR-----RRHOTVCNCSLYFCHLSGHRAMDM-----MNSPANGMV 333  
 QY 63 PTRLOTELVLCRQKTDALR-----VRVVHLAVHGHAEPEEA-----GKSDSELOES 112  
 DB 334 VSH-----VLRLPOTLFDIINGAHMGILAGLAYYSMOGNNAKAVIMVMSGVDAETIIT 388  
 QY 113 RNSLSAQOVLS--FOATPIARCALLEOVVPDVLVPGOS--VGSAVDFCEFA-SLGAEV 167  
 DB 389 GGSAAHGVSTLTSSFSGP-----QOKLQVKTNGSMHINSTALNCNESINTGPIA 439  
 QY 168 QIWSYTRPRQKELNLT---COLPDCRG-----EYVDSIOS-----CW----- 203  
 DB 440 GILYYHK-----FNSIGCPRLSSCKPTTFPRQSGSLDVAVTASADKPYCYMHAAPR 493  
 QY 204 ---VLPWLVN-----STGDGNVLLTLDVSEEDQFSFLL-VLRVPDALKS 244  
 DB 494 PCDVVPLANTGCPYCCFPSPVVGTTDRKGV-PTYNMGENSEDVLLLESTIRPSSGRWFG 552  
 QY 245 LMTKNLTGPONITLNHDLVPCLCIQVWSLEPDSERVEFCP---FREDPGAHRMLMHIAR 301  
 DB 553 CAMNNSGTG---FLKTCGAPPC-NIYGGGNNNESHLCFPTDCFRKHPDATYSR----- 602  
 QY 302 LRVLSPEVMDLAPCCLPKGTLCQWAPDQPCQPLVPPVPPQANAYVNEQDFOLVAGHP 361

DB 603 ---CGAGFWL--TPROMVDPYRLMHP-----CTVN-----FTLF----- 633  
 QY 362 NLGVSTWKEVQLOACSMWADSLGPPKDDMLLYEMKTLNNTSVCALEPGSCFLPMSAS 421  
 DB 634 KYRMFVGFEHRTAACNNTREKCNTERDROSEQHPHLSTTELATLPCSTFMPAL-S 692  
 QY 422 TRARIGEELLQDFRSHOCOMLMDNMGS-L-WACPDKXYIHRWLVLTACLILAA-- 478  
 DB 693 TGLIHLQNIYD-----VOYLGVSGMWGAL-----KMEVILLIFILLADAR 737  
 QY 479 -LFFLLKKNRRKA-----RGSTALLHSAD 506  
 DB 738 CVALMLMIMISOAEALLENVTLKAVAAAGTHGIGYLVAFCAAMHVKGLVPLVYSIF 797  
 QY 507 GAGYERLVGALASALSOPPLRVAVDLSRRELASGA-----LAFHHQRRIL 555  
 DB 798 G-----LMSLALVLLLPQRYA--WSESDSITLGAGVLYGFFLISWYKMWIGR-- 847  
 QY 556 QEGGVILLFSPAAVAGCQOWLOLQTVED---GPHDALAAMLSCVLPDEL 602  
 DB 848 -----LIMNQYTICRESALQV-WVPLRLARSGDGVILLSTLXPSLI 891

RESULT 8  
 ID 063155 PRELIMINARY; PRT; 1445 AA.  
 AC 063155;  
 DT 01-NOV-1996 (Tremblrel. 01. Created)  
 DT 01-JAN-1998 (Tremblrel. 05. Last sequence update)  
 DT 01-DEC-2001 (Tremblrel. 19. Last annotation update)  
 DE COLORECTAL TUMOR SUPPRESSOR.  
 GN DCC.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97015074; Pubmed=8861902;  
 RA Keino-Masu K., Masu M., Hinck L., Leonardo E.D., Chan S.S.X.,  
 RA Culotti J.G., Tessier-Lavigne M.,  
 RT "Deleted in Colorectal Cancer (DCC) encodes a netrin receptor.";  
 RL Cell 87:175-185(1996).  
 RN [2]  
 RP SEQUENCE OF 387-420 FROM N.A.  
 RX MEDLINE=90100559; Pubmed=2294591;  
 RA Fearon E.R., Cho K.R., Nigro J.M., Kern S.E., Simons J.W.,  
 RA Ruppert J.M., Hamilton S.R., Preisinger A.C., Thomas G., Kinzler K.W.,  
 RT "Identification of a chromosome 18q gene that is altered in colorectal  
 RT cancers.";  
 RL Science 247:49-56(1990).  
 DR EMBL: U68725; AAB41099.1; -  
 DR EMBL: M32291; AAA41086.1; -  
 DR HSSP: P56276; ITLK.  
 DR InterPro: IPR003962; FNIII\_repeat.  
 DR InterPro: IPR003961; FN\_III.  
 DR InterPro: IPR003598; Ig\_C2.  
 DR InterPro: IPR003600; Ig\_Like.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR Pfam: PF00041; fn3; 6.  
 DR Pfam: PF00047; fn3; 4.  
 DR PRINTS: PR00014; FNTYPEIII.  
 DR SMART: SM00060; FN3; 6.  
 DR SMART: SM00408; IGC2; 3.  
 DR SMART: SM00410; IG\_Like; 2.  
 KW Immunoglobulin domain; Repeat.  
 SO SEQUENCE 1445 AA; 157940 MW; 084F625954481988 CRC64;

Query Match 3.08; Score 112; DB 11; Length 1445;  
 Best Local Similarity 21.58; Pred. No. 0.67;  
 Matches 88; Conservative 47; Mismatches 155; Indels 120; Gaps 19;

OY 51 GSLOSAPGVLY--PTRL--QTELVLRCPQKTDALRRVYVHLAVHGMAREPEACKSD 106  
 DB 125 GSISRTAKVAGAPLRFSLQTESITAFMGDT-VLLKCEVIGDPMPTIHWQ-----KNO 177  
 OY 107 SELQ-----ESRNASLQAOVYLVSFOAYPIARCALLLEVQVPADLYNORGOSVGAVFDC- 158  
 DB 178 ODNLNIPGSR-----VVLLBSGALOISR-----LQPGD--SGVYRCSARN 216  
 OY 159 -FEASLGAEEVQIWSYTKPRYQKELNLTQOLPDCGLEVRDSIOSCV-----LPMLNV 210  
 DB 217 PASTRTGNEAEVRILSDPGIARPOLFLORPSNVIAIEGKDAVECCVGYPRPSTWLR- 275  
 OY 211 STDGNNVLTLLVSEODSFLIYLRRVPDALKSLMTKNLTGTPONTLNHNDLVPCLCIQ 270  
 DB 276 ---GEEVI-----OLRSKKYSLLGSGNLLISNVTD----- 302  
 OY 271 VMSLEPDERVEFCFREDPGAH-----RNLMTARLVLSPGVQLODAPCCLPGKV 322  
 DB 303 -----DMSGITTCVYTYKNENISASAEITVLP-PWFLNHPNML----- 340  
 OY 323 TLCAQAPD--QSFQCPVLPVP-----OKNATVNEPQDPOLVAGHNLCAVOVSTWERYQLQA 377  
 DB 341 -YAYESMDIEFECAYSGKVPFYVNMKNGDVLPISDYFOIYGSGNLRILGVKSDGEFYQ 399  
 OY 378 CSMDSLGPFKDMILYEMKGTGLNNTSVCALEPSCGTPPLSMASRAARL 427  
 DB 400 CVAENAGNAGSQAOLIVPKPAIPSSSILPSAPRDVVP--LVSSRFVRL 447  
 RESULT 9  
 OY 99X84 PRELIMINARY: PRT: 2012 AA.  
 AC 09BX84;  
 DT 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, last sequence update)  
 DE 01-OCT-2001 (TREMBLrel. 18, last annotation update)  
 DE CHANNEL-KINASE 2.  
 GN CHAK2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN RP  
 RP SEQUENCE FROM N.A.  
 RX TISSUE-KIDNEY; PubMed=10021370;  
 RX MEDLINE=9147092; PubMed=10021370;  
 RA Ryazanov A.G., Pavur K.S., Dorovkov M.V.;  
 RT "Alpha-kinases: a new class of protein kinases with a novel catalytic  
 domain";  
 RL Curr. Biol. 9:R43-R45(1999).  
 RN [2]  
 RN SEQUENCE FROM N.A.  
 RP TISSUE-KIDNEY;  
 RA Ryazanov A.G., Pavur K.S., Petrov A.N., Dorovkov M.V., Ryazanov A.G.;  
 RT "Novel type of signalling molecules: protein kinases covalently linked  
 to ion channels";  
 RL Mol. Biol. 0:0-0(2001).  
 DR EMBL: AF50881; AAK31202.1;  
 DR InterPro: IPR000636; Cation\_chan\_non\_119.  
 DR InterPro: IPR002111; Cat\_channel\_TripL.  
 DR Pfam: PF00520; Ion\_trans; 1.  
 KW kinase.  
 SQ SEQUENCE 2012 AA; 230493 MW; 8AD583235D8080AF CRC64;

OY 39 CHLMGDVLCLEGSLOSAPGVLYPTRLQTELVLRCPQ-----KTDALRRVYVHLA-- 91  
 DB 1327 AHSKYGQGLFVLSNLKR-----VPSAEVTLVLSRSVDVLTATEDIQTEVLVHLTQ 1380  
 OY 92 -VHGMA--EPEAKKDSLEQESRNASLQAOVYLVSFOAYPIARCALLLEVQVPADLYQ 146  
 DB 1381 TPVWSDMASVDEPKKEHEPIAHLLDQDKAEQVLPFLTSCPEPMTWSSPLS--QAKLMQ 1437  
 OY 147 PGOSVGAVFDCFEASLGAEEVQIWSYTKPRYQKELNLTQOLPDCGLEVRDSIOSCVLP 206  
 DB 1438 TGGGTVNNAF-----SEGDETVFS--IKRMQTCLEPSTCSDSSRSQHOQAOD----- 1486  
 OY 207 WLNSTDGNNVLTLLVSEODSFLIYLRRVPDALKSLMTKNLTGTPONTLNHNDLVPC 266  
 DB 1487 ---SSLSDNSTRSNOSSSCSEVG--PWLOP-----NTSFNINFLRRIRPARSHS----- 1531  
 OY 267 LCTQVMSLEPDERVEFCFREDPGAHRLMLHARLVLSPGVQLODAPCCLPGKVTLGW 326  
 DB 1532 ---FRFHKEKELMKIKICKIKLSGSS-----ICOGAM----- 1560  
 OY 327 QAPQSPQCPVLPVPYQKATVNEPQDPOLVAGHPN--LCVOVSTWERYQLQA--RSHQ 439  
 DB 1561 -----VKAKMLT-----KDRRLSKKKKKTGGQVLPIT-----VNAOSOSDQ 1597  
 OY 384 LGPFKDMILYEMKGTGLNNTSVCALEPSCGTPPLSMASRAARLGEELQ--DF--RSHQ 439  
 DB 1598 LNPEGENSEEESKKNFTYKSKFSTHGEVPIHQ--KMKTRKICGCAIQISDLKSHQ 1656  
 OY 440 CM--QLMND-----DNMGSIMACPMQYIHRNVLVWLACILLAAAL 479  
 DB 1657 DLSKNSLWNSSTNLNRSLLKSSIGVDKISALSKSPOEHHYSAL----- 1703  
 OY 480 FFFLLKKDRKRAKRSRALLHSADGAGERYELGALASALQMPRAVADLSRRRLS 539  
 DB 1704 -----ERNMLSLQTIPTPVOLEFAGEELTVRLRES--SPLNDKSMSSWGNGRA 1754  
 OY 540 A-----HGAL-----AMFHORRRILOEGV-VILLFSPAAYACCOOMQLQ 580  
 DB 1755 AMIOVLSREENDGGLRKAMRVYSTSEDD--ILKRGQFIVASFLPEVYRTHIKIQES 1811  
 OY 581 TVEPGPHDALAMLSCVLPDLQGRATGRYGVYGFEDGLHPDSVPSPFRAVLP 634  
 DB 1812 TV-----LHICLREIQOQRAAOKL--ITYENQVAPQIPIPTPRLLEV 1852  
 RESULT 10  
 OY 055225 PRELIMINARY: PRT: 2910 AA.  
 AC 055225;  
 DT 01-JUN-1998 (TREMBLrel. 06, Created)  
 DT 01-JUN-1998 (TREMBLrel. 06, last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)  
 DE OTOGELIN.  
 GN OTOG.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN RP  
 RP SEQUENCE FROM N.A.  
 RP STRAIN-BALB/C;  
 RX MEDLINE=98070772; PubMed=9405633;  
 RX Cohen-Salmon M., El-Amraoui A., Leibovici M., Petit C.;  
 RT "Otogelin: A glycoprotein specific to the acellular membranes of the  
 inner ear";  
 RL Proc. Natl. Acad. Sci. U.S.A. 94:14450-14455(1997).  
 DR EMBL: U96411; AAB96561.1;  
 DR HSSP: P56682; ICCV.  
 DR MGD: MGI:1202064; Otog.  
 DR InterPro: IPR002086; Aldehyde\_dehydr.  
 DR InterPro: IPR000359; Cys\_knot.  
 DR InterPro: IPR002919; TIL.

Query Match 3.0%; Score 111.5; DB 4; Length 2012;  
 Best Local Similarity 19.9%; Pred. No. 1.2; Mismatches 276; Indels 209; Gaps 31;  
 Matches 142; Conservative 87; Mismatches 276; Indels 209; Gaps 31;  
 OY 1 MPVSWFLTSLALGRNPVYSLERLMEPODPTAR-----CSLGLS 38  
 DB 1268 MPSS-LTRSLAGRHPRPVORGCALLEITNSKREATVNRNDQEOETOSIVSGVSPNRQ 1326

DR InterPro: IPR001846; VMD.  
 DR InterPro: IPR001007; VMFC.  
 DR Pfam: PF01826; TIL; 3.  
 DR Pfam: PF00094; vwd; 4.  
 DR SMART: SM00041; CT; 1.  
 DR SMART: SM00214; WMC; 1.  
 DR SMART: SM00216; VMD; 4.  
 DR PROSITE: PS00070; ALDEHYDE DEHYDR\_CYS; UNKNOWN\_1.  
 DR PROSITE: PS01225; CTCK-2; 1.  
 SO SEQUENCE 2910 AA; 313410 MW; 7270FC61A23264CD CRC64;

Query Match 3\*0%, Score 111.5; DB 11; Length 2910;  
 Best Local Similarity 19.8%; Pred. No. 1.9; Mismatches 140; Indels 153; Gaps 19;  
 Matches 83; Conservative 43;

DB 139 QVPALVPGQS-----VGSVDFCCFASLGAE--VOIW-SYTKPRY 177  
 DB 2267 QVPSSLTSEGTFRFRDSCATADCSPLRMVSNRTFSACHSFVSPESCMLIRDTKYVQ 2326  
 QY 178 QKELNLTQOLPDCRGLEY-----RDSIOSCVLFWLNVSTGDNLVLTLD 222  
 DB 2337 QPCVALTYVAMCHFRHVCIEWRGSDYCPFLCSSDSTYQACVAAACEPPDTCODGVLGPLD 2386  
 QY 223 VSEQDF-----SFLYLRL-----PVPDALKSLMYKNLTGPONT 257  
 DB 2387 PECCOVLGEQCVCTEGTILHRHSALCIPEDKCACTDSTGVPRALGETWNSLSG----- 2441  
 QY 258 LNHDLVLCICQVMSLEPDS-----EVEFCPFREDPGAHNLIARLVLS 307  
 DB 2442 -----CCQOCCOAPDTIIPVLDLDCPRPESCP-----RGEVILIQP 2479  
 QY 308 GVMOLDAPCCLGKRTLCQMAPDQSPQPLVPPVPOKNATVNEPQDFOLVAGH-----PN 362  
 DB 2480 -----TEPCCCLGSVCV-----NQTLCESGLAPCRGSHLITLHQEDSCSPSYCECPDG 2530  
 QY 363 LCVGVSTWEKVOQAACSNADSLGPFKDDMLVEMKTGLNNTSVCALEPSCG-----TLPLS 418  
 DB 2531 LC-----EAGQVPTC-----REDQILLEGRLG--DSCCTSYFCGEGCSDPME 2572  
 QY 419 MASTRA-----ARLGEELLQDFRSHQ-----CMQLMNDNMGSLMACPMD 458  
 DB 2573 CQEGEALTVHNTTELACPLCYOCVCENFRCPQVQCGMGTSLVEWMSPRDRCPRYKSCBD 2631

RESULT 11  
 093070 PRELIMINARY; PRT; 2873 AA.  
 AC 093070;  
 DT 01-NOV-1998 (Tremblrel. 08, Created)  
 DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)  
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
 DE GENOME POLYPEPTIDE.  
 OS Hepatitis GB virus C.  
 DC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
 CC GBV-C/HGV group.  
 NCBI\_TaxID=39839;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=K1737;  
 RC MEDLINE=98166861; Pubmed=9505962;  
 RA Katayama K., Fukushi S., Kurihara C., Ishiyama N., Okamura H.,  
 RA Hoshiro F.B., Oya A.;  
 RT \*Full-length GBV-C/HGV genomes from nine Japanese  
 RL isolates: characterization by comparative analyses.\*;  
 Arch. Virol. 143:1-13(1998).  
 DR EMBL: D87709; BAA25374.1; -;  
 DR HSSP: P27958; IHEI.  
 DR MEROPS: S29.002; -;  
 DR MEROPS: U39.001; -;  
 DR InterPro: IPR000923; Copper\_blue1.  
 DR InterPro: IPR001410; DEAD.  
 DR InterPro: IPR002518; HCV\_NS2.

DR InterPro: IPR004109; HCV\_NS3.  
 DR InterPro: IPR000745; HCV\_NS4a.  
 DR InterPro: IPR001490; HCV\_NS4b.  
 DR InterPro: IPR002868; HCV\_NS5a.  
 DR InterPro: IPR002166; HCV\_RdRp.  
 DR InterPro: IPR001650; Helicase\_C.  
 DR Pfam: PF01538; HCV\_NS2; 1.  
 DR Pfam: PF02907; HCV\_NS3; 1.  
 DR Pfam: PF01006; HCV\_NS4a; 1.  
 DR Pfam: PF01001; HCV\_NS4b; 1.  
 DR Pfam: PF01506; HCV\_NS5a; 1.  
 DR Pfam: PF00998; HCV\_RdRp; 1.  
 DR Pfam: PF00271; Helicase\_C; 1.  
 DR PROSITE: PS00196; COPPER\_BLUE; UNKNOWN\_1.  
 DR ATP-binding; Helicase; Nonstructural protein; Polyprotein;  
 KM RNA-directed RNA polymerase.  
 SO SEQUENCE 2873 AA; 310348 MW; 964B24CC1DF4F98 CRC64;

Query Match 3.0%; Score 111; DB 12; Length 2873;  
 Best Local Similarity 20.3%; Pred. No. 2.1; Mismatches 262; Indels 278; Gaps 44;  
 Matches 161; Conservative 92;

QY 1 MPVSWFLSLALGRNPNVVSLERLMEPQDTRARCSLGSCHLMDGDVLCIPGSIQAPGV 60  
 DB 2051 IPVSW-----EADARAPAMV-----YGGQSVTI-DGRTYIPIQLMRD---- 2089  
 QY 61 LVPTRLQTELVLRCKQKTCALRVRYVHLAVGHMAPEEAKSDSELRNALSQAQ 120  
 DB 2090 VAPSEVSSEVSLTEIGETE-----DELTEFA----- 2115  
 QY 121 VLSFOAIPARCALLLEVOPADLVOPGOSVGSVAFDCEASL--GAEOIWSYTPRY 177  
 DB 2116 -----DLPPAAALQAIENARILEP--HIDVIMEDCSPTSLGSSREHPWGEDIPRT 2167  
 QY 178 QKE--LNLTLQOLPDCRGLEVRDSDIOSCVLFWLNVSTGDNLVLTLDVSEED-----F 229  
 DB 2168 PSPALISVTESSPDERTKTPSVSPQED-----TPSSDSEVYQESPTASESEVFNAL 2220  
 QY 230 SFLYLRLVPPALKSLMY-----KNLTGPONTLNHDLVLCI--IQVMSLEPDS 279  
 DB 2221 SVLKALFPQSDATKRLTYRMSCCVKSVTRFSLGLTVAD--VASLCMEIQ-----N 2271  
 QY 280 RVEFCPFREDPGAHNLIARLVLSGVMOLDAPCCLGKRTL----- 324  
 DB 2272 HTAYCD-----KVRTP--LELYQGLVGNELTLECDKCEARQETLASF 2312  
 QY 325 --CWQADQSPQPLVPPVPOKNATVNEPQDFOLVAGHPNLCV-----QYSTWE 371  
 DB 2313 SYIMSGVPLTRAPPAKPPVVR-----PVGSLVAOTTKYVVTNPDNNGRRVDKVTFWR 2365  
 QY 372 KVLQACSNADSLGPFKDDMLVEMKTGLNNTSVCALEPSCGCTPLPSMASTRARLGEEL 431  
 DB 2366 APRVH-----DKFLVDSIERARKSAOCL-----SMGYTY-----EEA 2398  
 QY 432 LQDFRSHQCMQWMDNMGSLMACPMQY--IHRVAVLWLAALLAALFFLLKKD-- 488  
 DB 2399 IRTVRPHAMG--WGSKYSVKDLATPAGMAVHDR-----LQELTGTVPVFTLVKKEVF 2452  
 QY 489 --RRKARGSRRTALLHSADGAGYERLV-----GALASLSQPLVAVVDMRRELISANG 542  
 DB 2453 FKDRKEERGR-LIVFPDLPRIAEKLLIGDPGRYAKAV-----LGG 2493  
 QY 543 ALAMFHRRRIIOEGGVILLF-----SPAAY--AQC-----QOWIQLTVEPQPHDA 589  
 DB 2494 AYAFOYTPNQKVE--MLRMESKTKPCAICVADATCFDSSTIEDVALEF-----E 2542  
 QY 590 LAAMTSCVLPDFLQGRATGTYGVYFPDG--LHPSVSPFRVAPLFLSPQLQPAFLDAIQ 648  
 DB 2543 LVA-LASDHPWV--RALGT--YASGTWVTPGVPGERYC-----RSSGVLTISA 2589  
 QY 649 GGCST--SAGRPADRVERTQALRSALDSCSSSEAPGC-----CE-- 687



10

NCBI\_TaxID=9606;

[1]

SEQUENCE FROM N.A.

TISSUE=BRAIN, NEUROBLASTOMA;

Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.

-1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).

EMBL: BC005160; AA05160.1.

InterPro: IPR001680; WD40.

SMART: SM00320; WD40; 7.

PROSITE: PS00678; WD\_REPEATS\_1; UNKNOWN\_1.

PROSITE: PS50082; WD\_REPEATS\_2; 2.

PROSITE: PS50294; WD\_REPEATS\_REGION; 2.

Repeat: WD repeat.

NON\_TER

SEQUENCE 689 AA: 77638 MW: 8066FFDEEE623B7B CRC64:

Query Match 2.9%; Score 107.5; DB 4; Length 689;

Best Local Similarity 21.1%; Pred. No. 0.61;

Matches 129; Conservative 72; Mismatches 232; Indels 177; Gaps 33;

42 WDGDVLCPLPGSLQAPGVLPVTRIQTELVLCPQKDCALNRVVVHLAVGHMAPEE 101  
170 FSGDVMIHPYTNRPADKRSFIPSLVEKEKVS-----MYH-AIKMGWIOPRR 215  
102 AGKS-----DSELDSESRNASLQAOVLSFOAYPIARCALLEVOVPA-DLVQPGQSVGS 155  
216 PRDPTSFYDLMAQEDPNNAVIGRH-----KMHVPAPKIALPGHA----- 254  
156 FDGE-----EASLGAEOI-WSTYKPRYOKEINLTQOLPDCR-----GLEVRDSIOSC--- 202  
255 -ESYNPPETILSEERIAMEQOEGERKLSFLPKRPSIRAVPAIGRFIOERFERCLDL 313  
203 WLP----WLVSTGDGNYLTLDVSEEDFSFLYLRPVPDALKSLMYKNLTGPONITLN 259  
314 YLCPRQRKMRNVNVPEDILPKLRPRD-----LQPPF-TCQALVYR-----G 354  
260 HTDLVPCLCIQVWSLEPDSERVECPFRDPGCAHRNIMHIAKLK-----VLSPGVW 310  
355 HSDLVRLCL-----SVSPGQ--QMLVSGSDDSLR-LMEVATACVRTVPVGGVKKSVAM 405  
311 QLDAPCLPGKVT-----LCMQAPDQ-----SPCOPLVPVPQKNATVNE 350  
406 NPSPAVCLVAAAVEDSVLLINPALGDRIVAGSTDQLLSAFVPEEPFLQPARMLEASSEE 465  
351 PQ-DEQLVAGHPNLGVYSTWE-----KVQLQACSNWDSIGPFKDDML 393  
466 RQVGLRLRLICGKRPYQV-TWIGRGDYLAIVLATQGHQVYLHQLSRRSQSPFRSHQ 524  
394 VEMKTGLNNTSVCALEPSCPTPLPSNASTRARLGEELQDFNSH---OCQMLANDMNG 450  
525 VQR-----VAFHPA--RPFLLVAAQSQRVRLYLROELFTKIMPCK--W----VS 567  
451 SLWACPM-DKTYHRRM--VLYWLAACLLLAALFFELLKKORRAAGSFALLIHSADG 507  
568 SLAVHPADGNVTCGSDSKLWDFDLSTRPYRMLRHKKALRAVAHPRYPLEFASGSD 627  
508 AGYERLVGALASLSOMPLRAVAVDLMSRELISAHALAMFHHORRRILOEGGVVILLFSP 567  
628 GSVIVCHGKAVYNDLQNLVLPY-----KVLKGH-----VLT RDGLGVLDVIFHP 671  
568 AAVAOCQOML 577  
672 T-----QPMV 676

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 28, 2002, 19:43:34 : Search time 24.51 Seconds

(without alignments)  
1102.662 Million cell updates/sec

Title: US-09-899-471-5  
Perfect score: 3741  
Sequence: 1 MPVSMFLLSLGRPVVVS.....SSEAPGCCEDLPCITLLE 698

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	114.5	3.1	1447	1 DCC_MOUSE	P70211 mus musculu
2	112	3.0	1447	1 DCC_HUMAN	P43146 homo sapien
3	109.5	2.9	1711	1 PTPO_RAT	O64612 rattus norv
4	108.5	2.9	682	1 Y12A_HUMAN	Q14137 homo sapien
5	106.5	2.8	1409	1 AEX3_CAEEL	O02626 caenorhabd
6	103	2.8	557	1 OM6_CHIPS	P23701 chlamydia p
7	100.5	2.7	1448	1 APAR_HUMAN	O14727 homo sapien
8	99.5	2.7	1451	1 A2M2_MOUSE	P28666 mus musculu
9	99	2.6	2437	1 NOTC_BRARE	P45530 brachydanio
10	98.5	2.6	669	1 GLSK_HUMAN	O94925 homo sapien
11	97.5	2.6	1618	1 NEST_HUMAN	P46881 homo sapien
12	96.5	2.6	1249	1 APAR_RAT	O98955 rattus norv
13	93.5	2.5	204	1 C267_HUMAN	P58512 homo sapien
14	93.5	2.5	636	1 PAPB_HUMAN	O90115 homo sapien
15	93.5	2.5	726	1 CCT1_HUMAN	O60563 homo sapien
16	93.5	2.5	880	1 TYO3_MOUSE	P55144 mus musculu
17	93.5	2.5	1062	1 NAT2_HUMAN	O94x02 homo sapien
18	93.5	2.5	2647	1 ABP2_HUMAN	P21333 homo sapien
19	93	2.5	443	1 W70T_RAT	O35828 rattus norv
20	93	2.5	777	1 BISC_ECOLI	P20099 escherichia
21	92.5	2.5	566	1 TS13_MOUSE	O01755 mus musculu
22	92.5	2.5	890	1 TYO3_HUMAN	O06418 homo sapien
23	92.5	2.5	3707	1 PGBM_MOUSE	O05793 mus musculu
24	92	2.5	398	1 GSPK_KLEPN	P15571 klebsiella
25	91.5	2.4	235	1 FL3JL_HUMAN	P49371 homo sapien
26	91.5	2.4	1476	1 A2M1_MOUSE	P28665 mus musculu
27	91	2.4	362	1 CKRA_HUMAN	P46092 homo sapien
28	91	2.4	1058	1 GEM4_HUMAN	P57678 homo sapien
29	91	2.4	1216	1 AEGP_RAT	O63191 rattus norv
30	90.5	2.4	385	1 YEH1_ECOLI	P33381 escherichia
31	90.5	2.4	458	1 MUC_RABIT	P03988 oryctolagus
32	90.5	2.4	479	1 MUCM_RABIT	P04221 oryctolagus
33	90.5	2.4	844	1 YDZ5_SCHPO	O13712 schizosacch

34	90.5	2.4	880	1 TYO3_RAT	P55146 rattus norv
35	90	2.4	1928	1 LPH_RAT	O02401 rattus norv
36	89.5	2.4	837	1 GCSR_MOUSE	P40223 mus musculu
37	89.5	2.4	1370	1 G261_HUMAN	O14202 homo sapien
38	89.5	2.4	1927	1 LPH_HUMAN	P09848 homo sapien
39	89.5	2.4	4543	1 LRPL_CHICK	P098157 gallus gall
40	89	2.4	922	1 W70T_MOUSE	O94217 mus musculu
41	89	2.4	942	1 MAKE_MOUSE	O94216 mus musculu
42	89	2.4	1189	1 HAIR_HUMAN	O43593 homo sapien
43	88.5	2.4	938	1 EBN4_EBV	P03203 Epstein-Bar
44	88.5	2.4	1208	1 RCO4_HUMAN	O94761 homo sapien
45	88.5	2.4	1258	1 YS00_ANNSP	O87c2 anabaena sp

## ALIGNMENTS

RESULT	ID	DCG_MOUSE	STANDARD	PRT	1447 AA.
1	DCG_MOUSE	P70211			
AC	DCG_MOUSE	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)				
DT	01-MAR-2002 (Rel. 41, Last annotation update)				
DE	Tumor suppressor protein DCC precursor.				
GN	DCC.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.				
OX	NCBI_Taxid=10090;				
RN	(1)				
RP	SEQUENCE FROM N.A.				
RC	STRAIN-BALB/C; TISSUE-Brain;				
RX	MEDLINE-96112625; PubMed-8570174;				
RA	Cooper H.M., Ames P., Britto J., Gad J., Wilks A.F.;				
RT	"Cloning of the mouse homologue of the deleted in colorectal cancer gene (mDCC) and its expression in the developing mouse embryo.";				
RL	Oncogene 11:2243-2254(1995).				
RN	(2)				
RP	REVISIONS.				
RC	STRAIN-BALB/C; TISSUE-Brain;				
RL	Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.				
CC	-1- FUNCTION: IMPLICATED AS A TUMOR SUPPRESSOR GENE.				
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein.				
CC	-1- ALTERNATIVE PRODUCTS: TWO FORMS OF THE PROTEIN ARE PRODUCED FROM THE SAME GENE BY THE USE OF ALTERNATIVE INITIATION SITES. A THIRD FORM WHICH IS EXPRESSED ONLY IN THE EMBRYO IS PRODUCED BY ALTERNATIVE SPLICING.				
CC	-1- TISSUE SPECIFICITY: IN THE EMBRYO, EXPRESSED AT HIGH LEVELS IN THE DEVELOPING BRAIN AND NEURAL TUBE. IN ADULT, HIGHLY EXPRESSED IN BRAIN WITH VERY LOW LEVELS FOUND IN TESTIS, HEART AND THYMUS.				
CC	-1- DEVELOPMENTAL STAGE: LOW LEVELS IN EARLY GESTATION. HIGHEST LEVELS EXPRESSED DURING MID GESTATION. LEVELS DECREASE IN LATE GESTATION AND REMAIN AT THIS LEVEL IN THE ADULT.				
CC	-1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. DCC SUBFAMILY.				
CC	-1- SIMILARITY: CONTAINS 4 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.				
CC	-1- SIMILARITY: CONTAINS 6 FIBRONECTIN TYPE III-LIKE DOMAINS.				
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CC	EMBL; X85788; CAA59786.1; -				
DR	HSSP; P56276; 1TLK.				
DR	MGD; MGI:94869; DCC.				
DR	InterPro; IPR003961; FN_III.				
DR	InterPro; IPR003962; FNIII_repeat.				





	FTID=VAR_003911.
FT CONFLICT	138 MISSING (IN REF. 3).
FT CONFLICT	233 MISSING (IN REF. 3).
FT CONFLICT	421 MISSING (IN REF. 3).
SO SEQUENCE	1447 AA; 158456 MW; 4A8612766ED0471F CRC64;

[illegible]

OY	617	GL	618
Db	580	GL	581
RESULT	3		
PTPO_RAT			
ID	PTPO_RAT	STANDARD:	PRT: 1711.AA.
AC	064612:		
DT	01-NOV-1997	(Rel. 35, Created)	
DT	01-NOV-1997	(Rel. 35, Last sequence update)	
DT	15-JUL-1999	(Rel. 38, Last annotation update)	
DE	Osteostectin protein tyrosine phosphatase precursor (EC 3.1.3.48) (OST-PTP).		



```

QY 547 FH0RRRILOEGGVILLFSPAANOCCOMIOLQVBERP-HDAL-----AAMLS----- 595
DB 812 SVRCRAGPQLQASHVLVL-----SVEPGPVEDVLCHEPATYALALMTMP 855
QY 596 -----CVLPDEFLQGRATGRVY-----GYVF-----DGLHPDSVP-SPEVAPLFSLP 637
DB 856 AGDVQCVL-----VVELVYPCGGGTHFVQVNTSGDALLPLNLPMTTSTRLS--LTVL 906
QY 638 TQLPAPLALQGGCSTSA 655
DB 907 GNRSMRSRAVSLVCSSTA 924
RESULT 4
Y124_HUMAN
ID Y124_HUMAN STANDARD; PRT; 682 AA.
AC Q14137;
DT 01-NOV-1997 (Rel. 35, Created).
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein KIAA0124 (Fragment).
GN KIAA0124.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96127530; PubMed=8590280;
RA Nagase T., Seki N., Tanaka A., Ishikawa K.-I., Nomura N.;
RT "Prediction of the coding sequences of unidentified human genes. IV.
RT The coding sequences of 40 new genes (KIAA0121-KIAA0160) deduced by
RT analysis of cDNA clones from human cell line KG-1."
RL DNA Res. 2:167-174(1995).
CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
CC -1- SIMILARITY: STRONG, TO YEAST YMR049C.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
DB EMBL: D50914; BAA09473.1;
DB InterPro: IPR001680; WD40.
DB Pfam: PF00400; WD40; 7.
DB SMART: SM00320; WD40; 5.
DB PROSITE: PS00678; WD_REPEATS_1; 1.
DB PROSITE: PS50082; WD_REPEATS_2; 2.
DB PROSITE: PS50294; WD_REPEATS_REGION; 2.
KW Hypothetical protein; Repeat; WD repeat.
FT NON_TER 1
FT REPEAT 347 386 WD 1.
FT REPEAT 388 428 WD 2.
FT REPEAT 468 512 WD 3.
FT REPEAT 513 551 WD 4.
FT REPEAT 554 593 WD 5.
FT REPEAT 597 636 WD 6.
FT REPEAT 652 681 WD 7.
SQ SEQUENCE 682 AA; 76949 MW; 929219E600E732BD CRC64;
Query Match 2.9%; Score 108.5; DB 1: Length 682;
Best local Similarity 21.1%; Pred. No. 0.5; Mismatches 232; Indels 177; Gaps 33;
Matches 129; Conservative 72;
QY 42 WDCGYLCPGSLQSPGVLPVTRLOTLELVLRCPORPCALRVVVVLAHGHWAEPPEE 101
DB 163 FSGGVYTHPVNRPDKRSFISLVEKEKYSR-----MVH-AIKMGMIQPRR 208
QY 102 AGKS-----DELDGSRNASLQAVVLSQAFIARCALLLEVQPA-DLVQPGSGSVGS 155

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DB 209 PRDPTSFYDLMAQEDPNAVLGRH-----KMHVAPRKALRGHA----- 247
QY 156 FDCE-----EASLGAEOI-WSTPKRYQKELNTQOLPDCR-----GLEVRDSIOSC--- 202
DB 248 -RSYNPPPEYLLSEERLAMEQOEPGERKLSFLPRKFPSLAVAPAGYFIQRFERCLDL 306
QY 203 WYLP---WLVNVPDGNVLLTLTLDVSEODFSFLYLVRVPALKSILMKNLGPNITLN 259
DB 307 YLCPROKRMKRVNVPEDLILKLRPRD-----LOFPF-TCOLVYR-----G 347
QY 260 HTDLVPCICIQWVSLPEPDSERVEFCPPREDGAGRNLMIARLR-----VLSPGW 310
DB 348 HSDLVKCL-----SVSPGG---QMLVSGSDGSLR-LMEVATARCVRVPVGGVKSVM 398
QY 311 OLDAPCCLEPKYT-----LCWAPDQ-----SPCQPLVPVPQKNATVE 350
DB 399 NEPSAVCLVAVAVEDSVLLNLPALGRLVAGSTQLLSAFVPPEEPPIQAPARMLASSEE 458
QY 351 PQ-DEOLVAGHPNLGVYSTWE-----KYQLOACSMADSLGFEFDMLL 393
DB 459 RQVGLRLRICHGRPVYOV-TWGRGDYLAVALTOGHTOVLIHOLSRRSRSPFRHSHQ 517
QY 394 VEMKTGLNNTSVCALEPSCGTPPLPSMASTRARLGEELLQDFRSH---QCMLWMDNMG 450
DB 518 VOR-----VAFHPA--RPFLVASQSRVRLYHLRQELTKIMNCK--W-----VS 560.
QY 451 SLMACPM-DKTYHRRR--VLYVLACILLAAALFFELLKDKRKAARSGFRALLHSADG 507
DB 561 SLAVHPADGNVTCGSYSKLVWFDDLSTKPYRLRHKKALRAVAHPRPLFASGSD 620
QY 508 AGERYLVGALASALSOMPRVAVDLMSRRELSAAGALWTFH0RRRILOEGGVILLFSP 567
DB 621 GSVYVCHGMVNYDILLQNPILVPV-----KVLKGH-----VLTLDGLVDLVIFHP 664
QY 568 AAVACQGM 577
DB 665 T-----QPVW 669
RESULT 5
AEX3_CAEL
ID AEX3_CAEL STANDARD; PRT; 1409 AA.
AC 002626; Q27467;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Regulator of presynaptic activity aex-3.
GN AEX-3 OR C02H7.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditiida; Rhabditoidea;
OC Rhabditiidae; Peloderiinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-BRISTOL N2;
RX MEDLINE=97282461; PubMed=9136770;
RA Iwasaki K., Staunton J., Saifee O., Nonet M., Thomas J.H.;
RT "aex-3 encodes a novel regulator of presynaptic activity in C.
RT elegans."
RL Neuron 16:613-622(1997).
RP [2]
RP SEQUENCE FROM N.A.
RX STRAIN-BRISTOL N2;
RA Leinbag D., Mink M.;
RL Submitted (FEB-1996) to the EMBL/Genbank/DBJ databases.
RL [3]
RP INTERACTION WITH CAB-1.
RX MEDLINE=20428446; PubMed=10970871;
RA Iwasaki K., Toyonaga R.;
RT "The rab3 GDP/GTP exchange factor homolog AEX-3 has a dual function
RT in synaptic transmission."
RL EMBO J. 19:4806-4816(2000).

```

- FUNCTION: GUANINE NUCLEOTIDE EXCHANGE FACTOR (GEF) FOR RAB3. MAY  
 REGULATE TWO DIFFERENT PATHWAYS FOR NEURAL ACTIVITIES.  
 - SUBUNIT: BINDS TO CAB-1.  
 - TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF NEURONS.  
 - SIMILARITY: CONTAINS 1 DENN DOMAIN.  
 -----  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

EMBL: 093842; AAC52421.1; \*  
 DR EMBL: 049945; AAC47926.1; \*  
 DR Wormpep: CO2H7.3; CE16806.  
 DR Interpro: IPR001194; DENN.  
 DR Pfam: PR02141; DENN; 1.  
 IT Guanine-nucleotide releasing factor.  
 IT DOMAIN 216 364 DENN.  
 IT DOMAIN 604 632 SER-RICH.  
 SEQ SEQUENCE 1409 AA; 157458 MW; 2DDE6395AC96313 CRC64;

Query Match 2.88; Score 106.5; DB 1; Length 1409;  
 Best Local Similarity 20.08; Pred. No. 1.9;  
 Matches 115; Conservative 77; Mismatches 201; Indels 181; Gaps 25;

101 EAGKSELEDSNRASLAQAVYLSFOAPFIARCALLEVOVPADIVYQSGVSGAVDCE 160  
 780 QOSKNQVAFKEDQALVQSGVSGVSAFKLR--LMEDSELELV-----CSK 825  
 161 ASLGAEOVIMSYTKPRYOKELNLTQO-----LPDC-RGLEVRDSIQSC----- 202  
 826 LNLGLEVKL--SEDEVKEVQLTKGQKAYVKILAKLEGIEVSEVNTGCCGFASVHY 882  
 203 -----WVLPMLNVTSDGDVNLITLDVSEODESFLLYLRPPVDALKSLMYKNTGP- 253  
 883 LEIATHHYAMMGGEVITPSSASPTMTTPEHSNDILKESRPKLPA-STIDRTPTKPL 941  
 254 -ONITLNTHTD-----LVPCLCIOYWSLEPDSERVEFCPPREDP--GAHRLMHIARL 302  
 942 GQNVITSTNNHLEAOSTRSPALPPV---PPREAPPI-PKRNPPILGAPKVPBGAR- 955  
 303 RVLSPEWOLADACCLPGKVTLCWQAPDQSP-----COPLV 338  
 996 -----APPLEPRPKVKTAVDEFQNLVNNOPAPQSSPSFLADADEQTRPL 1044  
 339 PPVPQKNATVNEQDQOLVAGHPN-----LCVOVSTWEKVOIQACSWAD--- 382  
 1045 KRAPPTTLTPVGKQEPCK-VLPTEPNEPVRYHYIOELLILAVOHQIMONLCFEMNAFVLDVAG 1103  
 383 ---SLGPFKDDMLLVETKGTGLNNTSVCALEPSGCTPLPSMASTRARL-----GEELLD 434  
 1104 EKEIYAMDEPSEKIDRYSLANDSEKRLLEEDRLSLTLNMTAYMTMCTGOKRALD- 1162  
 435 FRSHOCMOLMNDNGSLMACPMQKYIHRWVVLWACLILAALFFLLKDKRKRAAR 494  
 1163 ---QKVRRLGLKRAHIGLVKSEIKNLDE-----LPSTGQNFPLPK-----PL 1202  
 495 GSR-----TALLHSADGAG-----YERLVGALASALSO 523  
 1203 GSRLVQKQSEFTVCGQSSDQOMMEVCEDDAVVLRSLITGAATERMYEELTVN-----ITY 1257  
 524 MPLRVAVDLSRRELASGALWAFHQRRLIOE 557  
 1258 SPKTKILCMRRHDDVYH--MKKHTKKCRELYO 1289

RESULT 6  
 OM6\_CHLPS STANDARD; PRT; 557 AA.  
 ID OM6\_CHLPS

AC P23701;  
 DT 01-NOV-1991 (Rel. 20, Created)  
 DT 01-NOV-1991 (Rel. 20, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE 60 kDa outer membrane protein precursor (cysteine-rich outer membrane  
 protein) (CRP) (60 kDa cysteine-rich OMP).  
 GN OMCB OR OMP2 OR ENVB.  
 OS Chlamydia psittaci (Chlamydia psittaci).  
 OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia. [NCBI\\_TaxId-83554](http://www.ncbi.nlm.nih.gov/ncbi/TaxId-83554).  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=EA6/A22/M;  
 RX MEDLINE=90384851; PubMed=2402464;  
 RA Watson M.W., Lambden P.R., Clarke I.N.;  
 RT "The nucleotide sequence of the 60 kDa cysteine rich outer membrane  
 protein of Chlamydia psittaci strain EA6/A22/M.";  
 RL Nucleic Acids Res. 18:5300-5300(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=6BC;  
 RX MEDLINE=91267949; PubMed=2050637;  
 RA Everett K.D.E., Hatch T.P.;  
 RT "Sequence analysis and lipid modification of the cysteine-rich  
 envelope proteins of Chlamydia psittaci 6BC.";  
 RL J. Bacteriol. 173:3821-3830(1991).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Watson M.W.;  
 RL Submitted (FEB-1993) to the EMBL/GenBank/DBJ databases.  
 CC - FUNCTION: ASSOCIATED WITH DIFFERENTIATION OF RETICULATE BODIES  
 (RBS) INTO ELEMENTARY BODIES (EBs). IT IS NECESSARY FOR STRUCTURAL  
 INTEGRITY OF THE EBS OUTER ENVELOPE. IT MAY ALSO BE AN IMPORTANT  
 VIRULENCE FACTOR.  
 CC - SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.  
 -----  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

EMBL: X53512; CA437592.1; \*  
 DR EMBL: M61116; AAB61619.1; \*  
 DR PIR: S12603; S12603.  
 DR Interpro: IPR003506; Chlam\_OMP6.  
 DR PRINTS: PR01336; CHLAMIDIA06.  
 KW Outer membrane; Transmembrane; Signal; Virulence.  
 FT SIGNAL 23 40  
 FT PROPEP 1 22  
 FT CHAIN 41 557  
 FT VARIANT 45 45 A -> S (IN STRAIN 6BC).  
 FT VARIANT 73 73 E -> G (IN STRAIN 6BC).  
 SQ SEQUENCE 557 AA; 59843 MW; 0D444F09EAA073C6 CRC64;

Query Match 2.88; Score 103; DB 1; Length 557;  
 Best Local Similarity 20.18; Pred. No. 1.1;  
 Matches 61; Conservative 42; Mismatches 97; Indels 104; Gaps 15;

158 CF-EASLGAEOVIMSYTKPRYOKELNLTQOLPCRGLEVDSIOSCVLTPVLIANTSDDN 216  
 198 CFTATVACPELRSTTKCG-OPALICQDGPFCAR-----CPVYKIEVCNRTGSA 249  
 217 VLLTLDVSEODESFLLYLRPPVDALKSLMYKNTLGPONTLNTDLPV-----CLCQVW 272  
 250 IARNVVD-----NPVPDG-----YTHASGQRVLSFNGDRPQSGSKFC----- 289  
 273 SLEPDSERVEFCPPREDP-----GAHRLMHIARLRLVLSPGWOLDAPC----- 316  
 290 -----VEFCPQKRGKVTNATVASYCGGHKCSANVTY-----VNEPCVQVNI 332

OY 317 -----CLPGKVTLCMQAP-DQSPQPIVPPQKNAIVNEPQFQVAGHPNLCVOVS 368  
 DB 333 GADMSVVCAPVETTVVSNPDGLKLVVIEDTAPSGATI-----LEAGAEICCNKA 385  
 OY 369 TW-----EKVQLQACSNWASISGPFKDDML-----VEKMT-----GLNNTSV 405  
 DB 386 VMCIKEMCGEITQIFVVAAGASPGKFTNOVVATNSDGGCTSCAEVTTMKGLATM 445  
 OY 406 CALE 409  
 DB 446 CVID 449  
 RESULT 7  
 APAP\_HUMAN STANDARD; PRT; 1248 AA.  
 ID APAP\_HUMAN  
 AC 014727; Q9UBZ5; Q9UJ58; Q9UJ59; Q9UJ60; Q9UJ61; Q9UJ62; Q9UJ63;  
 AC Q9UJ64; Q9UJ65; Q9UJ66; Q9UJ67; Q9UJ68; Q9UJ69; Q9UJ70; Q9UJ71;  
 AC Q9UGP0; Q9UGP1; Q9UGP2; Q9UGP3; Q9UGP4; Q9UGP5; Q9UGP6; Q9UGP7;  
 DT 15-JUN-1998 (Rel. 36, Created)  
 DT 01-MAR-2002 (Rel. 41, Last sequence update)  
 DT 01-MAR-2002 (Rel. 41, Last annotation update)  
 DE Apoptotic protease activating factor 1 (Apaf-1).  
 GN APAF1 OR KIA0413.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN 11  
 RP SEQUENCE FROM N.A. (ISOFORM 3), AND PARTIAL SEQUENCE.  
 RC TISSUE=Cervical carcinoma;  
 RX MEDLINE=97410306; PubMed=9267021;  
 RA Zou H., Henzel W.J., Liu X., Lutschg A., Wang X.;  
 RT "Apaf-1, a human protein homologous to C. elegans CED-4, participates  
 RT in cytochrome c-dependent activation of caspase-3.";  
 RT Cell 90:405-413(1997).  
 RN 12  
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 4 AND 5).  
 RC TISSUE=Peripheral blood, Heart, and Cervical carcinoma;  
 RX MEDLINE=99373149; PubMed=1044196;  
 RA Hahn C., Hirsch B., Jahnke D., Duerkop H., Stein H.;  
 RT "Three new types of Apaf-1 in mammalian cells";  
 RT Blochem. Biophys. Res. Commun. 261:746-749(1999).  
 RN 13  
 RP SEQUENCE FROM N.A. (ISOFORM 2).  
 RC TISSUE=T-cell;  
 RX MEDLINE=99292765; PubMed=10364241;  
 RA Saleh A., Srinivasula S.M., Acharya S., Fishel R., Alnemri E.S.;  
 RT "Cytochrome c and dATP-mediated oligomerization of Apaf-1 is a  
 RT prerequisite for procaspase-9 activation.";  
 RT J. Biol. Chem. 274:17941-17945(1999).  
 RN 14  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC TISSUE=Kidney;  
 RA Benedict M.A., Nunez G.;  
 RT Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.  
 RN 15  
 RP SEQUENCE OF 385-1248 FROM N.A. (ISOFORM 1).  
 RC TISSUE=Brain;  
 RX MEDLINE=98116655; PubMed=9455477;  
 RA Ishikawa K.-I., Nagase T., Nakajima D., Seki N., Ohira M.,  
 RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;  
 RT "Prediction of the coding sequences of unidentified human genes. VIII.  
 RT 78 new cDNA clones from brain which code for large proteins in  
 RT vitro.";  
 RT DNA Res. 4:307-313(1997).  
 RN 16  
 RP SEQUENCE OF 810-864 AND 866-883 FROM N.A.  
 RA Roberts D.L., Daigleish R., Cohen G.M., MacFarlane M.;  
 RT "The mammalian CED4 homologue, APAF1, exists as two distinct forms in  
 RT human cells";  
 RT Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.

RN 17  
 RP SEQUENCE OF 1-138 FROM N.A. (ISOFORM 1/4/5).  
 RA Won M., Lee J.-W., Oh H.-H., Kim D.-U., Chung K.-S., Lee M.,  
 RA Yoo H.-S.;  
 RT "Cloning of variant Apaf1.";  
 RT Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN 18  
 RP APAF-1-MEDIATED OLIGOMERIZATION.  
 RX MEDLINE=98315378; PubMed=9651578;  
 RA Srinivasula S.M., Ahmad M., Fernandes-Alnemri T., Alnemri E.S.;  
 RT "Autoactivation of procaspase-9 by Apaf-1-mediated oligomerization.";  
 RT Mol. Cell 1:949-957(1998).  
 RN 19  
 RP INDUCTION BY E2F AND P53.  
 RX MEDLINE=21283226; PubMed=11389439;  
 RA Moroni M.C., Hickman E.S., Denchi E.L., Capra G., Coll E.,  
 RA Cecconi F., Mueller H., Hella K.;  
 RT "Apaf-1 is a transcriptional target for E2F and p53.";  
 RT Nat. Cell Biol. 3:552-558(2001).  
 RN 110  
 RP X-RAY CRYSTALLOGRAPHY (1.3 ANGSTROMS) OF 1-97.  
 RX MEDLINE=20013059; PubMed=10543941;  
 RA Vaughn D.E., Rodriguez J., Lazebnik Y., Joshua-Tor L.;  
 RT "Crystal structure of Apaf-1 caspase recruitment domain: an alpha-  
 RT helical Greek key fold for apoptotic signaling.";  
 RT J. Mol. Biol. 293:439-447(1999).  
 RN 111  
 RP STRUCTURE BY NMR OF 1-97.  
 RX MEDLINE=20047184; PubMed=10578182;  
 RA Day C.L., Dupont C., Lackmann M., Vaux D.L., Hinds M.G.;  
 RT "Solution structure and mutagenesis of the caspase recruitment domain  
 RT (CARD) from Apaf-1.";  
 RT Cell Death Differ. 6:1125-1132(1999).  
 CC -1- FUNCTION: Oligomeric Apaf-1 mediates the cytochrome c-dependent  
 CC autocatalytic activation of pro-caspase 9 (Apaf-3), leading to the  
 CC activation of caspase-3 and apoptosis. This activation requires  
 CC ATP.  
 CC -1- SUBUNIT: Monomer. Oligomerizes upon binding of cytochrome c and  
 CC dATP. Oligomeric Apaf-1 and pro-caspase-9 bind to each other via  
 CC their respective NH2-terminal CARD domains and consecutively  
 CC mature caspase-9 is released from the complex.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- ALTERNATIVE PRODUCTS: 5 isoforms; 1/Apaf-1XL (shown here), 2/Apaf-  
 CC 1L, 3/Apaf-1S, 4/Apaf-1M and 5/Apaf-1XS; are produced by  
 CC alternative splicing.  
 CC -1- TISSUE SPECIFICITY: Ubiquitous. Highest levels of expression in  
 CC adult spleen and peripheral blood leukocytes, and in fetal brain,  
 CC kidney and lung. Isoform 1 is expressed in heart, kidney and  
 CC liver.  
 CC -1- INDUCTION: By E2F and p53 in apoptotic neurons.  
 CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 13 WD REPEATS (TRP-ASP DOMAINS).  
 CC -1- CAUTION: Ref.7 sequence differs from that shown due to a  
 CC frameshift in position 109.  
 CC -----  
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 CC -----  
 DR EMBL: AF013263; AAC51678.1;  
 DR EMBL: AJ243003; CAB55579.1;  
 DR EMBL: AJ243004; CAB55580.1;  
 DR EMBL: AJ243005; CAB55581.1;  
 DR EMBL: AJ243006; CAB55582.1;  
 DR EMBL: AJ243007; CAB55583.1;  
 DR EMBL: AJ243008; CAB55584.1;  
 DR EMBL: AJ243009; CAB55585.1;  
 DR EMBL: AJ243010; CAB55586.1;

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>R EMBL: AJ243011; CAB55587.1; -
>R EMBL: AJ243048; CAB55588.1; -
>R EMBL: AJ243107; CAB56462.1; -
>R EMBL: AF134397; AAD38344.1; -
>R EMBL: AF149794; AAD34016.1; -
>R EMBL: AB007873; BAA24843.1; -
>R EMBL: AJ133643; CAB55085.1; -
>R EMBL: AJ133644; CAB55086.1; -
>R EMBL: AF248734; CAB55087.1; -
>R PDB: 1CWS; 01-DEC-99.
>R PDB: 1CWS; 21-JAN-00.
>R MIN: 602233; -
>R InterPro: IPR001315; CARD.
>R InterPro: IPR002182; NB-ARC.
>R InterPro: IPR001680; WD40.
>R Pfam: PF00619; CARD; 1.
>R Pfam: PF00931; NB-ARC; 1.
>R Pfam: PF00400; WD40; 11.
>R PRINTS: PRO0320; GPROTEINRPT.
>R SMART: SM00320; WD40; 10.
>R PROSITE: PS00678; WD_REPEATS_1; 4.
>R PROSITE: PS50082; WD_REPEATS_2; 9.
>R PROSITE: PS50294; WD_REPEATS_REGION; 1.
>R Apoptosis; ATP-binding; Repeat; WD repeat; Alternative splicing;
>R 3D-structure.
>R DOMAIN 1 90
>R NP_BIND 154 415
>R REPEAT 613 652
>R REPEAT 655 694
>R REPEAT 697 738
>R REPEAT 741 780
>R REPEAT 796 836
>R REPEAT 838 877
>R REPEAT 880 919
>R REPEAT 959 998
>R REPEAT 1001 1040
>R REPEAT 1042 1080
>R REPEAT 1083 1122
>R REPEAT 1125 1164
>R REPEAT 1175 1212
>R DOMAIN 95 98
>R VARSPPLIC 99 109
>R VARSPPLIC 575 575
>R VARSPPLIC 824 866
>R VARSPPLIC 1113 1154
>R CONFLICT 108 108
>R CONFLICT 134 134
>R CONFLICT 145 145
>R CONFLICT 161 161
>R CONFLICT 370 370
>R CONFLICT 383 383
>R CONFLICT 544 544
>R CONFLICT 580 580
>R CONFLICT 608 608
>R CONFLICT 620 620
>R CONFLICT 639 639
>R CONFLICT 708 708
>R CONFLICT 742 742
>R CONFLICT 746 746
>R CONFLICT 757 757
>R CONFLICT 795 795
>R CONFLICT 798 798
>R CONFLICT 825 825
>R CONFLICT 871 871
>R CONFLICT 876 876
>R CONFLICT 949 949

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Query Match 2.7%; Score 100.5; DB 1; Length 1248;  
Best Local Similarity 20.3%; Pred. No. 5;

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Matches 118; Conservative 65; Mismatches 210; Indels 187; Gaps 29;
>Q 79 DCALRVAVVHLAVHGH-----NAPEEACKSDSLQE-SRNASIQ-AQVLSFOAY-- 128
>Db 537 DCANSENFQEFSLUNGILGKQPPNIVQIGCEPETSIVYQDAKQAOEVNMGMLYLE 596
>Q 129 -----PIARCALLEVOVPADLV-----QPGQSVGSVAVDCEASIGAEQVMSYTPKRX 177
>Db 597 WINKKNTNLSRLVVRPHITDAVYHACFEEDGRI-----ASGCAKTLQVFAETG 647
>Q 178 QKELNLTQQLPD--CRGLEVRDS-IQSCVYLPWLV--STDGNNVLLTLDVSEEQ----- 227
>Db 648 EKLEIKAHDEEVLCGAFSTDRFATCSVDKRVKIMNSMTGE-LVHTYDEHSEQVACH 706
>Q 228 ---DFSLVLYRPVDAKLKSLMYKNLGPONTLHTDVLPCLCIOVSLPEPSEREFC 284
>Db 707 FTNSSHLLATGSSDCEFLKMDLNQKRCRNTMFGHTN-----SVNHC 749
>Q 285 PFREDPGAHRLMHLIARLVLSPGVQDLAPCLPGKVTYLCWQAPDQSPQPLVPVPQK 344
>Db 750 RFSPPD-----KLASCSADGTCLK-WDATSANERKST--NVKQF 786
>Q 345 NAYVNEPQDQVLVAGHRLVCQVSTWEVYQAGSM-ADS-----LGPFRDQM 391
>Db 787 FLNLDEPQEDM-----EVIYKCCSWSDGARIMVAAKNKIFLFDIHTSG 830
>Q 392 LLYEMKTGLNNT-SVCALPEPGCTPLPSMASTRARLQELQDPRSHOCMLMNDNMG 450
>Db 831 LGEIHTGHSTIOYCPSPNHLAVNL-----SOYCEVLEMTDSDRS 873
>Q 451 SLWACPMKTYIHRWVLTWLTACLLLAALFFELLKDKRKARAGSRTALLHSADAGY 510
>Db 874 KVADCRG---HLISWV-----HG-----VHSPGSSSF 897
>Q 511 ERYVGLASLSQMPPLAVVDVMSRRELSSANGALAMFHQRRRIQEGGVILLSPAAV 570
>Db 898 ----LTSSDDQ-----TRLMEKRYCKKNSAV-MLKQEVVDVQENEVMTL-----AV 940
>Q 571 AOCQOMLQIQVEPDPHAL--AAWLSGVLPDPLGCRATG 608
>Db 941 DHTLR-LQLINGRTGQIDYLTEAOVSCCCLSPHDIAYIAG 979

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RESULT 8
A2M2_MOUSE STANDARD; PRT: 1451 AA.
ID A2M2_MOUSE
AC P28666;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, last sequence update)
DT 01-NOV-1997 (Rel. 35, last annotation update)
DE Muriinoglobulin 2 precursor (Mug2).
GN MUG2 OR MUG-2.
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=91358495; PubMed=1840592;
RT Overberg L., Torrekens S., van Leuven F., van den Berghe H.;
RT "Molecular characterization of the murlinoglobulins.";
RL J. Biol. Chem. 266:16903-16910(1991).
-!- FUNCTION: A PROTEINASE ACTIVATES THE INHIBITOR BY SPECIFIC
PROTEOLYSIS IN THE BAIT REGION, WHICH, BY AN UNKNOWN MECHANISM
LEADS TO REACTION AT THE CYSTEINYL-GLUTAMYL INTERNAL THIOL ESTER
SITE AND TO A CONFORMATIONAL CHANGE, WHEREBY THE PROTEINASE IS
TRAPPED AND/OR COVALENTLY BOUND TO THE INHIBITOR. WHILE IN THE
TETRAMERIC PROTEINASE INHIBITORS STERIC LINKAGE BETWEEN THE
STRONG, MONOMERIC FORMS NEED A COVALENT LINKAGE BETWEEN THE
ACTIVATED GLUTAMYL RESIDUE OF THE ORIGINAL THIOL ESTER AND A
TERMINAL AMINO GROUP OF A LYSINE OR ANOTHER NUCLEOPHILIC GROUP ON
THE PROTEINASE, FOR INHIBITION TO BE EFFECTIVE.

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CC -1- SUBUNIT: MONOMER.  
 CC -1- TISSUE SPECIFICITY: PLASMA.  
 CC -1- SIMILARITY: TO OTHER PROTEINS OF THE ALPHA-MACROGLOBULIN FAMILY,  
 CC INCLUDING COMPLEMENT COMPONENTS C3, C4, AND C5.  
 CC -----  
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 CC -----  
 CC EMBL: M65238; AAA73041.1; -  
 CC PIR: B41185; B41185.  
 CC HSSP: P01023; 1BY8.  
 CC MCD: MGI:99836; MUG2.  
 CC InterPro: IPR002890; A2M.N.  
 CC InterPro: IPR001599; Alpha\_2\_macroloblin.  
 CC Pfam: PF00207; A2M; 2.  
 CC Pfam: PF01835; A2M.N; 1.  
 CC PROSITE: PS00477; ALPHA\_2\_MACROGLOBULIN; 1.  
 CC Serine protease inhibitor; glycoprotein; Plasma; Bait region; signal;  
 CC Multigene family.  
 CC SIGNAL 1 27 BY SIMILARITY.  
 CC CHAIN 28 1451 MURINOLOBULIN 2.  
 CC DOMAIN 677 734 BAIT REGION (APPROXIMATELY).  
 CC DISULFID 48 86 BY SIMILARITY.  
 CC DISULFID 251 276 BY SIMILARITY.  
 CC DISULFID 269 288 BY SIMILARITY.  
 CC DISULFID 461 555 BY SIMILARITY.  
 CC DISULFID 587 773 BY SIMILARITY.  
 CC DISULFID 634 680 BY SIMILARITY.  
 CC DISULFID 849 885 BY SIMILARITY.  
 CC DISULFID 923 1274 BY SIMILARITY.  
 CC DISULFID 1081 1104 BY SIMILARITY.  
 CC DISULFID 1298 1444 BY SIMILARITY.  
 CC THIOLEST 974 977 BY SIMILARITY.  
 CC CARBOHYD 55 55 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC CARBOHYD 294 294 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC CARBOHYD 313 313 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC CARBOHYD 500 500 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC CARBOHYD 749 749 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC CARBOHYD 776 776 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC CARBOHYD 871 871 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC CARBOHYD 1401 1401 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC CARBOHYD 1451 AA; 162368 MW; 9B2A82EFAA6258F6 CRC64;  
 CC SEQUENCE  
 CC -----  
 CC Query Match 2.7%; Score 99.5; DB 1; Length 1451;  
 CC Best Local Similarity 19.4%; Pred. No. 7.4; Mismatches 159; Indels 113; Gaps 17;  
 CC Matches 77; Conservative 47; Mismatches 159; Indels 113; Gaps 17;  
 CC -----  
 CC 67 QTELVLCPCQ-----KTDCAIRRVVHLAV-----HGMAEPEEA---102  
 CC 454 ETSILPCNOIHTVOAHRIILGDLGLVLAQSVIIVMAQSGIITQGNHTHOVEGEAEVVK 513  
 CC 103 GKSDSELAQESRNASLAQVLSFOAIPARCALLLEVOPADLVOPGSGVSAVDFCEAS 162  
 CC 514 GNPDL-----IPVEFSMAPMKMLIYTLIPQEV--ADVNFEIKCLANK 559  
 CC 163 LGAEVQIMSTYKPKRYQKELNLTOQLPDCGLEVRDSIQSCWVLPMLNVSTDGQNVLLTD 222  
 CC 560 VDLSSFS--SGSLPASQTLQVLAPOSISGLRAVD--QS-----595  
 CC 223 VSEEDSFLLYLTPVPALKSLATKNTLGNPNTLNHTDLV-----CLCQVW 272  
 CC 596 -----VILLKP--EELSPSWIYNLPGM-----HNKFIYSSLSIEDREDCLVSSW 640  
 CC 273 SLEPDSRVEFCPEPREDGAHR-----NIMHARLRLVLSPGVWQLDAPCLLP--GKVTLCW 326  
 CC 641 VAE---KHTDVPVPGREKDYRYVEDMDLKAFITNLKIKLPKICFDSPAMSGPRKFLDLAF 697

OY 327 QAPDSPCQ-----PLVPVPQKNATVNEPQDFQVAGHPNLCVOYSTKREKOLQACSW 380  
 DB 698 SSVSGTLQKSSKRRQPEEPREDPPKDPLEATTIRKYPEETWY----MDIVYNSTGV 753  
 OY 381 A-----DSLGPFRDMLVEKRTGLNNTSYCALE 409  
 DB 754 AVEVTEVPTITETWAGALCLSDTGLSSVPLQ 789  
 CC -----  
 CC RESULT 9  
 CC NOTC BRARE  
 CC ID NOTC BRARE STANDARD; PRT; 2437 AA.  
 CC AC P46530;  
 CC DT 01-NOV-1995 (Rel. 32, Created)  
 CC DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 CC DT 01-MAR-2002 (Rel. 41, Last annotation update)  
 CC DE Neurogenic locus notch homolog protein precursor.  
 CC GN NOTCH OR NOTCH1A.  
 CC OS Brachydanio rerio (zebrafish) (Zebra danio).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;  
 CC Cypriniformes; Cyprinidae; Danio.  
 CC OC NCBI\_TaxId=7955;  
 CC RN [1]  
 CC RP SEQUENCE FROM N.A.  
 CC RC TISSUE=Embryo;  
 CC RA MEDLINE=94128602; PubMed=8297791;  
 CC RT Bierkamp C., Campos-Ortega J.A.;  
 CC RT "A zebrafish homologue of the Drosophila neurogenic gene Notch and  
 CC RT its pattern of transcription during early embryogenesis.";  
 CC RT Mech. Dev. 43:87-100(1993).  
 CC -1- FUNCTION: IMPLICATED IN CELL FATE SPECIFICATIONS DURING  
 CC EMBRYO DEVELOPMENT. MAY BE INVOLVED IN THE FORMATION OF THE  
 CC NEURAL PLATE, NOTOCHORD AND BRAIN VESICLES.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED IN ALL CELLS IN PREGASTRULATION  
 CC STAGES. DURING GASTRULATION IS DIFFERENTIALLY EXPRESSED,  
 CC ACCUMULATING PREDOMINANTLY IN THE PRECHORDAL MESODERM AND  
 CC NOTOCHORD. AT THE END OF GASTRULATION, EXPRESSED ALONG THE  
 CC ANTERIOR-POSTERIOR AXIS INCLUDING THE DEVELOPING NEURAL PLATE  
 CC AND DIFFERENTIATING MESODERM. ALSO PRESENT IN THE DEVELOPING  
 CC BRAIN AND HEAD REGIONS.  
 CC -1- SIMILARITY: HIGH, WITH OTHER NOTCH-TYPE PROTEINS.  
 CC -1- SIMILARITY: CONTAINS 36 EGF-LIKE DOMAINS.  
 CC -1- SIMILARITY: CONTAINS 3 LIN/NOTCH REPEATS.  
 CC -1- SIMILARITY: CONTAINS 6 ANK REPEATS.  
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 CC -----  
 CC EMBL: X69088; CAA4831.1; -  
 CC HSSP: P00740; 1EDM.  
 CC ZFIN: ZDB-GENE-990415-173; notch1a.  
 CC InterPro: IPR002110; ANK.  
 CC InterPro: IPR000152; Asx\_hydroxyl.  
 CC InterPro: IPR000561; EGF-like.  
 CC InterPro: IPR000742; EGF-2.  
 CC InterPro: IPR001881; EGF\_Ca.  
 CC InterPro: IPR001438; EGF-II.  
 CC InterPro: IPR000800; Notch.  
 CC Pfam: PF00023; ank; 6.  
 CC Pfam: PF00008; EGF; 36.  
 CC Pfam: PF00066; notch; 3.  
 CC PRINTS: PR00010; EGFBL00D.  
 CC PRINTS: PR01452; NOTCH.  
 CC SMART: SM00248; ANK; 5.  
 CC SMART: SM00179; EGF\_CA; 19.  
 CC SMART: SM00001; EGF\_like; 16.





OY 430 ELIADFRSHOCQMLNDNDMGLS-WACPMKXTHRRVWLWVLAALLAALFFLLKKD 488  
 DB 2001 ELI---NCHADPNNAVDGSKSLHMAAAVNN-----YDAAY---VLLKNG 2039  
 OY 489 RRKAARSR--TALLHSDAGGER---LYGALASA-----LSQMLRVAVDMSREL 538  
 DB 2040 ANKLOKNNKEETPEFLAARBS-YETAKVLHLNANDIADHDLDQPRDAHER----- 2092  
 OY 539 SANGALAMFHORRRILOEGGVILLFSPAAVAQC--OOMLQLOVTPGPHDAAALMSC 596  
 DB 2093 -----MHNDIYVLENNLVNTPPLSPPLCCPNYLGIRK-SPGNNTAKKTRK 2143  
 OY 597 VLDPFLOGRAGR-----YGV-----YFDGLHPDSVPS 626  
 DB 2144 PGCGVGSGKSDKIRTKKSGDKNGINGVLSPYDLSLSPHGYLSVSSPPMPTS 2203  
 OY 627 PFVAPFSLPTOLPAFLDALOGCSTAGRPADREHYT 666  
 DB 2204 PFQSPPLSL-NQLOGLADSHMGALOGIGKFPDSAPRUS 2242  
 RESULT 10  
 GLSK\_HUMAN STANDARD: PRF: 669 AA.  
 ID GLSK\_HUMAN 09JUN40; 09JUL05; 09JUL06; 09JUL07;  
 AC 094925; 09JUN40; 09JUL05; 09JUL06; 09JUL07;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Glutaminase, kidney isoform, mitochondrial precursor (EC 3.5.1.2)  
 DE (GLS) (L-glutamine amidohydrolase) (K-glutaminase).  
 GN GLS OR KIAA0838.  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. AND ALTERNATIVE SPLICING.  
 RC TISSUE=Placenta;  
 RX MEDLINE=20473703; PubMed=11015561;  
 RA Elgadi K.M., Meguid R.A., Qian M., Souba W.W., Abcouwer S.F.;  
 RT Cloning and analysis of unique human glutaminase isoforms generated  
 RT by tissue-specific alternative splicing.\*;  
 RL Physiol. Genomics 1:51-62(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC TISSUE=Brain;  
 RX MEDLINE=99156230; PubMed=10048485;  
 RA Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Hirosewa M.,  
 RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;  
 RT Prediction of the coding sequences of unidentified human genes. XII.  
 RT The complete sequences of 100 new cDNA clones from brain which code  
 RT for large proteins in vitro.\*;  
 RL DNA Res. 5:355-364(1998).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC TISSUE=Brain;  
 RA Chavez R.A., Wang C., Cong R., Hawkinson J.E., Forsayeth J.R.;  
 RT Identification and expression of human renal and hepatic glutaminase  
 RT isoforms.\*;  
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC TISSUE=Brain;  
 RX MEDLINE=20185643; PubMed=10719215;  
 RA Holcomb T., Taylor L., Trochilomou J., Curthoys N.P.;  
 RT Isolation, characterization and expression of a human brain  
 RT mitochondrial glutaminase cDNA.\*;  
 RL Brain Res. Mol. Brain Res. 76:56-63(2000).  
 RN [5]  
 RP SEQUENCE OF 225-466 FROM N.A.  
 RC TISSUE=Colorectal carcinoma;  
 RA Turner A., McGivan J.D.;

RT "adenoma and carcinoma cell lines derived from colorectal tumours  
 RT express different isoforms of glutaminase.\*;  
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: CATALYZES THE FIRST REACTION IN THE PRIMARY PATHWAY  
 CC FOR THE RENAL CATABOLISM OF GLUTAMINE.  
 CC -1- CATALYTIC ACTIVITY: L-glutamine + H(2)O = L-glutamate + NH(3).  
 CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS; KGA (SHOWN HERE), GAM AND  
 CC GAC; ARE PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- TISSUE SPECIFICITY: KGA IS EXPRESSED PREDOMINANTLY IN BRAIN AND  
 CC KIDNEY BUT NOT IN LIVER, GAC IS EXPRESSED PRINCIPALLY IN CARDIAC  
 CC MUSCLE AND PANCREAS BUT NOT IN LIVER OR BRAIN, GAM IS  
 CC EXPRESSED SOLELY IN CARDIAC AND SKELETAL MUSCLE.  
 CC -1- SIMILARITY: BELONGS TO THE GLUTAMINASE FAMILY.  
 CC -1- SIMILARITY: CONTAINS 1 ANK REPEAT.  
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 CC  
 DR EMBL: AF158555; AB047056.1; -  
 DR EMBL: AF097492; AAF00088.1; -  
 DR EMBL: AF097493; AAF00089.1; -  
 DR EMBL: AF097495; AAF00090.1; -  
 DR EMBL: AB020645; BA074861.1; -  
 DR EMBL: AF223943; AAF33825.1; -  
 DR EMBL: AF327434; AAG47842.1; -  
 DR EMBL: AF279697; AAG17700.1; -  
 DR MIM: 138280; -  
 DR InterPro: IPR002110; ANK.  
 DR Pfam: PF00023; ank. 2.  
 DR SMART: SM00248; ANK. 1.  
 DR PROSITE: PS50088; ANK\_REPEAT. 1.  
 DR PROSITE: PS50297; ANK\_REPEAT\_REGION. 1.  
 KW Hydroxylase; Transit peptide; Mitochondrion; ANK repeat;  
 KW Alternative splicing  
 FT TRANSIT 1 16  
 FT CHAIN 17 669  
 FT REPEAT 585 618  
 FT VARSPPLIC 162 169  
 FT VARSPPLIC 170 669  
 FT VARSPPLIC 551 669  
 FT  
 FT MITOCHONDRION (BY SIMILARITY).  
 FT GLUTAMINASE, KIDNEY ISOFORM.  
 FT ANK.  
 FT ALKSTGLR -> VSFYILS (IN ISOFORM GAM).  
 FT MISSING (IN ISOFORM GAM).  
 FT VKSYINLFAVITGVGSLRRLALSNMDEQDYSRTALH  
 FT VAAEGHEVYKFLKACKVNPFPDRMNITPDALHGH  
 FT HDVKILQEVQVITPDGSDNGKENVKHNLDGL ->  
 FT HSPFLDESLSQDELALKEVKKVSPESNIDISTVYRM  
 FT ESTLEKRS (IN ISOFORM GAC).  
 FT G -> S (IN REF. 1; AAF00090).  
 FT E -> D (IN REF. 1; AAF00090).  
 FT F -> L (IN REF. 4).  
 FT V -> A (IN REF. 1).  
 FT CONFLICT 6 6  
 FT CONFLICT 66 66  
 FT CONFLICT 219 219  
 FT CONFLICT 268 268  
 SQ SEQUENCE 669 AA; 73461 MW; 4E5E63505E84E0B7 CRC64;  
 Query Match 2.68; Score 98.5; DB 1; Length 669;  
 Best Local Similarity 19.78; Pred. No. 3.2; Indels 273; Gaps 31;  
 Matches 137; Conservative 67; Mismatches 219;  
 OY 69 ELVLRCPQKTDKAL-RVVVVHIA-----VHGHW-----APEEAG 103  
 DB 12 DILLRSPAGVSAITLRRQPLVTLCRPRGGGRPAAGPAAARLHVMWGGGMPAEPLARG 71  
 OY 104 KSISE---LOESRNASLOAOVLSFOAYPIARCAALLEVOVPADLVOPGSGVSAVDCFE 160  
 DB 72 LSSSPSEILLQELGKSTHPQPGVSPAPAPAA-----PGKDPGETDARG 116  
 OY 161 ASLGAEV-----QIMSYPKPRXKEILNQQLPDCRLKLEVRDS---IQ 200  
 DB 117 NSBCKELVASGENKIKIGGLPLSEDLLEFTTAEGEKIPVHFITALKSTGLRTSDPRK 176  
 OY 201 SCWVLPMLNVSTGDGDNVLLTLIDVSEEDFSPFLYLRP-----VPDAKLSIMYKNTLGP 253

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Db 177 ECDMDRLRLIQTSDGVMLDKDKCVQSNIVLTQAFRRKREVPD-----FKSFT-- 228
Cc 254 ONITLHNTDLVPLCICIQWVSLPDSERVEPCPFREDPGAHRLMHLRLVLSPGWOLD 313
Db 229 -----SHID-----ELYESAKKSGGKAVADIIPLAKSPDLMGVS 264
Cc 314 APCCLPG-----KVTLCWQA----- 328
Db 265 V-CTVDGGRHSTGDTFVPPCLQSCVPLKAYAIANDLCTEYHRYGKESGLREKFL 323
Cc 329 -PDQSPCOPLYPVQKNA*------TYNEPQDFOLV-----AGHNLCYQVST 369
Db 324 NEDDRPHNMV-----NCAIYVTSLIKQGVNNAEKFDYVQFLINKMAGNEYGFSNAT 377
Cc 370 WEK-----VOLQAC--SWADSLGPPKDDMLVEMKTGLNNTSYCA--LEPS 411
Db 378 FQSERESGDRNFAIGYLLKKEKPECTDVGILDFYQLSIEFTCSASVMAATLANG 437
Cc 412 GCTPUPS--MASTRARLGEELLQDFRSNOC-----MQLMN 445
Db 438 GCPPTGERVLSPEAVRNTLSLM-----HSCGMYDFSGQAFHVGLPAKSGVAGILLVY 492
Cc 446 DDNMGSL-WACPMCKY-----IHRRWLVWLAC----- 472
Db 493 PRVKGMMCKSPDLKNGSNVKGIFHCIDLVS-CNFHNYDNLRHFAKLPDRREGDQRY 551
Cc 473 -----LLLA-----ALFEFLLLKDRRKRAANGSRATALLHSADGAGYERLVGALASAL 521
Db 552 KSVINLFAAYGVDSALRFAALSAMDMEQRDYSKTA--LHVAABEGHVEYVKLELAC 609
Cc 522 SOMPLRAVDLMSRRLSAHGALEMFHQRRIIOE 557
Db 610 KVNPE--PRDRNNTPMDE--ALHFGHVDYKILQE 641

RESULT 11
NEST_HUMAN
AC P48681; O00552; STANDARD; PRT; 1618 AA.
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Nestin.
GN NES.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=93123384; PubMed=1478958;
RA Dahlstrand J., McKay R.D.G., Zimmerman L.B., Lendahl U.;
RT "Characterization of the human nestin gene reveals a close
evolutionary relationship to neurofilaments";
J. Cell Sci. 103:589-597(1992).
[2]
RP SEQUENCE OF 296-309 FROM N.A.
RX MEDLINE=99117355; PubMed=9917366;
RA Yaworsky P.J., Kappen C.;
RT "Heterogeneity of neural progenitor cells revealed by enhancers in
the nestin gene";
Dev. Biol. 205:309-321(1999).
RL Dev. Biol. 205:309-321(1999).
CC -1- TISSUE SPECIFICITY: CNS STEM CELLS.
CC -1- DEVELOPMENTAL STAGE: UPON TERMINAL NEURAL DIFFERENTIATION, NESTIN
IS DOWN-REGULATED AND REPLACED BY NEUROFILAMENTS.
CC -1- SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
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Cc entities requires a license agreement (See http://www.isb-sib.ch/announce/
Cc or send an email to license@sib-sib.ch).
Cc -----
DR EMBL; X65964; CA646780.1; -
DR EMBL; AF004335; AAB64426.1; -.
DR MIM; 600915; -
DR InterPro; IPR001664; IF.
DR PROSITE; PS00226; IF. 1.
KW Intermediate filament; Coiled coil; Neutroine.
FT DOMAIN 1
FT 1 312
FT 8 312
FT 313 1618
FT 8 43
FT 44 55
FT 56 151
FT 152 172
FT 173 191
FT 192 194
FT 195 312
FT 312
SQ SEQUENCE 1618 AA; 176704 MW; C9E9AA48C6534D0 CRC64;

Query Match 2.6%; Score 97.5; DB 1; Length 1618;
Best Local Similarity 24.1%; Pred. No. 12;
Matches 93; Conservative 45; Mismatches 139; Indels 109; Gaps 21.

Cc 349 NEPODFOLVAGHPNLCVQY-----STWEK-----VOLQAC--SWADSLGPPD--DM 391
Db 83 NLAELLEGVAGR--CEQLRLARERTTEVARRNRRAVEAKCARAWLSOGAELERELEA 139
Cc 392 LLY--EMKGLNNTSVCA--LEPSGCTPLPSMASTRARLGEELLQDFRSNOCQLM 444
Db 140 LRVAAHEERVGILNAQACAPRLPAPRPAPAEVEEL-ARRLGEANRGAVKIQ----- 193
Cc 445 NDDNMGSLWACPMCKYIHRRWLV--VWLACLLLAALFEFLLLKDRRKRAANG--SR 497
Db 194 -----ERVANHETSLDQTRERLRAVQGAR--EVRLELQQLQAEHGGILLER 237
Cc 498 TALLHSADGAGYERL-----VGAALASLSQPLRAVDLMSRRLSAHGALEMFH 548
Db 238 RAALQRLGKQERLRATEKFLQAVEALEQEKQGLQSQIAOYLEGRQQLA----- 288
Cc 549 HORRIIOEGGVILLFSPAAYACQOWLO-----LOTVERGPHDALA--AWLSCVLPD 600
Db 289 HLKMSLSL-----VATRTLLAENSRLQTEGGSKTSLSFDQPKLELPFR 336
Cc 601 FLQGRATGRVGVYFDGLHPDVSPPFRAVAPLFSLPOLPAFL--DALQGGCSTAGR 657
Db 337 TPEGRRIGSLPLV-----LSPTSLSPLPA--TLETVPATLKNQEFLOAKRTPLAST 387
Cc 658 PADVERVYQLRSALDSCSTSSSEAP 683
Db 388 P--IPPTQAPSPAVDAEIRAQDAP 410

RESULT 12
APAF_RAT
ID AFAE_RAT STANDARD; PRT; 1249 AA.
Cc 09EPV5;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Apoptotic protease activating factor 1 (Apaf-1).
GN APAF1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RA Itoh T., Itoh A., Pleasure D.;

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Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.

12)

RA Faden A.I.;  
RA Yakovlev A.G., Ota K., Movsesyan V., Bao W.-L., Yoshihara K.,  
RA "Differential expression of apoptotic protease-activating factor-1 and  
RA caspase-3 genes and susceptibility to apoptosis during brain  
RA development and after traumatic brain injury.";  
RA Neurosci. 21:7439-7446(2001).

CC -1- FUNCTION: Regulates programmed cell death; necessary for normal  
CC brain development. Particulates with caspase-3, leading to  
CC cytochrome c-dependent activation of caspase-3, leading to  
CC apoptosis. This activation requires ATP (By similarity).  
CC -1- SUBUNIT: Monomer. Oligomerizes upon binding of cytochrome c and  
CC dATP. Oligomerizes upon binding of cytochrome c and  
CC their respective NH2-terminal CARD domains (By similarity).  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
CC -1- DEVELOPMENTAL STAGE: Highly expressed in brain cortex in embryos  
CC (E17) and new-born rats up to day 7. Very low expression  
CC thereafter.

CC -1- INDUCTION: By brain injury.  
CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.  
CC -1- SIMILARITY: CONTAINS 13 WD REPEATS (TRP-ASP DOMAINS).  
CC -1- SIMILARITY: CONTAINS 1 NB-ARC DOMAIN.

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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC EMBL: AF320222; AAG35067.1;  
CC InterPro: IPR001315; CARD.  
CC InterPro: IPR002182; NB-ARC.  
CC InterPro: IPR001680; WD40.  
CC Pfam: PF00619; CARD. 1.  
CC Pfam: PF00931; NB-ARC. 1.  
CC Pfam: PF00400; WD40. 13.  
CC PRINTS: PR00320; GPROTEINRPT.  
DR SMART: SM00114; CARD. 1.  
DR SMART: SM00320; WD40. 13.  
DR PROSITE: PS50209; CARD. 1.  
DR PROSITE: PS00678; WD\_REPEATS.1; 4.  
DR PROSITE: PS50082; WD\_REPEATS.2; 9.  
DR PROSITE: PS50294; WD\_REPEATS\_REGION.1.  
KM Apoptosis: ATP-binding; Repeat; WD repeat.  
FT DOMAIN 1 90  
FT NP\_BIND 106 415 NB-ARC.  
FT REPEAT 613 652 ATP (POTENTIAL).  
FT REPEAT 613 652 WD 1.  
FT REPEAT 655 694 WD 2.  
FT REPEAT 697 738 WD 3.  
FT REPEAT 741 780 WD 4.  
FT REPEAT 796 837 WD 5.  
FT REPEAT 838 877 WD 6.  
FT REPEAT 880 919 WD 7.  
FT REPEAT 959 998 WD 8.  
FT REPEAT 1001 1040 WD 9.  
FT REPEAT 1042 1080 WD 10.  
FT REPEAT 1083 1122 WD 11.  
FT REPEAT 1125 1164 WD 12.  
FT REPEAT 1176 1213 WD 13.  
FT REPEAT 1249 AA; 141151 MW; 784AB116FAD008E9 CRC64;  
FT SEQUENCE

Query Match 2.6%; Score 96.5; DB 1; Length 1249;  
Best Local Similarity 19.4%; Pred. No. 11;  
Matches 137; Conservative 78; Mismatches 245; Indels 245; Gaps 32;  
99 DCALRVVVVHLAVGH-----WAEPEAGKSDSELOE-SRNASLQA-QVVLSPQAT-- 128

Db 537 DCVAVCEPFOEFLSLNGHLGKPPENIVOLICFEEETSEVVOAKIQAKOEVDGRLYLE 596  
Oy 129 -----PIARCALLEVOYPADLV-----QPGOSVGSANFDECEASLGAFOVMSYKRPY 177  
Db 597 WINKTKITKNSLRVLRPHHTDAVYACFSQDCQRI-----ASCQADKTLQVFAEKG 647  
Oy 178 OKELNLTQOLPD--CRGLEVADS-IOSCVLPMVNSTDGNVLL-TLDVSEQ----- 227  
Db 648 EKLDIKAHNDEVLCFAFFSDSYIACNSVDKVKVIMSGTKLVHTYEHESEQVNCIF 707  
Oy 228 -DFSLTLIRPVDPALSKLMTKLTGPONITLNTDVLPCLCIQVWSLEPDSERVEFCP 285  
Db 708 TKNSNHLLATGSDNSFLKMLDNLNKECRNMFHTN-----STHCR 750  
Oy 286 FREDPCAHNRMLHARLRVLSFGWOLDAPCCLGKVTLCWAPQSPQPLVPPPOAN 345  
Db 751 FSPDD-----ELLASCSADGTLTL-MDVRSAN-----EKRS 780  
Oy 346 ATY-----NEPODFOLVAGHPNLCVOYSTWEKVQLQACSM-ADS-----L 384  
Db 781 INVKRFLESEDPDEVEV-----VKCSMSADGRIIYAANKVIL 823  
Oy 385 GPEKDMLEVMKTLGNT-SVCALEPSCCTPLPSMASTRARLGEELLQDFRSQCMQ 443  
Db 824 IDHISGLLTHHTGHSTIQCDFSEY-----DHLAVIALSOYVEL 866  
Oy 444 WNDNNGSLWACPMKDYIHRWVYLWACLILAAALFFELLKDKDRRAAGSRALLH 503  
Db 867 WHDSKVKADCG-----HLSW-----HG-----VWF 890  
Oy 504 SADGAYERLVGALASALSCMPLRAVDLWSRRELASGALAMFHQRRILOEGGVIL 563  
Db 891 SPGSSF-----LTASDQITRV-----METRVCNKSALV-LKELDIVQVQENEMVL 938  
Oy 564 LFSPAVACCOOMLOQYVEPGHDAL--AAMLSCLPDLQGRATGRTVG----- 612  
Db 939 ---AVDNI-KGLDLIAGKTQIDYLPEDAVSCCSPHLEYVAFGEDEGAKIIELEPN 992  
Oy 613 --VFEDGLHPDSV-----PSPERVAFLPSLTOLAPFDALQ----- 648  
Db 993 NNVFSSGIGHKRAVRIHIOPTADKTLISSEDSYIQVWMTQETEEVFLQAHQETVKKFRL 1052  
Oy 649 -----GGCSTAGRPADREVERVQALRSALDSCYSSSEA 682  
Db 1053 LBSRLLSWSPDQTVKVMVYITGRIERDFCHQGTVLSCAISSDA 1097

RESULT 13  
C267\_HUMAN  
ID C267\_HUMAN STANDARD; PRT; 204 AA.  
AC P58512;  
DT 01-MAR-2002 (Rel. 41, Created)  
DT 01-MAR-2002 (Rel. 41, Last sequence update)  
DT 01-MAR-2002 (Rel. 41, Last annotation update)  
DE Protein C21orf67.  
GN C21ORF67.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORMS A AND B).  
RX MEDLINE-21564202; PubMed-11707072;  
RA Raymond A., Friedl M., Neegaard Henriksen C., Chapot F.,  
RA Deutsch S., Ueda C., Rossler C., Lyle R., Gulipont M.,  
RA Antonarakis S.E.;  
RT "From PREDS and open reading frames to cDNA isolation: revisiting the  
RT human chromosome 21 transcription map.";  
RL Genomics 78:46-54(2001).  
CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; A (shown here) and B; are  
CC produced by alternative splicing.  
CC -1- TISSUE SPECIFICITY: Not detected in any tissue tested.

-----  
 -1- CAUTION: Maps to the wrongly predicted PRED54 locus.  
 -----  
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 -----  
 EMBL: AF380178; AAL34496.1; ~~AF380178~~  
 EMBL: AY040088; AAK74136.1; ~~AF380178~~  
 Alternative splicing  
 VARSPLIC 72 82 LAADIAGDALP -> CTSGASAGOKL (IN ISOFORM B).  
 MISSING (IN ISOFORM B).  
 VARSPLIC 83 204 21307 MW; F955EC4E414F2340 CRC64;  
 SEQUENCE  
 Query Match 2.5%; Score 93.5; DB 1; Length 204;  
 Best Local Similarity 36.6%; Pred. No. 1.7;  
 Matches 30; Conservative 5; Mismatches 38; Indels 9; Gaps 5;  
 252 GPNITLHTLVPCICIQWLSLEP-DSEVERCEPREDPGARHNTIARLVSPGV 310  
 104 GPALDEHCHERC-CGCGASFSPFAPR---CP-SERLGASHSMWAINGRSKINPPW 158  
 311 QLDAPCCLPGKVTLCWQAPDOS 332  
 159 ---APACLPGGFPACLPAPKSS 177  
 RESULT 14  
 APB\_HUMAN STANDARD; PRT; 636 AA.  
 O9NRJ5;  
 16-OCT-2001 (Rel. 40, Created)  
 16-OCT-2001 (Rel. 40, Last sequence update)  
 16-OCT-2001 (Rel. 40, Last annotation update)  
 Poly(A) polymerase beta (Ec 2.7.7.19) (PAP beta) (Polynucleotide adenylyltransferase beta) (Testis-specific poly(A) polymerase).  
 PAP0LB OR PAP.  
 Homo sapiens (Human).  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 NCBI\_TaxID=9606;  
 [1]  
 SEQUENCE FROM N.A.  
 Lee Y., Kim H., Chung J., Lee Y.;  
 "Testis-specific poly(A) polymerase gene is conserved in human and mouse";  
 Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
 -1- CATALYTIC ACTIVITY: N ATP + (nucleotide)(M) - N diphosphate + (nucleotide)(M+H).  
 -1- SUBCELLULAR LOCATION: NUCLEAR (Probable).  
 -1- TISSUE SPECIFICITY: Testis-specific.  
 -1- SIMILARITY: BELONGS TO THE POLY(A) POLYMERASE FAMILY.  
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 -----  
 EMBL: AF218840; AAF81013.1;  
 InterPro: IPR002934; NRP\_transf.  
 InterPro: IPR001201; PAP\_25A\_core.  
 Pfam: PF01909; NTP\_transf\_2; 1.  
 mRNA processing; Transferase; Transcription; RNA-binding;  
 Nuclear protein.  
 ACT\_SITE 113 113 BY SIMILARITY.

FT ACT\_SITE 115 115 BY SIMILARITY.  
 FT ACT\_SITE 167 167 BY SIMILARITY.  
 SQ SEQUENCE 636 AA; 71681 MW; 3A0823F4309C35DD CRC64;  
 Query Match 2.5%; Score 93.5; DB 1; Length 636;  
 Best Local Similarity 20.5%; Pred. No. 7.7;  
 Matches 77; Conservative 50; Mismatches 123; Indels 125; Gaps 17;  
 50 PGSLQAPGPLYVPR--LOTELYRCPOKTPCALRVRYVHLAVGHNAEPEACKSDS 107  
 4 PVITQGPAPPPNRRGVSSPSILAVKEDCLLQRLIFLRPGVEEEEE----- 57  
 108 ELQESRNASLOAQVLSFOAPVPIARCALLEVOVPADLVQPG-QSVGSAVFDEEASIGAE 166  
 58 -----LQRLIVLEKLNIVKEMWIREISEKSLPGSVLENGGKIFTEGSRVIGV 107  
 167 VQIKSTYK-----PRYQELNLTQQLPDCRGLEYRDSIQSCWVLP 206  
 108 -----HTKGADIDALCVAPSHVDRSDFTSFYAKLKLQEEVLDRAVEA-----FVP 155  
 207 WLVNSTDG-----DNVLTLD-----VSEQDPFSFL 232  
 156 VIKCEFGIEIDILFARALDITPEDLDLDDSLKNTDKIRSLNGCRVDE-----I 210  
 233 LYDRPVDALK-----SLW-----YKNLGPNITLHTLVPCICIQWLSLEPDS-- 278  
 211 LHLVPNIDNFLTLRAIKLMKCHNITYNIGLEFG-QVSMALVARTC---QLYPNVA 265  
 279 ---ERVEFCPREDPGARHNTIARLVSPGQDLAPCCLPGKVTLCWQAPDOSPCO 335  
 266 STLVKKEFLVSEWMPVLLKEPEERNLMPVD---PRVNS-----DRYHLM 313  
 336 PLVPPV-PQKNATVN 349  
 314 PITTPATPOONSTYN 328  
 RESULT 15  
 CCT1\_HUMAN STANDARD; PRT; 726 AA.  
 ID CCT1\_HUMAN  
 AC 060563; O60581;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Cyclin T1 (Cyclin T) (CyclT).  
 GN CCT1.  
 OS Homo sapiens (Human).  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 NCBI\_TaxID=9606;  
 [1]  
 SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.  
 RC TISSUE-T-cell lymphoma.  
 RX MEDLINE-98150851; PubMed-9491887;  
 RA Wei P., Gardner M.E., Fang S.-M., Fischer W.H., Jones K.A.;  
 "A novel CDK9-associated C-type cyclin interacts directly with HIV-1 Tat and mediates its high-affinity, loop-specific binding to TAR RNA";  
 Cell 92:451-462(1998).  
 [2]  
 SEQUENCE FROM N.A.  
 RC TISSUE-Breast cancer;  
 RX MEDLINE-98167917; PubMed-9499409;  
 RA Peng J.-M., Zhu Y., Milton J.T., Price D.H.;  
 "Identification of multiple cyclin subunits of human P-TEFb";  
 Genes Dev 12:755-762(1998).  
 [3]  
 FUNCTION.  
 RP MEDIANE-99263518; PubMed-10329125;  
 RX Ivanov D., Kwak Y.T., Nee E., Guo J., Garcia-Martinez L.F.,  
 RA Gaynor R.B.;  
 "Cyclin T1 domains involved in complex formation with Tat and TAR RNA

RT are critical for tat-activation.";  
 RL J. Mol. Biol. 288:41-56(1999).  
 RN [4]  
 RP MUTAGENESIS.  
 RX MEDLINE-99263519; PubMed-10329126;  
 RA Kwak Y.T., Ivanov D., Guo J., Nee E., Gaynor R.B.;  
 RT "Role of the human and murine cyclin T proteins in regulating HIV-1  
 RL Tat-activation.";  
 RL J. Mol. Biol. 288:57-69(1999).  
 RN [5]  
 RP FUNCTION.  
 RX MEDLINE-99051315; PubMed-9832804;  
 RA Garber M.E., Wei P., Kewalramani V.N., Mayall T.P., Herrmann C.H.,  
 RT Rice A.P., Littman D.R., Jones K.A.;  
 RT "The interaction between HIV-1 Tat and human cyclin T1 requires zinc  
 RT and a critical cysteine residue that is not conserved in the murine  
 RT Cyclin T protein.";  
 RL Genes Dev. 12:3512-3527(1998).  
 RN [6]  
 RP FUNCTION.  
 RX MEDLINE-99292873; PubMed-10364329;  
 RA Bieleas P.D., Grdina T.A., Bogerd H.P., Cullen B.R.;  
 RT "Analysis of the effect of natural sequence variation in Tat and in  
 RT cyclin T on the formation and RNA binding properties of Tat-cyclin T  
 RT complexes.";  
 RL J. Virol. 73:5777-5786(1999).  
 RN [7]  
 RP FUNCTION: REGULATORY SUBUNIT OF THE CYCLIN-DEPENDENT KINASE PAIR  
 CC (CDK9/CYCLIN T) COMPLEX, ALSO CALLED POSITIVE TRANSCRIPTION  
 CC ELONGATION FACTOR B (P-TEF), WHICH IS PROPOSED TO FACILITATE THE  
 CC TRANSITION FROM ABORTIVE TO PRODUCTION ELONGATION BY  
 CC PHOSPHORYLATING THE CTD (CARBOXY-TERMINAL DOMAIN) OF THE LARGE  
 CC SUBUNIT OF RNA POLYMERASE II (RNAP II). BINDS ALSO TO THE  
 CC TRANSCRIPTIONAL DOMAIN OF THE HIV-1 NUCLEAR TRANSCRIPTIONAL  
 CC ACTIVATOR, TAT. IT IS PROBABLY THE CIS-ACTING TRANSCRIPTION  
 CC RESPONSE ELEMENT (TAR) RNA-BINDING COFACTOR FOR TAT. ALSO SERVES  
 CC AS AN ESSENTIAL COFACTOR FOR HIV 2-TAT AND SIMIAN IMMUNODEFICIENCY  
 CC VIRUS (AFRICAN MANDRILL) TAT FUNCTION.  
 CC -1 SUBUNIT: ASSOCIATES WITH CDK9 TO FORM P-TEF. CYCLIN T1 IS THE  
 CC PREDOMINANT CYCLIN ASSOCIATED WITH CDK9.  
 CC -1 SUBCELLULAR LOCATION: Nuclear.  
 CC -1 TISSUE SPECIFICITY: UNIDIRECTIONALLY EXPRESSED.  
 CC -1 MISCELLANEOUS: INTERACTION BETWEEN TAT AND CYCLIN T1 REQUIRES  
 CC ZINC.  
 CC -1 SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN C SUBFAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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 CC -----  
 CC EMBL: AF045161; AAC39638.1; -  
 CC EMBL: AF048730; AAC39664.1; -  
 CC TRANSFAC: T02727; -  
 CC MIM: 602506; -  
 CC InterPro: IPR000553; Cyclin.  
 CC Pfam: PF00134; cyclin; 1.  
 CC SMART: SM00385; CYCLIN; 1.  
 CC PROSITE: PS00292; CYCLINS; FALSE\_NEG.  
 CC Cyclin: cell cycle; cell division; Colled coil;  
 CC Transcription regulation; Nuclear protein.  
 CC NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).  
 CC TAT: TAR RECOGNITION MOTIF (TRM).  
 CC COILED COIL (POTENTIAL).  
 CC POLY-HIS.  
 CC POLY-SER.  
 CC POLY-PRO.  
 CC C->Y: LOSS OF HIV-1 TAT TRANSCRIPTION.  
 CC C->Y: R (IN REF. 2).  
 CC CONFLICT 77 77  
 CC SEQUENCE 726 AA; 80684 MW; 4637EB3DDEDEF3 CRC64;

Query Match 2.58; Score 93.5; DB 1; Length 726;  
 Best Local Similarity 19.3%; Pred. No. 9.1;  
 Matches 43; Conservative 39; Mismatches 70; Indels 71; Gaps 11;  
 QY 50 PGSIQSAAPVLYPRRLQTELVLRCPQRTDCLRVVYVLAHVGMAPEPEKGSSEL 109  
 DB 79 PGN-SVAPALFLAKVEEQ-----PKLLEHYK--VAHTCLHPQESLPDT--RSEAYL 127  
 QY 110 QESRNASLQAOVLSFOAYP-----IARCALLLEVOPADLVOPGSGSAVFPCFE 160  
 DB 128 QOVQDVLVLESIILQTLGFEITIDPHRHVYKCTOL-VKSKDLAOTSIFMATNSLHLLT 186  
 QY 161 ASLGAEOVIMSYTRPRRQKEMLTQQLPDCRGLEVRDSIQSC-----VWLEPLN 209  
 DB 187 FSL-----QYTPP-----VACCHLACKMSMWELP--- 213  
 QY 210 VSTDDG-----NVLITDVEEQDFSLILYLRPPVDALKSLM 246  
 DB 214 VSTDGKHMEYVDATVTLLELDELTHEFLQILEKTPNRLKRW 256

Search completed: September 28, 2002, 19:43:38  
 Job time: 286 sec

Sun Sep 29 09:32:54 2002

us-09-899-471-5.rsp

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 28, 2002, 19:41:27 : Search time 43.34 Seconds  
(without alignments)  
1547.539 Million cell updates/sec

Title: US-09-899-471-5  
Perfect score: 3741  
Sequence: 1 MPVSWFLSLALGRNPVVS.....SSAAPGCCCEMDIAPCTTLE 698

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database:

1: PIR-71:\*  
2: pir1:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	119.5	3.2	1013	2 B70841	probable helz prot
2	112	3.0	1447	2 A54100	tumor suppressor p
3	111.5	3.0	2910	2 T42214	otogelin - mouse
4	107.5	2.9	1187	2 JE0347	hypothetical prote
5	106.5	2.8	478	2 D75564	hypothetical prote
6	106.5	2.8	1409	2 T37188	presynaptic activi
7	106	2.8	267	2 A38442	probable tumor sup
8	103	2.8	557	1 B39439	60K cysteine-rich
9	103	2.8	906	2 G83156	probable transcrip
10	102	2.7	1615	2 B49502	protein-tyrosine-p
11	102	2.7	1767	2 A49502	protein-tyrosine-p
12	102	2.7	4848	2 T30289	pristinamycin I sy
13	101.5	2.7	658	2 A82553	hypothetical prote
14	101.5	2.7	1274	2 T04018	hypothetical prote
15	100.5	2.7	647	2 T26240	hypothetical prote
16	100	2.7	851	2 T31520	hypothetical prote
17	99.5	2.7	1451	2 B41185	hypothetical prote
18	99.5	2.7	3014	1 JC5620	alpha-2 macroglobu
19	99	2.6	1271	2 T43269	genome polyprotein
20	99	2.6	1617	2 T43269	microcystin synthe
21	99	2.6	2437	2 A57041	complement C4 - ch
22	98.5	2.6	442	2 A57041	transcription regu
23	98.5	2.6	665	2 S69222	probable transcrip
24	97.5	2.6	1618	2 S21424	nestin - human
25	96.5	2.6	1476	2 A41185	alpha-2 macroglobu
26	96	2.6	364	2 D96017	probable peptidase
27	95.5	2.6	1711	1 A55148	protein-tyrosine-p
28	95.5	2.6	2629	2 T30987	telomerase-associ
29	95	2.5	1573	2 S01845	DNA (cytosine-5-)-

30	94.5	2.5	445	2 E70854	probable membrane
31	94.5	2.5	3738	2 T05501	hypothetical prote
32	94	2.5	10223	2 T30225	polyketide synthas
33	93.5	2.5	478	2 T30763	hypothetical prote
34	93.5	2.5	523	2 T47560	serine protein kin
35	93.5	2.5	819	2 C83346	probable non-ribos
36	93.5	2.5	876	2 I49152	protein-tyrosine k
37	93.5	2.5	880	2 B53743	gelatin factor AB
38	93.5	2.5	2647	2 A37098	conserved hypothet
39	93.5	2.5	6260	2 T30228	polyketide synthas
40	93	2.5	604	2 G83091	conserved hypothet
41	93	2.5	739	2 SA7772	biotin sulfide r
42	93	2.5	739	2 D91183	biotin sulfide r
43	93	2.5	739	2 H86029	biotin sulfide r
44	93	2.5	1637	2 T00070	hypothetical prote
45	92.5	2.5	361	2 T39784	hypothetical prote

## ALIGNMENTS

RESULT 1  
B70841  
probable helz protein - Mycobacterium tuberculosis (strain H37RV)  
C:Species: Mycobacterium tuberculosis  
C:Date: 17-Jul-1998 #sequence.revision 17-Jul-1998 #text\_change 22-Oct-1999  
C:Accession: B70841  
R:COLE, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gord  
Rajandream, M.A.; Rogers, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroy  
Nature 393, 537-544, 1998  
A:Authors: Squires, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrall, B.G.  
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete ge  
A:Reference number: A70500; M01D:98295987  
A:Accession: B70841  
A>Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-1013 <COI>  
A:Cross-references: GB:AL021924; GB:AL123456; NID:g3261519; PIDN:CA17284.1; PID:el  
A:Experimental source: strain H37RV  
C:Genetics:  
A:Gene: helz

Query Match 3.2%; Score 119.5; DB 2; Length 1013;  
Best local Similarity 20.8%; Pred. No. 0.36; Indels 267; Gaps 38;  
Matches 150; Conservative 80; Mismatches 224;  
OY 90 LAHGHMAEP--EEAGKSDSELQESRNASLQAVVLSFOAYPIARCALEGVADL---144  
2 LVHGFWSNGKRMEDSDLL---VKPSQALRSARPHFA-----APADLIAG 49  
DB 145 VDPGQ-----SVGSAYFDCE-----ASLGAEOVMSYKPRYOKELNLT---184  
OY 50 IHGKPATAVLLPILSLASAPLSDPELRLAPRAPARTDPMILAMVPP--VVDLDPTAALA 107  
DB 185 ---QQLPDCR-GLEV-----RDSIOSCWVLPMLNVSDG-----DNVL 218  
OY 108 ADQPAPVDVRYGASVDYLAELAVFARLEVERGRVLPQLRDTGGAACRPVYLGSDYVA 167  
DB 219 LTLVSEEDDFSLYLRLPV-----PDALSLMYKMLTGPONTLNTDLY 264  
DB 168 MT-----SLVSAMPVPCRAEVGGHDPHELTSLADAM-----VDAAVRAALSMDLL 214  
OY 265 PCLICIVMSLEPSESEVEFCPPREDPCAHNLMHITARLVLSPGVWQDAPCCLPGRVTL 324  
DB 215 P-----PRRGSRKRR-----AVEAM-LTALTCPPGRFPA 243  
OY 325 CWAQAPDQSCQPLVPPVPAKATVNEPODFQLVAGHPHLCVQVSYWEVQQLQACMSADSL 384  
DB 244 -----EPDELDALA-----BALRPMDDVGI-----GTV 266  
OY 385 GPFKDDMLLVEMKTKGINTSVCALEPSGCTPLPSPMASTRARLGEELLQDFRSRHOOM---441



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Db 267 GPAAATFLSEVETNEET-----PAG-----SLMRL-ETLLQSTQDPSLTPA 309
QY 442 -QLMNDMNGSLIMACPMKXIIHRRVY---LWMLACILLAAALFFELLKDKRKAAGS 496
Db 310 EQAWNND--GSL-----RRLMDRPOELLTELGRASRIPELV-----PALRTA 351
QY 497 RTALLHSDAGVRYLGAALASLSOMPLRYAVDIMSRRRLSAHGALAMFHQRRLIQ 556
Db 352 CPSLELDADA--YRFLSGTAAYLDEAGFVLLPSM-----W---DRRRL- 393
QY 557 EGVVILLFSP--AAVACQOMLOEFTVE-----PGPHDALAAMLSCVLP----- 599
Db 394 --GLVLSAYTVDVGVGASKRGQOLVFRMELAVGDDPLSEETIALLETKSPILRLR 451
QY 600 -----DFTQGRATGRVGVYFDGLL--HSDVSPSPFRVAPLFSLPTOLPA 642
Db 452 GOWVALDTEQNRRLGLEFPERKPTGRKTAETLALASHHPDDVDTPEVTAV-----RADG 506
QY 643 FLDALGGCSTAGRAPRVERVQALRSALDSCTS-----SSEAPGCCCEEMDAGPCTTL 697
Db 507 WLGDLLAGAASLQPLDPPDGFATLRPYQQRGLAMIAFLSLGLGSLADMDGLKTV 566
QY 698 E 698
Db 567 Q 567

RESULT 2
A54100
Tumor suppressor protein DCC precursor - human
N:Alternate names: colorectal cancer suppressor DCC
C:Species: Homo sapiens (man)
C>Date: 02-Aug-1994 #sequence_revision 02-Aug-1994 #text_change 05-Nov-1999
C:Accession: A54100; A40098
R:Hedrick, L.; Cho, K.R.; Fearon, E.R.; Wu, T.C.; Kinzler, K.W.; Vogelstein, B.
Genes Dev. 8, 1174-1183, 1994
A>Title: The DCC gene product in cellular differentiation and colorectal tumorigenesis.
A:Reference number: A54100; MUID:95011532
A:Accession: A54100
A:Molecule type: mRNA
A:Residues: 1-1447 <HED>
R:Fearon, E.R.; Cho, K.R.; Nigro, J.M.; Kern, S.E.; Simons, J.W.; Ruppert, J.M.; Hamiltc
Science 247, 49-56, 1990
A>Title: Identification of a chromosome 18q gene that is altered in colorectal cancers.
A:Reference number: A40098; MUID:90100559
A:Accession: A40098
A:Molecule type: mRNA
A:Residues: 1-750 <FEA>
A:Cross-references: GB:M32292; NID:g181492; PIDN:AAA35751.1; PID:g181493
C:Genetics:
A:Gene: GDB:DCO
A:Cross-references: GDB:119838; OMIM:120470
A:Map position: 18q21.1-18q21.1
C:Keywords: transmembrane protein; tumor suppressor
F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-1447/Product: tumor suppressor protein DCC #status predicted <MAT>

Query Match 3.0%; Score 112; DB 2; Length 1447;
Best Local Similarity 18.8%; Pred. No. 2.2; Indels 302; Gaps 34;
Matches 136; Conservative 74; Mismatches 210;

QY 20 STERIMPODARCSLSLSCHMDGVCLTCLPSLQSAFG--PVLVPTRLQTEVL---RC 74
Db 39 ALNFISSPSDAVT-----MRGNNVL-LDCSASDRGVPVTKKKDGIHIALGMDERK 89
QY 75 POKTDCALRVVVVLAHVGHMAEPE-----EAGKSDELSQESRNASL---Q 118
Db 90 QQLSNGSLILIONILHSRIH---KPDGLYOCESLSDGSGSIISRAKAVAVAPLRLSLQ 145
QY 119 AQVYLSQAIPI-ARCALLLEVQVPA-----DL-----VQPG 148

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Db 146 TESVTAFMGDTVLLKCEVIGEMPTIHMOKNQODLPIPIGDSRVVLLPSGALQISRLQPG 205
QY 149 QSVSAVAFDC-----FEASLGAEOIWSYTKRKYKEINLITQOLPDCRGLFVNDISQSCW 203
Db 206 -DIG--IYKSAARPASRTGNEAEVRLISDPLRHQLTFLQRPNSVVAIEGDAVLECC 262
QY 204 V-----LPMANVSTQDNNVLTLDVSEEDQFSLLYLRVPDALKSLMYKNLITGPONI 256
Db 263 VSGPPEPSFTMLR--GEVYI-----QLRSKKYSILGGSNLL 236
QY 257 TLNHTDLPVLCICIOYWSLEPDSERYEPCFPEDPGAH-----RNLMIHARLVLSPG 308
Db 297 ISNVTI-----DQSGMYTCVVYTKMNIASASLTVLP- 330
QY 309 VMQIDAPCLPGKVTLCWQAPD--QSPCQPLVPPV-----QKNATVNEPODFOLVAGHPNL 363
Db 331 PWTLMHPSNL-----YAESMDIEPECTVSGKPVPTVMKMGDVYIPSDYQIVGSGNL 385
QY 364 CVQVSTWEKVQLQACSWADSLGPFKRD---MLVEMKTLNNTSVCALEPSCGP----- 415
Db 386 RI-----LGVYKSDGEGFYQCVAEENAGNQTSAQLIVPKPAIPSSSV 427
QY 416 -----LPSMASTRARLGEELLQDFRSHOCQMLMNDNNGSLMACPMKXIIHRRVYL 467
Db 428 LPSAPRDVPEVLVSSRRVRLS-----WRPPAE----- 454
QY 468 VWLACILLAAALFFELLKDKRKAAGS-RTALLHSDAGYERLVGALASLSOMPL 526
Db 455 -----AKNINQITFTYFFSEGNRRERALTTPQGSILQIV 489
QY 527 R-----VAVDIMSRRRLSAHGALAMFHQRRLIQEGGVILLFSPAAYAQO 574
Db 490 GNLKPEAMTYFRVAYAYNEMGGESS-----QPIKVA-TQ 522
QY 575 QWIO-----LQYVEGPHALAMLSCLVPDFQGR-----ATGRVGVYRD 616
Db 523 PELQVQPGVENLQAVSPTSILITWEP--PAYANGPVQYRLCTEYSTGKEONIEVD 579
QY 617 GL 618
Db 580 GL 581

RESULT 3
T42214
Otogelin - mouse
N:Alternate names: mucin-like extracellular matrix protein
C:Species: Mus musculus (house mouse)
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C:Accession: T42214
R:Cohen-Salmon, M.; El-Amraoui, A.; Ielbiovici, M.; Pettit, C.
Proc. Natl. Acad. Sci. U.S.A. 94, 14450-14455, 1997
A>Title: Otogelin: A glycoprotein specific to the acellular membranes of the inner
A:Reference number: Z22079; MUID:98070772
A:Accession: T42214
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-2910 <COH>
A:Cross-references: EMBL:U96411; NID:g2760883; PID:g2760884; PIDN:AB96561.1
A:Experimental source: strain BALB/c
A>Note: component of all the acellular membranes of the inner ear
C:Superfamily: von Willebrand factor; von Willebrand factor type A repeat homology;

Query Match 3.0%; Score 111.5; DB 2; Length 2910;
Best Local Similarity 19.8%; Pred. No. 6;
Matches 83; Conservative 43; Mismatches 140; Indels 153; Gaps 19;

QY 139 OVPADLVQPGS-----VGSVAFDCFEASLGAE--VQIM-STTKPRY 177
Db 2267 OVSSSLTSEQTRFRPDSQATADCSPLRLMVSNTFTSACHSFVSESPCELMIRDTKYQV 2326

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QY 178 OKELNLTQOLPDCRGLEY-----RDSIOSCWVLPMVLNVSTDDGNVLLTLD 222  
 Db 2327 OPCVALLTYVAMCHKRVHCLEMGRSDYCPFLCSDSDSTYQACVAACEPPTCODGVLPID 2386  
 QY 223 VSEEDF-----SFLLYL-----PYDALKSLMYKNLTGPNIT 257  
 Db 2387 PEQCVLIGBCVCTECTETILHRRHSALCIPEDKCACTDSTGPRALGETNNSLSG----- 2441  
 QY 258 LNHDLVPLCLCTQVMSLEPSS-----ERYEFCFPREDPGAHRLMHTARLVLSP 307  
 Db 2442 -----CCOQOCCAPPTIIRBPLDCPCRPRESCE-----RFGVILLQP 2479  
 QY 308 GVMQDAPCCLCGRKYLTCMAQPSQPLVPYPOKRNATVNEPQDFOLVAGH-----PN 362  
 Db 2480 -----TEDPCLL-GSVVC-----NPTLCEGLAPTCRPGHSLTHFEQEDSCPSYSCEDDPG 2530  
 QY 363 LCVQVSTWKEVOLQACSMWDSLGFPRKDDMLVEAKTGLNNTSVCLPESGCG-----TPLS 418  
 Db 2531 LC-----EAEVPTC-----REDQILLIEGRIG-----DSCCTSYRCGCECSDPME 2572  
 QY 419 MASTRA-----ARIGEELADFRSHQ-----CMQWMDNDMGLMACPMD 458  
 Db 2573 COGEHALVHRMTTELCCPLQCVCEHFRCPOVCGMGTSLVEVWSPRCPCYKSCCED 2631

## RESULT 4

hypothetical protein c31612.1 (K1AA0734 (C2 domain protein)) [imported] - human  
 N:Alternate names: BAI-associated protein 3  
 C:Species: Homo sapiens (man)  
 C>Date: 05-Feb-1999 #sequence\_revision 05-Feb-1999 #text\_change 01-Dec-2000  
 C/Accession: J0347; T45060  
 R:Shirtsuchi, T.; Oda, K.; Nishimori, H.; Suzuki, M.; Takahashi, E.; Tokino, T.; Nakam  
 Blochem. Biophys. Res. Commun. 251, 158-165, 1998  
 A:Title: Cloning and characterization of BAP3 (BAI-associated protein 3), a C2 domain-co  
 A:Reference number: J0347; MUID:99009239  
 A:Accession: J0347  
 A:Molecule type: mRNA  
 A:Residues: 1-1187 <SHIT>  
 A:Cross-references: GB:AB017111; NID:g3929916; PIDN:BAA34710.1; PID:g3929917  
 A:Experimental source: brain  
 R:Frankland, J.  
 submitted to the EMBL Data Library, July 1999  
 A:Reference number: Z22901  
 A:Accession: T45060  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 36-581, 'D', 583-1187 <FRA>  
 A:Cross-references: EMBL:AL031709; PIDN:CAB56182.1  
 A:Experimental source: clone LA16-31612  
 C:Genetics:  
 A:Gene: BAP3  
 A:Map position: 16p13.3-16p13.3  
 A:Intons: 79/2; 108/3; 135/3; 171/3; 191/3; 214/1; 279/2; 294/2; 320/2; 354/3; 390/3;  
 976/3; 1003/3; 1044/1; 1085/2; 1154/1  
 A:Note: c31612.1

Query Match 2.9%; Score 107.5; DB 2; Length 1187;  
 Best Local Similarity 21.0%; Pred. No. 4;  
 Matches 158; Conservative 85; Mismatches 216; Indels 295; Gaps 47;

QY 1 MPVS-----WFLI-----SLALGRNVVSLERLMEPQDARCSIG-----LSCHL 41  
 Db 356 VPVAGVDMFKLEPRSSASRVGCHLVLKL--ITQORDTAMSGRGSGFLSHLLLSHL 413  
 QY 42 -----WDGD-----VLCLPGSIQASAPGVLPVRLQTELYLRCKQKTD 80  
 Db 414 LRLHSAEPNSSNMRGELSTPATILCLHGA--QSNLSPLQLAV-LHMVSSRHQ--TC 469  
 QY 81 ALRVVVVHLA--VHGHAPEPEAGKSDSELQSRNASLQA-----QVVSFOAY-PIA 131  
 Db 470 TLDSYLLGLEDMQAHN--EAPSLPQOEESLADSLASFSEFGQLLQKLRDYPFAT 526

QY 132 RCA-----LLEQVPADLVDPQSVASAFDC-PEASLGAEV-----QIW 170  
 Db 527 NSTAVHRLLELLKCLKCLQLQFPSPFEI-----CPFESELNMDIAALKRGREMYDRL 580  
 QY 171 SYTKRYQKELNLTQOLPDCRGL-----EVRDSIQSC----- 202  
 Db 581 NAKSPREQPG--PQRLP--GLVVLADAVYDDLOFCYSVYASLFSHSLYNDVFTLFRQ 634  
 QY 203 -----WVLPMVLNVSTDDGNVLLTLDYSEEDDFSLYLRLRVYDMLKSLMYKNLTGP 253  
 Db 635 LERLVAEAMVL-----TEELSPKMTLEVASG--LEFELYL-GLAD-LOREW-DSIGOR 682  
 QY 254 ONITLN-----HFDVPLCTQVW-----STEPDERVEFCFPREDP 290  
 Db 683 DSRSLAIGAHNPFLE--AVKLMFOYLRLDQAKRRLQGAVIDMDTLEP-----VDASSRHSS 736  
 QY 291 GAHRLM--HIALRLVSPGWQDAPCCLPGRVTLQWAPDQSPQPLVPPVPOK--NA 346  
 Db 737 AATAGLCLSHIOEL-----W-----VRLAM--PDPAQAGLGQLGQDVCEA 776  
 QY 347 T-----VNEPDQVLAG--HFNLCQVSTWKEV-----LQACSMWDSLGFPRKDD 390  
 Db 777 TLFYTELLKRVDTQGAAGEAVSEALCVLNNVEIVRKAAQALKGLAMEG----- 829  
 QY 391 MLVEAKTGLNNTSVCLPESGCTPLPSMASTRA-----ARIGEELADFRS 437  
 Db 830 -----ATPEGVLPRLPLSCTQALDDLDQREAITVYHLSKNVGDTRK 873  
 QY 438 H-QCMQWMDNDMGLMACPMDKYIHRRWLVMLACLILAALFFLLKKRRKARAGS 496  
 Db 874 YVOHISLSPDSIQNDQAVAPLKMRYLDEK-----LALLNANSL-----VGN 913  
 QY 497 FTALLHNSADGGERVELVQALASLSOMPLRAVADLMSRRELSHGALAMHHQRRRLQ 556  
 Db 914 LSRVL-----EALWEILLQATILQALG-ANQDVADPFSRPHFTLEALVSEFH-----A 960  
 QY 557 EGVVILLFSPAAVACQOQMLQLOTEPEPQDAL 590  
 Db 961 EG-----QGLPLESLRDGSYKRL 978

## RESULT 5

hypothetical protein - Deinococcus radiodurans (strain R1)  
 C:Species: Deinococcus radiodurans  
 C>Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 31-Mar-2000  
 C/Accession: D75564  
 R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, F  
 , M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Uterback, T.; Zalewski, C  
 S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.  
 Science 286, 1571-1577, 1999  
 A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1  
 A:Reference number: A75250; MUID:20036896  
 A:Accession: D75564  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-478 <WHIT>  
 A:Cross-references: GB:AE001869; GB:AE000513; NID:g6457721; PIDN:AAF09658.1; PID:g6  
 A:Experimental source: strain R1  
 C:Genetics:  
 A:Gene: DR0061  
 A:Map position: 1

Query Match 2.8%; Score 106.5; DB 2; Length 478;  
 Best Local Similarity 23.2%; Pred. No. 1.5;  
 Matches 118; Conservative 38; Mismatches 184; Indels 169; Gaps 23;

QY 237 PVP-----DALKSLMYKNLTGPNITLNHTDLYPLCLCTQVMSLEPDSERVEFCFPREDPGAH 293  
 Db 17 PVPAGDVLSLQNSVVRQIARTLGLLILLEGGAQVQWA--LDRVEDDPPPPPOGDD 73

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OY 294 RNLHIAIRL-----VLSPGV-----W-----310
DB 74 ALFAOIAITROGSGSPHERAOLEVLRAGAGPOSLRADPRERPLIREAORIRRLARR 133
OY 311 QLDAPCCLPEKVTLCWQAPDQSPQPLVPVPOKNAVNEPODFOLVAGHPNLCOVSTW 370
DB 134 LARAPOLEPCTVAHSVLYAOEASALSAPAAGDGLTLH-----LGGPD-----RLAHV 182
OY 371 EKVYQACGMSADSLPPEKMDILVEMKTG--LNTSVCALESQCTPLPFSMASTRARLG 428
DB 183 OGIRL---SWR-SLGP--NMOLVQDETSDPVSQGLALLRPD--LP--ASER-----225
OY 429 BEILDFERSHOCQOLWMDNNGSLMACPMDKYIHRRWLVWLACLLIAALFFELLKKD 488
DB 226 -QLFLVGGQOLQVLPSCD-----YVLLRRR 250
OY 489 -----RRKARSGSRVALLHSDAGYERLVGALASALQMPLRVAVDLMSRRLS 539
DB 251 ADAAOTRHRLARLALGRACALLLPAGOHGRRLARLRLARGDP-----PRADDP 302
OY 540 AHGALAMFH-----HORRILDEGGVYVILFSPAANAQCOQWLOLOQVPEPBDALAAW 593
DB 303 ASGOVAFAQTPAECLAAARSLORLEPLGRFSPAQVA-----HEAQVAQ 347
OY 594 LSCVLPDFLOGRATGRVGVYFDGLHPDSVSPSPFRVA---PLFSL---PQOLPA---FL 644
DB 348 ALHLHP-----HYAAOVQQAHEHAASAEPLUREANPDLVGREAGPVPVLPATGHFI 399
OY 645 DALGGCSTAGCPADPDRVERVTOALRSAL 673
DB 400 VFPLGPDPLEVRPLGDRLLTLRPDYRAEL 428

RESULT 6
T37188
presynaptic activity regulator aex-3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 18-Feb-2000
C:Accession: T37188
R:Leimnac, D.; Minx, M.
submitted to the EMBL Data Library, February 1996
A:Description: The sequence of C. elegans cosmid CO2H7.
A:Reference number: Z20523
A:Accession: T37188
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1409 <LEI>
A:Cross-references: EMBL:U49945; PIDN:ANC47926.1; GSPDB:GN00029
A:Experimental source: strain Bristol N2; clone CO2H7
C:Genetics:
A:Gene: aex-3; CESP:CO2H7.3
A:Map position: X
A:Introns: 77/1; 136/2; 183/2; 232/3; 283/3; 386/3; 427/3; 527/3; 577/1; 699/3; 782/2; 8

Query Match 2.8%; Score 106.5; DB 2; Length 1409;
Best Local Similarity 20.0%; Pred. No. 6;
Matches 115; Conservative 77; Mismatches 201; Indels 181; Gaps 25;

OY 101 ENAGSSELSERNASIAQOVVLSFOAYPARCALLEVOPADLVQGGQSVGSAVFDFCE 160
DB 780 QOSNOCQVKECCDALVQSGVGMSPAKLR--LMEDSLRELV-----CSK 825
OY 161 ASLGAEOVMSTYKPRYOKEMLTQO-----LPDC-RGLEVRDSIOSC-----202
DB 826 LNLGLEVL-----SEDEYVEVOLTQGFAYVYKILKACLEGIEVSFTMPCCGGASVHV 882
OY 203 -----WVLPMLVSTGDNVLTLDVSEODESFLYLRLVPDALKSLMYKNLTGP- 253
DB 883 LEIAHTHWAMGGGEVITPSSSAPSTMTTPEHSNDILKESRKLPA-STIDLRTPTKPL 941

OY 254 -QNTLNHTD-----LVPLCQVMSLEPDSERVEPFPREDP--GAHRNMHIARL 302
DB 254 -----LVPLCQVMSLEPDSERVEPFPREDP--GAHRNMHIARL 302

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DB 942 GQNVPTSTNNHIAOSTRSPALPPV-----PPREAPPI-PKRNPPGLGAPKVEGAR- 995
OY 303 RVLSPGVQWOLDAPCLPGKVTLCWQAPDQSP-----COPLY 338
DB 996 -----APPLPRPKRVKVTAVDERPONLVPNQNPAPQSSPFLADADEQTKPLL 1044
OY 339 PPVPOKNAVNEPODFOLVAGHPN-----LCQVSTWKEVOLQACSMAD-----382
DB 1045 KPAPPTTLPEVGOEPC-KVLPTENEPVRYHYQGLILAVQIQWQONQLEWENAFVDLVNQ 1103
OY 383 ---SIGPFRKDDMLVEMKGTGNTSVCALESQCTPLPFSMASTRARL-----GELLAD 434
DB 1104 EREIVGMDPESEMIDRYSLANDSEKKRLLEEDRLSTLLHMTAVYIMCGTGQKALO- 1162
OY 435 FRSHOCQOLANDNMGSLMACPMDKYIHRRWLVWLACLLIAALFFELLKKDRKRAAR 494
DB 1163 ---QVRRRLGRKAHIOVCSKEINKLDE-----LPSTQGNFPLK-----PL 1202
OY 495 GSR-----FALLHSADGAG-----YERLVGALASALSQ 523
DB 1203 GSRIVQKOSFTVCPGQSSDQGMFMFECDDAVVLRSTIGATERMWERLVN-----ITY 1257
OY 524 MPLRVAVDLMSRRELSAHGALAMFHORRILDE 557
DB 1258 SPKTKIILCIMRRHDKVH--MKRFHTKKRELYQ 1289

RESULT 7
A38442
Probable tumor suppressor - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 16-Feb-1997
C:Accession: A38442
R:Nigro, J.M.; Cho, K.R.; Fearon, E.R.; Kern, S.E.; Ruppert, J.M.; Oliner, J.D.; Ki
Cell 64, 607-613, 1991.
A:Title: Scrambled exons.
A:Reference number: A38442; MUID:91121517
A:Accession: A38442
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-267 <NTG>
A:Cross-references: GB:M63696; GB:M63700; GB:M63702; GB:M63718; GB:M63698
C:Keywords: transmembrane protein

Query Match 2.8%; Score 106; DB 2; Length 267;
Best Local Similarity 24.3%; Pred. No. 0.77;
Matches 73; Conservative 35; Mismatches 100; Indels 92; Gaps 17;

OY 155 VFDCFEASLGAEOVMSTYKPRYOKEMLTQOLPDCRGLEVRDSIOSCWVLPMLNVSTG 214
DB 8 LYOC-EASLQSGSIIISRT-----AKVAVALPRLFSQTESVAFM-----G 47
OY 215 DNVLTLDVSEODESFLYLRLVPDALKSLMYKNLTGPONTLNHTD-----LVPLCQIQ 270
DB 48 DTVLKCVEIG-----PMPTI---HMOKN---QODLPIPEDSRVYVLPSCALQ 91
OY 271 VMSLEPDSERVEPFCFPREDPGHRNLMHIARLVLSPGWQOLDAPCCLPEKVTLCWQAPD 330
DB 92 ISRLQPDGDIGYKCSAR-NPASSRT-GNEAEVRIISP-PWFLNHPSTNL-----YAYESMD 143
OY 331 -QSPCOPLVPPVP-----QKNATVNEPODFOLVAGHPNLQVSTWKEVOLQACSMASISG 385
DB 144 IEFECTVSGKVPVYVNMKNQDVLPSPDFQIVGGSNLRL-----LG 185
OY 386 PFKDD-----MLLVEMKGTGNTSVCALESQCTPLPS-----MASTRARL 427
DB 186 VKSDEGFYQCVAENENAGNAQTSAGLIYVK---PIPSSVLPSPADPVDVYVVLVSSRYRL 242

RESULT 8
B39439
60k cysteine-rich outer membrane protein 1 precursor - Chlamydomonas psittaci

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Db 1459 ELEFGEVTEALGSRVLRLDLDVADDPERTIGSVLLDATERHRLVGLN--TTDG----- 1511

QY 221 LDVSEODESFL--YLKRPVDPAL-----KSLMYKNL-----TGPNIT 257

Db 1512 -PLDEERTLTLFEQQAATPDATALVMGDRSLTVAELARARLRLVALGAGPEQIV 1570

QY 258 L-----NHTDLPVLCICIQWMS-----LEPDSERVECFPREDPGARHNLHIAIRLRLS 306

Db 1571 ALQDPRSLDVLTVN-LANWAGCAALYLPDPD-----YPPER-----IAHMRADA 1613

QY 307 PGWQLDAPCLPGKVTLCWMA--SPDQSPCOPLVPVP-----OKNATVNEPODFOLVA 358

Db 1614 RPLALVVA--IPDDTTLMAVADSRLTDADRSAPLLPAHPAVITYTSGSGAPRG--VVV 1668

QY 359 GHPRLCY-----QVSTWENVQLQACSW-----ADSLGPF 387

Db 1669 AHSILATVPAAQAAGLGTSHSRVLTNFASISPDAAVMELTSLAFTGAGLVADADLLPG 1728

QY 388 KDDMLVEMKGTGLNNTSVCALEPSCGCTPLPSMA 420

Db 1729 PSIALRVHDR---HTLIALPSPALPALPDGA 1757

RESULT 13

A82593

hypothetical protein XF2169 [imported] - Xylella fastidiosa (strain 9a5c)

C:Species: Xylella fastidiosa

C>Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000

C:Accession: A82593

R:Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen

Nature 406, 151-157, 2000

A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A:Reference number: A82515: MIMD:20365717

A>Note: for a complete list of authors see reference number A59328 below

A:Accession: A82593

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-698 <SIM>

A:Cross-references: GB:AE004030; GB:AE003849; NID:9107292; PIDN:AAF84968.1; GSPDB:GN001

R:Experimental source: strain 9a5c

R:Simpon, A.J.G.; Relnach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A

Bionex, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, F

as-Neto, E.; Docena, C.; El-Dorry, H.; Facinani, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000

A:Authors: Pereira, V.C.A.; Perro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitzling, J.P.; Krieger, J.E.; Kurama, E.E.; Laigt

chado, M.A.; Madeira, A.M.P.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, F

A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.

, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmeri, D.A

Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak

M.; Tsubako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z

A:Reference number: A59328

A:Contents: annotation

C:Genetics:

A:Gene: XF2169

Query Match 2.7%; Score 101.5; DB 2; Length 698;

Best Local Similarity 19.3%; Pred. No. 6.1;

Matches 109; Conservative 66; Mismatches 197; Indels 193; Gaps 27;

QY 176 ROKELNTLOQLPDCRGLEYRDSIQSCW-----VLPWLVNSTDGDVLTLDV-- 223

Db 249 RLTFGEPELLAGHPD-RALTLHRLQVLAWPEDPRTLEALLTAMKQDMD--DDARITIDAL 306

QY 224 -----SEEDSFSLYLKRPVDPALKSLMYKNLNGPONTITLHNTDL 263

Db 307 DLKPRHDLMLALAVAPGSDSEARIVIERLTSAMPEHLPAL--ETLMSLHDIQ--NNPEA 363

QY 264 VPCLCIQWMSLEP-----DSERVECFPREDPGARHNLHIAIRLRLSIPGWQLDAPCCLP 319

Db 364 AETVAAQIVAIIEPGRISGEGRIVIEALLQDRPPT-----AVACL- 401

QY 320 GKVTLCWQAPDQSPCOPLVPVPQKNAVNEP-----QD-----FOLVAGHPNLQVSTW 370

Db 402 -----QOLIESVPEHERITLRWMLGLVQDRAGQFE-----ALATW 437

QY 371 EKVOLOACSWADSGFPFDDMLVEMKGTGLNNTSVCALEPSCGCTPLPSMASTRARLGE 430

Db 438 LQFOAEQAKYRLPLP-----QFTWNSKO-----WPDIAIPAELLARP 476

QY 431 ILQDFRSHQCQLNNDNDWMSLACPMDKYIHRMVLVYLACLLAALFFLLKKDR 490

Db 477 L-----IMPPGSHVERVTMMMAVSSMLC----- 502

QY 491 KAARGSTALLHNSADGAYRELVGALASALSOMPLRVAVDLSRRELASHGA----- 543

Db 503 -ADRYSETP--PADPLQRYETVELS--GTLRQALIDAM--RQDLPARGLIEDGV 554

QY 544 -LAFPHQ-----RRILQEGGVILLFSPAAVACQOQIQLQTVEPGPDAL--AAWLS 595

Db 555 WLLMWDNSLLTALPRLPREGRLITVLRPDRD--LLDWIAYGSPPLADSLQQAANWLG 612

QY 596 CVLPDFLOGRATGRVGYVFGDLHPDSV--PSPFVVA-----PLFSLPQLPAFLALQGG 650

Db 613 -----DILNQIAALHEDLDYHPHLRLDGEDNPQALATTLIEDIFGSPFPPLPSLEAPR-- 666

QY 651 CSTSAGRPADRVREVTQALRSALDS 675

Db 667 -----LPACRWMDRYREVLSAFDA 685

RESULT 14

T04018

hypothetical protein F17A8.60 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cross)

C>Date: 30-Apr-1999 #sequence\_revision 30-Apr-1999 #text\_change 30-Apr-1999

C:Accession: T04018

R:Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, I

submitted to the Protein Sequence Database, March 1999

A:Reference number: Z15184

A:Accession: T04018

A:Molecule type: DNA

A:Residues: 1-1274 <BEV>

A:Cross-references: EMBL:AL049482

A:Experimental source: cultivar Columbia; BAC clone F17A8

C:Genetics:

A:Map position: 4

A:Introns: 55/3; 801/1

A>Note: F17A8.60

Query Match 2.7%; Score 101.5; DB 2; Length 1274;

Best Local Similarity 20.2%; Pred. No. 13;

Matches 112; Conservative 62; Mismatches 183; Indels 197; Gaps 33;

QY 187 LPPDCRGLEYRDSIQS-----CWLPWLVNSTDGDVLTLDVSEEDSFSLYLRL 236

Db 694 LPEHFGRRKRDISSIVDRIRQSHSWSIRFL--SSAKQILKLKAVLSSMSYAMMCKRL 751

QY 237 PV-----PDALKSLM--YKNLTGPNIT--TLNHTDLPVLCIQWMSL- 274

Db 752 PSLCKQIOSVLTFRFWWDSPKDRKMAVMSMDKLTLPINEGGLGPRETEAKLS--WRL 808

QY 275 -EPDS--ERV-----EFCFPREDPGARHNLH--IALRVLSPG----- 308

Db 809 KPHSLLSRYLLAKYNTSSFSMDCSASPSASHGWRGILAGRDILKRLGSLGSGDSIN 868

QY 309 WQQLDAPCLPGKVTLCWQAPDQSPCOPLVPVP--PQKNAVNEPQDFOLVAGHPNLQVOY 367

Db 869 VW-----TEAWLSF--SSPFRIPPTPTNKDLVS-----HDLICHDV 904

QY 368 STM--EKVOLOACSWADSLG-----PFDMLVEMKGTGLNNTSV--CALEPSCGCTPLP 417

Db 905 KSMVAEIAIRKHLPOYEDQIRKITINALPLQDSLVWLVPKSGEYTTTKGYALAKLNSFPAS 964

QY 418 SM-----ASTRAARLGEELIQ-----DPRSHQCOQLMNDNM 449  
Db 965 QLEFNQKINIKWIKHTSPKVFHFLMKAMKALPYGEALSRNIEAEVTCRCGO--TESSL 1022  
QY 450 GSIMACPMOKYIHRRWVLMVLAACLLAAALFEFLLKKDRKARGSRFALLHSADGAG 509  
Db 1023 HMLMLCP---YAKKWE-----LAPVLE-----NPEATHSSVALLLVDA---- 1059  
QY 510 YERLVGALSALSOMPLR--VAVDLMSRRELASGALAMFHQRRIIOEGGVILLFSP 567  
Db 1060 -KRMVALPPTGASAPLYPWALMHM-----KARNRLIFDNHS-----CSEGLVL----- 1104  
QY 568 AAVAQCOQWLIQLOTV-----EKGPHAL-----AAMLS--CVLPDFLO---- 603  
Db 1105 KAILDARAMEADLLIHPSPISDYSPPTMLKYTSCEFVDAMWTSYCGMGMFLQDPYK 1164  
QY 604 -----GRATGRYVG 612  
Db 1165 VKIKENQSSSEFVG 1178

## RESULT 15

T26240  
Hypothetical protein W06F12.1a - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
C:Accession: T26240  
R:Lloyd, C.  
Submitted to the EMBL Data Library, December 1996  
A:Reference number: Z20179  
A:Accession: T26240  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-647 <MIL>  
A:Cross-references: EMBL:Z83244; PIDN:CAB05827.1; GSPDB:GN00021; CESP:W06F12.1a  
A:Experimental source: clone W06F12  
C:Genetics:  
A:Gene: CESP:W06F12.1a  
A:Map position: 3  
A:Introns: 47/2; 87/1; 145/1; 179/1; 216/3; 255/2; 317/2; 353/1; 564/3; 634/2

Query Match 2.7%; Score 100.5; DB 2; Length 647;

Best Local Similarity 23.0%; Pred. No. 6.7;

Matches 45; Conservative 30; Mismatches 72; Indels 49; Gaps 8;

QY 85 RVVVLAVHGHAEPEEAG-----KSDSELQSRNASLQAOVVLSPQAYPIARCALLEV 138  
Db 176 QLVGEMALVSH--THRAVSGSTCYEKQKQOQVOQIPTOPV-----AHVSSNAIILAA 229  
QY 139 Q-----VPADLVQPGQSVGSAVDFCEASLGAEOIWSYTKRYOKEL-----NLTOQLP 188  
Db 230 QPFYPPYQDSQPDRIIGYGAGCV-----VMSVTDRSGKRVALKKMPNFQNL 279  
QY 189 DC-----RGLGVDSIOSCWVLPRLANVSTGDNVLLTIDVSEBODFSLLYLRPVPDALKS 244  
Db 280 SCKRVREIKMLSSFRH-----DNVLSLIDILQPNPSPFOELVYLTLMQS 326  
QY 245 LMYKNLTGPNITLNH 260  
Db 327 DLKRTIVSPQALTPPH 342

Search completed: September 28, 2002, 19:41:32  
Job time: 6105 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

: protein - protein search, using sw model

on: September 28, 2002, 19:40:27 ; Search time 27.72 Seconds  
(without alignments)  
615.046 Million cell updates/sec

file: US-09-899-471-5

reflect score: 3741  
sequence: 1 MPVSWFLSLALGRNPVVS.....SSAPGCGCEMDLGPCTTLE 698

oring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

arched: 231628 seqs, 24425594 residues

\*total number of hits satisfying chosen parameters: 231628

imum DB seq length: 0  
ximum DB seq length: 200000000

st-processing: Minimum Match 08  
Maximum Match 100%  
Listing first 45 summaries

atabase : Issued Patents, AA:\*

- 1: /cgn2\_6/ptodata/2/1aa/5A.COMB.pep:\*
- 2: /cgn2\_6/ptodata/2/1aa/5B.COMB.pep:\*
- 3: /cgn2\_6/ptodata/2/1aa/6A.COMB.pep:\*
- 4: /cgn2\_6/ptodata/2/1aa/6B.COMB.pep:\*
- 5: /cgn2\_6/ptodata/2/1aa/PCRTUS.COMB.pep:\*
- 6: /cgn2\_6/ptodata/2/1aa/Backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Hit No.	Score	Query Match	Length	ID	Description
1	312	8.3	617	4	US-09-188-930-303
2	177	4.7	864	2	US-08-620-694A-2
3	177	4.7	864	3	US-09-022-255-2
4	177	4.7	864	3	US-09-022-696-2
5	177	4.7	864	3	US-08-978-773-2
6	177	4.7	864	3	US-09-022-253-2
7	177	4.7	864	3	US-09-022-250-2
8	177	4.7	864	4	US-09-022-259-2
9	177	4.7	864	4	US-09-022-257-2
10	150.5	4.0	330	4	US-09-188-930-125
11	147.5	3.9	866	2	US-08-620-694A-10
12	147.5	3.9	866	3	US-09-022-255-10
13	147.5	3.9	866	3	US-09-022-696-10
14	147.5	3.9	866	3	US-08-978-773-4
15	147.5	3.9	866	3	US-09-022-253-10
16	147.5	3.9	866	3	US-09-022-260-10
17	147.5	3.9	866	4	US-09-022-259-10
18	147.5	3.9	866	4	US-09-022-257-10
19	112	3.0	1447	5	US-09-041-886-25
20	112	3.0	1447	5	PCT-US94-05277-2
21	107.5	2.9	1711	2	US-08-342-930-2
22	103	2.8	1410	4	US-09-568-102-3
23	103	2.8	1410	4	US-09-567-969-3
24	103	2.8	1410	4	US-09-568-480-3
25	103	2.8	1410	4	US-09-568-486-3
26	103	2.8	1410	4	US-09-568-472-3
27	103	2.8	1410	4	US-09-568-472-3

28	97.5	2.6	1618	1	US-07-853-913-4	Sequence 4, Appl
29	95.5	2.6	1498	2	US-08-404-531B-28	Sequence 28, Appl
30	95.5	2.6	1498	3	US-08-476-900A-28	Sequence 28, Appl
31	95.5	2.6	1498	3	US-08-488-546A-28	Sequence 28, Appl
32	95.5	2.6	1581	2	US-08-404-531B-6	Sequence 6, Appl
33	95.5	2.6	1581	3	US-08-476-900A-6	Sequence 6, Appl
34	95.5	2.6	1581	3	US-08-488-546A-6	Sequence 6, Appl
35	95.5	2.6	2629	2	US-08-751-189-4	Sequence 4, Appl
36	95.5	2.6	2629	2	US-09-060-836-4	Sequence 4, Appl
37	95.5	2.6	2629	2	US-09-184-445-4	Sequence 4, Appl
38	94.5	2.5	2627	2	US-08-751-189-3	Sequence 3, Appl
39	94.5	2.5	2627	2	US-09-060-836-3	Sequence 3, Appl
40	94.5	2.5	2627	4	US-09-184-445-3	Sequence 3, Appl
41	93.5	2.5	726	4	US-09-126-980-2	Sequence 2, Appl
42	93.5	2.5	726	4	US-09-476-482-2	Sequence 2, Appl
43	93.5	2.5	880	1	US-08-445-640-10	Sequence 10, Appl
44	93.5	2.5	880	3	US-08-170-558-10	Sequence 10, Appl
45	93.5	2.5	880	3	US-08-447-314-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1  
US-09-188-930-303  
; Sequence 303; Application US/09188930A  
; Patent No. 6150502  
; GENERAL INFORMATION:  
; APPLICANT: Watson, James D.  
; APPLICANT: Strachan, Lorna  
; APPLICANT: Sleeman, Matthew  
; APPLICANT: Onrust, Rene  
; APPLICANT: Morrison, James Greg  
; TITLE OF INVENTION: Compositions Isolated From Skin Cells  
; FILE REFERENCE: 11000.1011c1  
; CURRENT APPLICATION NUMBER: US/09/188, 930A  
; CURRENT FILING DATE: 1998-11-09  
; NUMBER OF SEQ ID NOS: 348  
; SOFTWARE: PASTSeq for Windows Version 3.0  
; SEQ ID NO 303  
; LENGTH: 617  
; TYPE: PRT  
; ORGANISM: Mouse  
US-09-188-930-303

Query Match	8.3%	Score 312;	DB 4;	Length 617;
Best local similarity	23.9%	Pred. No. 1.4e-24;	Indels 136;	Gaps 21;
Matches 134;	Conservative 66;	Mismatches 224;		
QY 175	PRYQKELMTLQQLDPCRGLEY-----RDSIOSC--WVLPMILNVSTGDNVLLTLDVSEE	226		
DB 137	PERSFPL-----LPEQAVKRTIPAGPKASVRLCQWALKEEDLSSPDT-----	181		
QY 227	QDSFLLLRPVVDALKSLMYKNLTGPONTILNHTDLPCLGIQVWSLEPDSERVEECFP	286		
DB 182	-----OKIVSGGHTVDLP-----LPLCMCIENASYLOEDTVRRKKCF	221		
QY 287	REDPGAH-RULMHTIARLVSPG---WMDAPCCLREKTLQWAPQSPQPLVPPVP	342		
DB 222	QSMPELVGSDFMOSIRFTDYSOHNOMVALTRCPDLKIASLCWRQDDPLTPCETL-----	276		
QY 343	QKNATYNEQDFQLVAG---HPNLCYQVSTWEKYLQAC-----SWADSLGPFKDM	391		
DB 277	FNATQSEGWILLENVDLHPQLCFKS-FENSSHCEPQSGSLPMTYSMDT-QAQO	333		
QY 392	LVEAKTGTGLNNTSVCLERSGC---PLPSMASTRANLGEELLQD-----FRSHQMOQL	443		
DB 334	LTLHSSRTYATFSAAWSPDGLCPDTPMPVYSISQYGSVPVTLDLITFLRQNCILY	393		
QY 444	WMDNNGLSLMACPMKXTHRRWLV-----WLACILLAAALFFELLKKDRRAAGS	496		



Db 394 WRSD-----VHFARKHVLCPDDAPYPTOLL-----RSLGSGRT 427

Qy 497 RTALLHSADAGYERLVGALASALSQM---PLRVAVDLMSRRELNAHGLAMFHHQRR 553

Db 428 RPVLLHHADEAQRRLVGALELRTALGGRDVLVDMEGTHVAIGPLPMMAARER 487

Qy 554 ILQSGGVILLFSPRAVACQOMLQOTYEPFPHDLAAMLSCVLPDFLOGRATGRYGV 613

Db 488 VARQGYVLLLMNCNCPGFS-----TACSGDPQOASLRTILCAAPRPL-----LLA 531

Qy 614 YFDLLHPDSVSPRVPVPLFSLPTQLPAFLDLAGGCSFSA-----GRPADVERVYQ 667

Db 532 YFSNLCAKGDIPRPLRALPRYLLDLPLRLALDQAPATLASSHSLGAKRCLKNRLQ 591

Qy 668 A-----LRSAIDSCYSSSEAP 683

Db 592 CHLELEAKDYGSTNSP 611

RESULT 2

US-08-620-694A-2

Sequence 2, Application US/08620694A

Patent No. 5869286

GENERAL INFORMATION:

APPLICANT: Yao, Zhengbin

APPLICANT: Spriggs, Melanie

APPLICANT: Fanslow, William

TITLE OF INVENTION: No. 5869286el Receptor That Binds IL-17

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunex Corporation

STREET: 51 University Street

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Power Macintosh

OPERATING SYSTEM: Apple Operating System 7.5.5

SOFTWARE: Microsoft Word for Apple, Version 6.0.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/620,694A

FILING DATE: 21 MARCH 1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: USSN 08/538,765

FILING DATE: 7 AUGUST 1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: USSN 08/410,535

FILING DATE: 23 MARCH 1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia Anne

REGISTRATION NUMBER: 34,695

REFERENCE/DOCKET NUMBER: 2617-B

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206)587-0430

TELEFAX: (206)

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 864 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-620-694A-2

Query Match 4.7%; Score 177; DB 2; Length 864;

Best Local Similarity 20.5%; Pred. No. 1.1e-09;

Matches 121; Conservative 65; Mismatches 189; Indels 216; Gaps 29;

Qy 198 SIQSCW-----VLPMINVTSGDGNVLLTLDVSEODFSFLTYLRPV----- 239

Db 2 AIRCCPRVYVPGALGWL-----LLILNVLAPGRASPRLLDPPRAVCAQEGISCRV 52

Qy 240 ---DALKSLWY--KNLT--GRQNTLN-----HTDLVPCLCIOVWSLEPD----- 277

Db 53 KNSICLDDSWIHPKNTLPPSSPKNIYINLVSSTQGEGLVPLVHVE-WLQOTASILYLEG 111

Qy 278 -----SER--VECCPREDPGAHRLNHLRLR-VLSFG-----VQDLAPCCL 318

Db 112 AELSVLQLTNNEKLVAF--OFLSMLOHRRKWRFSFSHFVVDGQREYTVHHLPR--- 167

Qy 319 PGKVTLCQWAPDQSPCCP-----LVPPVPQKNATVNEPODFOLVAGHPNLQVSTWEKYO 374

Db 168 -----IPDGPNNKSKILFVPDCEDSKMKMTSCVSSGSLMDPNITVETLDTQHLR 218

Qy 375 LQACSWADSLGPFRRDMLYEMKTGLNNTSV----- 405

Db 219 VDFTLNNEST-PYO--VLISEFSDSEHNSCFDVKQIFAPROEFHORANTFTLSKEH 274

Qy 406 -CA-----LEP--SGC-----TPLPMSASTRAARLSEGLLODFRSHOCQMOIMND 447

Db 275 WCHHHVQVPPFSSCLNDCLRHAVTVPCEVITSMTTVK----- 313

Qy 448 NMGSIMACPMKXYIHRMW--LVWILACILLAAALFFFL-----LTKDRRKRAAGS--- 496

Db 314 -----PVADVI-PLMWGLILILAILLVGSYVILICMTWRISGADQENHGDSTKN 364

Qy 497 -----RTALLHSADGAGYERLVGALASAL--SQMPLRVAVDLMSRRELSA 540

Db 365 GLIPVADLTPPLRPKRKWIYVSADHPLYEVVLKFAQFLTYACGTEVALDLEQVISE 424

Qy 541 HGALWPFHHORRRRILOGGVVILFS-----PAAVACQOMLQOTYVEG 585

Db 425 VGVMTVSRKQKQEVESNKTITILCSRGTOAKKRAILCGMAEPAVDLRCDHW-----KPA 478

Qy 586 PHDLAAMLSCVLPDFLOGRATGRYGVYFEDGLHPDSVSPFRAVPLFSL 636

Db 479 -GDLFPAAMMILPDRFRACFGYVVCYFSGICSERVDPOLFNTSRPL 528

RESULT 3

US-09-022-255-2

Sequence 2, Application US/09022255

Patent No. 6072033

GENERAL INFORMATION:

APPLICANT: Yao, Zhengbin

APPLICANT: Spriggs, Melanie

APPLICANT: Fanslow, William

TITLE OF INVENTION: No. 6072033el Receptor That Binds IL-17

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunex Corporation

STREET: 51 University Street

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Power Macintosh

OPERATING SYSTEM: Apple Operating System 7.5.5

SOFTWARE: Microsoft Word for Apple, Version 6.0.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/022,255

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: USSN 08/620,694

FILING DATE: 21 MARCH 1996

APPLICATION NUMBER: USSN 08/538,765

FILING DATE: 7 AUGUST 1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: USSN 08/410,535  
 FILING DATE: 23 MARCH 1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Perkins, Patricia Anne  
 REGISTRATION NUMBER: 34,695  
 REFERENCE/DOCKET NUMBER: 2617-B  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (206)587-0430  
 TELEFAX: (206)  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 864 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 DB-09-022-255-2

Query Match 4.7%; Score 177; DB 3; Length 864;  
 Best Local Similarity 20.5%; Pred. No. 1.1e-09;  
 Matches 121; Conservative 65; Mismatches 189; Indels 216; Gaps 29;

198 SIQSCW-----VLPWLNVSDGDNVLLTLDVSEEDPFSFLYLRRPV----- 239  
 2 AIRCWPVVPGRPALGWL-----LLLLNLVAPGRASPRLLDFPAPVCAQEGLSGRV 52  
 240 --DAKSLWY--KNLT--GPNITLN-----HTDLVPCICIOVWSLEPD----- 277  
 53 KNSTCLDSDWHPKMLTPSPKNIYINLSVSTOGEIVLVHVE-WTLOTDAISLYLEG 111  
 278 -----SER--VECPREDPGAHNLMHIARLR-VLSPG-----VWOLAPCCL 318  
 112 AELSVLQNTNERLCVKE-QFLSMLOHNRKRFRFSHFVVDGQEXEYVHHLRKP--- 167  
 319 PGKVTLCQAPDQSPQCP---LVPPVPOKNATVNEPQDQOLVAQHNLQCVQSTWEKVQ 374  
 168 -----IPDGDPNHKSIIIFVPCDEDSKMKMTTSCVSSGSLMDPNITVETLDTQHNR 218  
 375 LQACSWADSLGPRKDDMLVEMKTGLNNTSV----- 405  
 219 VDFTLNNEST-PLYO---VLLESFSDSEHNSCFDVYVKQIFAPROEEFHORANTFTLSKPH 274  
 406 -CA-----LEP--SGC-----TPLPMSASTRAARLGEELLQDFRSHQCMQMDND 447  
 275 WCCHHHVOVQPFSSCLNDCLRAHVAIVPCPVISNTTVPK----- 313  
 448 NMGSLMACPMKTYIHRNV--LVWLACLLLAALFEFL-----LKKDRRKAARG-- 496  
 314 -----PVADYI-PLWVYGLITLIALIVGSAIVILICMTWRLSGADQEKHGDSKIN 364  
 497 -----RTALLHSHADGAGYERLVGALASAL--SQMPLRVAVDLMSRRELSA 540  
 365 GILPVADITPRPLPRKRWIYISADHPLEYEVLAKRAQFLITACGEVALDLLEQVISE 424  
 541 HGALAMFHQRRILOEGGVYLLFS-----PAVAQAQCOQMLDQVTEPG 585  
 425 VGVATWVSROKQEWESNKIILICSRGTQAKMKAILGMAEPVQIARCDHW-----KPA 478  
 586 PHDLAMLSGVLDLDFLOGRATGRVGYTFDGLLHSDVSPSPRVAPLFEFL 636  
 479 -GDLETAAMNMLPDKFRPACFGTYVCFSGICSERDVPDLFNITSRYPL 528

## RESULT 4

US-09-022-696-2

Sequence 2, Application US/09022696

Patent No. 6072037

## GENERAL INFORMATION:

APPLICANT: Yao, Zhengbin  
 APPLICANT: Springs, Melanie  
 APPLICANT: Fanslow, William  
 TITLE OF INVENTION: No. 6072037a1 Receptor That Binds IL-17  
 NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Immunex Corporation  
 STREET: 51 University Street  
 CITY: Seattle  
 STATE: WA  
 COUNTRY: USA  
 ZIP: 98101  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: Apple Power Macintosh  
 SOFTWARE: Microsoft Word for Apple, Version 6.0.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/022,696  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/620,694  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/620,694  
 FILING DATE:  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Perkins, Patricia Anne  
 REGISTRATION NUMBER: 34,695  
 REFERENCE/DOCKET NUMBER: 2617-B  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (206)587-0430  
 TELEFAX: (206)  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 864 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-09-022-696-2

Query Match 4.7%; Score 177; DB 3; Length 864;  
 Best Local Similarity 20.5%; Pred. No. 1.1e-09;  
 Matches 121; Conservative 65; Mismatches 189; Indels 216; Gaps 29;

198 SIQSCW-----VLPWLNVSDGDNVLLTLDVSEEDPFSFLYLRRPV----- 239  
 2 AIRCWPVVPGRPALGWL-----LLLLNLVAPGRASPRLLDFPAPVCAQEGLSGRV 52  
 240 --DAKSLWY--KNLT--GPNITLN-----HTDLVPCICIOVWSLEPD----- 277  
 53 KNSTCLDSDWHPKMLTPSPKNIYINLSVSTOGEIVLVHVE-WTLOTDAISLYLEG 111  
 278 -----SER--VECPREDPGAHNLMHIARLR-VLSPG-----VWOLAPCCL 318  
 112 AELSVLQNTNERLCVKE-QFLSMLOHNRKRFRFSHFVVDGQEXEYVHHLRKP--- 167  
 319 PGKVTLCQAPDQSPQCP---LVPPVPOKNATVNEPQDQOLVAQHNLQCVQSTWEKVQ 374  
 168 -----IPDGDPNHKSIIIFVPCDEDSKMKMTTSCVSSGSLMDPNITVETLDTQHNR 218  
 375 LQACSWADSLGPRKDDMLVEMKTGLNNTSV----- 405  
 219 VDFTLNNEST-PLYO---VLLESFSDSEHNSCFDVYVKQIFAPROEEFHORANTFTLSKPH 274  
 406 -CA-----LEP--SGC-----TPLPMSASTRAARLGEELLQDFRSHQCMQMDND 447  
 275 WCCHHHVOVQPFSSCLNDCLRAHVAIVPCPVISNTTVPK----- 313  
 448 NMGSLMACPMKTYIHRNV--LVWLACLLLAALFEFL-----LKKDRRKAARG-- 496  
 314 -----PVADYI-PLWVYGLITLIALIVGSAIVILICMTWRLSGADQEKHGDSKIN 364  
 497 -----RTALLHSHADGAGYERLVGALASAL--SQMPLRVAVDLMSRRELSA 540

Db 365 GILPVDLTPPLPRKRWIYVSADHPLVEVYLAKEAFLITACGTEVALDLLEOVISE 424  
QY 541 HGALAMFHORRRILOEGVILLES-----PAVAOCCOMLOLQTEVPG 585  
Db 425 VGVMTWVSROKOEVEENSKIIILCSRGTOAKKAILGMAEPAVOLRCDHW-----KPA 478  
QY 586 PHDALAAMLSVLPDLQGRATGRYGVYFDGLLHPDSVSPFRRVAPLESL 636  
Db 479 -GDLETAAMMILPDKFRPACFTYVVCYFSGICSERDVPDLFNITSRYPL 528

RESULT 5  
US-08-978-773-2  
Sequence 2, Application US/08978773  
Patent No. 6083906  
GENERAL INFORMATION:  
APPLICANT: Trout, Anthony  
TITLE OF INVENTION: Method of Regulating Nitric Oxide Production  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple PowerMacintosh  
OPERATING SYSTEM: Apple Operating System 7.5.5  
SOFTWARE: Microsoft Word for PowerMacintosh, Version 6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/978,773  
FILING DATE:  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 60/052,525  
FILING DATE: 27 NOVEMBER 1996  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia Anne  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 2623-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 864 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-978-773-2

Query Match 4.7%; Score 177; DB 3; Length 864;  
Best Local Similarity 20.5%; Pred. No. 1.1e-09;  
Matches 121; Conservative 65; Mismatches 189; Indels 216; Gaps 29;

QY 198 SIQSCW-----VLPMNLNSTDGNVLLTLDVSEBQDSFLLYLPRVP-----239  
Db 2 AIRCMBRVVPGPALGWL-----LILLNLVLAAGRASPRLLDPAPCAQEGSLSCR 52  
QY 240 ---DALSKLWY--KNLT--GPNQITLN-----HTDLVPCLCIQWLSLEPD-----277  
Db 53 KNSICLDDSWHPPNLTSPSSKNNTITNLSSVSTQGEVLVPLAVE-WTLQTDASIIYLEG 111  
QY 278 -----SER--VECCPREDDPGAHRLNLMHIALR-VLSPG-----VMOLDAPCCL 318  
Db 112 AELSLVQLNTNERLCVKE-QELSMLOHHRKRRFSEFSHVVYVDPGCEYEYVHLLPRP---167  
QY 319 PGVYVILCWAQAPDSQPCP-----LVPPVYQKNAVTNEPQDFQLVAGHPNLGVQVSTWEKYQ 374

Db 168 -----IPDGPNHKSKITFPDCEDESKMKTTSCVSSGSLMDPNTIVETLDTQHLR 218  
QY 375 IQACSNADSLGPEKDMILVEMKGLNNTSV-----405  
Db 219 VDTFLMNEST-PIQ---VLIESFSDSENHSCPDVYKQIPAPROEFPHORANTFTLSKH 274  
QY 406 -CA-----LEP--SGC-----TPLPMASTRAARLAGEELLQDFRSHOCQMLMND 447  
Db 275 WCCHHHVQVQPFSSCLNDCRHAHTVPCVPIISNTYK-----313  
QY 448 NMGSLNACPMCKYIHRWV--LVMLACLLLAALFFPL-----LLKDRRAARGS---496  
Db 314 -----PVADYI-PLMVYGLITLIALLVGSVYVLIICMTWRLSGADQEKHGDDSKIN 364  
QY 497 -----RRALLHSADGAGYERLYNGLASAL-SQMLRAVADLSRRELSA 540  
Db 365 GILPVDLTPPLPRKRWIYVSADHPLVEVYLAKEAFLITACGTEVALDLLEOVISE 424  
QY 541 HGALAMFHORRRILOEGVILLES-----PAVAOCCOMLOLQTEVPG 585  
Db 425 VGVMTWVSROKOEVEENSKIIILCSRGTOAKKAILGMAEPAVOLRCDHW-----KPA 478  
QY 586 PHDALAAMLSVLPDLQGRATGRYGVYFDGLLHPDSVSPFRRVAPLESL 636  
Db 479 -GDLETAAMMILPDKFRPACFTYVVCYFSGICSERDVPDLFNITSRYPL 528

RESULT 6  
US-09-022-253-2  
Sequence 2, Application US/09022253  
Patent No. 6096305  
GENERAL INFORMATION:  
APPLICANT: Yao, Zhengbin  
APPLICANT: Spriggs, Melanie  
TITLE OF INVENTION: No. 6096305e1 Receptor That Binds IL-17  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Power Macintosh  
OPERATING SYSTEM: Apple Operating System 7.5.5  
SOFTWARE: Microsoft Word for Apple, Version 6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/022,253  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/620,694  
FILING DATE: 21-MARCH-1996  
APPLICATION NUMBER: USSN 08/538,765  
FILING DATE: 7 AUGUST 1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/410,535  
FILING DATE: 23 MARCH 1995  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia Anne  
REGISTRATION NUMBER: 34,695  
REFERENCE/DOCKET NUMBER: 2617-B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:

LENGTH: 864 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-09-022-253-2

Query Match 4.7%; Score 177; DB 3; Length 864;  
 Best Local Similarity 20.5%; Pred. No. 1.1e-09;  
 Matches 121; Conservative 65; Mismatches 189; Indels 216; Gaps 29;

198 SIQSCW-----VLPMLNSTGDNVLLTDYSEEDFSLILRPP----- 239  
 2 AIRRCMPRVVPGPALGML-----LILLNLVLPGRASPRLLDFPAPVCAOEGLSGRV 52  
 240 ---DAKSLMY--KNLT--GPONITLN-----HTDLVPCLCIOVNSLEPD----- 277  
 53 KNSTGLDSDSHIRKNTLPSSPKNIYINLSVSTOGELVPLVHVE-WLQTDASILYLEG 111  
 278 -----SER--VECPREDPGAHNLMHIARLR-VLSPG-----WQIDAPCCL 318  
 112 AELSVQLQNTNRLCYKF-QFLSMLOHHRKRMRESFSHFVVDPCGEYEVYHHLPRK--- 167  
 319 PGKVTLCWQAPDQSPQF---LVPPVQKNAVNEPDQFQVAGHRLCYOVSTWEKYQ 374  
 168 -----IPGDDPNHRSKILFVPPCEDSKMKMTTSCVSSGSLMDPNITVETLDTQHLR 218  
 375 IQACSWADSLGPFKDDMLVEMKTGLNNTSV----- 405  
 219 VDFTLNNEST-PLYQ---VLSEFSDESNHSCFDVYKQIFAPROEFHORANVTTLSTKH 274  
 406 -CA-----LEP--SGC-----TLPSPMASTRARLGEELLQDFRSQCMQLMND 447  
 275 WCCHHNVQVOFPFSSCLNCLRHAVTVPCPVISNTVYVK----- 313  
 448 NMGSLACPMKTYIHRWV--LVWLACILLAAALFFPL-----LLKDRRAARG-- 496  
 314 -----PVADYI-PLWYVGLITLILALVGSVIVLICTMWRLSGADQEKHGDSDSKIN 364  
 497 -----RTALLHSADGAGERYLVGALASAL-SQMLRVAVDMSRRELSA 540  
 365 GILPVADLTPPLRPKRWIYVSADHPLVEVVLKFAQFLITACCTEVALDLLEQVISE 424  
 541 HGALAMFHQRRIILOGGVVILFS-----PAVAQCOOMLQLOTVERG 585  
 425 VGVMTWVSROKQEWESNSKIIILCSRGTOAKKAILGMAEPAVOLRCDHW-----KPA 478  
 586 PHDALAAMLSCVLPDLQGRATGRVGYFPDGLLHPDSVSPFRAVAPLPSL 636  
 479 -GDLFTAAAMNMLPDKFRPACFGTYVVCYFSGICSERDVPDLFNITSRYPL 528

RESULT 7  
 US-09-022-260-2  
 Sequence 2, Application US/09022260  
 Patent No. 6100235  
 GENERAL INFORMATION:  
 APPLICANT: Yao, Zhengbin  
 APPLICANT: Sprilgus, Melanie  
 APPLICANT: Fanslow, William  
 TITLE OF INVENTION: No. 6100235el Receptor That Blinds IL-17  
 NUMBER OF SEQUENCES: 10  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Immunex Corporation  
 STREET: 51 University Street  
 CITY: Seattle  
 STATE: WA  
 COUNTRY: USA  
 ZIP: 98101  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: Apple Power Macintosh  
 OPERATING SYSTEM: Apple Operating System 7.5.5

SOFTWARE: Microsoft Word for Apple, Version 6.0.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/022,260  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/620,694  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: USSN 08/410,535  
 FILING DATE: 23 MARCH 1995  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Perkins, Patricia Anne  
 REGISTRATION NUMBER: 34,695  
 REFERENCE/DOCKET NUMBER: 2617-B  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (206) 587-0430  
 TELEFAX: (206)  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 864 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-09-022-260-2

Query Match 4.7%; Score 177; DB 3; Length 864;  
 Best Local Similarity 20.5%; Pred. No. 1.1e-09;  
 Matches 121; Conservative 65; Mismatches 189; Indels 216; Gaps 29;

198 SIQSCW-----VLPMLNSTGDNVLLTDYSEEDFSLILRPP----- 239  
 2 AIRRCMPRVVPGPALGML-----LILLNLVLPGRASPRLLDFPAPVCAOEGLSGRV 52  
 240 ---DAKSLMY--KNLT--GPONITLN-----HTDLVPCLCIOVNSLEPD----- 277  
 53 KNSTGLDSDSHIRKNTLPSSPKNIYINLSVSTOGELVPLVHVE-WLQTDASILYLEG 111  
 278 -----SER--VECPREDPGAHNLMHIARLR-VLSPG-----WQIDAPCCL 318  
 112 AELSVQLQNTNRLCYKF-QFLSMLOHHRKRMRESFSHFVVDPCGEYEVYHHLPRK--- 167  
 319 PGKVTLCWQAPDQSPQF---LVPPVQKNAVNEPDQFQVAGHRLCYOVSTWEKYQ 374  
 168 -----IPGDDPNHRSKILFVPPCEDSKMKMTTSCVSSGSLMDPNITVETLDTQHLR 218  
 375 IQACSWADSLGPFKDDMLVEMKTGLNNTSV----- 405  
 219 VDFTLNNEST-PLYQ---VLSEFSDESNHSCFDVYKQIFAPROEFHORANVTTLSTKH 274  
 406 -CA-----LEP--SGC-----TLPSPMASTRARLGEELLQDFRSQCMQLMND 447  
 275 WCCHHNVQVOFPFSSCLNCLRHAVTVPCPVISNTVYVK----- 313  
 448 NMGSLACPMKTYIHRWV--LVWLACILLAAALFFPL-----LLKDRRAARG-- 496  
 314 -----PVADYI-PLWYVGLITLILALVGSVIVLICTMWRLSGADQEKHGDSDSKIN 364  
 497 -----RTALLHSADGAGERYLVGALASAL-SQMLRVAVDMSRRELSA 540  
 365 GILPVADLTPPLRPKRWIYVSADHPLVEVVLKFAQFLITACCTEVALDLLEQVISE 424  
 541 HGALAMFHQRRIILOGGVVILFS-----PAVAQCOOMLQLOTVERG 585  
 425 VGVMTWVSROKQEWESNSKIIILCSRGTOAKKAILGMAEPAVOLRCDHW-----KPA 478  
 586 PHDALAAMLSCVLPDLQGRATGRVGYFPDGLLHPDSVSPFRAVAPLPSL 636  
 479 -GDLFTAAAMNMLPDKFRPACFGTYVVCYFSGICSERDVPDLFNITSRYPL 528





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10 AVPGPLGLLLLLGLVLAAGSASLRLLDHRALVCSQP---GLNCTVKNSTCLDDSWIHR 66
101 EAGKSDSELOESRNASLQAVVLSF---QAVPIARCALLEVOVPADLVPOGSGVSAVF 156
67 -----NLTPSSPKDLQDLHFPAHTQGGDLFPVAH---IEMTLQTD----- 103
157 DCFEASL-----GAEOVMSYTKPRYOKEINLTQQLPDCRGLEVRDSIQ---SCWVLPMLN 209
104 -----ASILEGAEISV-----LQJLNTNERL---CVREFELSKLRHHRRRFFESH 148
210 VSTDGDNVLLTLDVSEEDFSFLYLRLVPYDALKSLMYKNLTGPONITLNTHTDLYPCLC- 268
149 FVYVDP-----QEYEVYVHNLKPRIPDGDPRNHSKNFLVPCDHAKRKVTPPCMS 199
269 -----IQWLSLEPDSERVEFC-----PREDPGAHNRLMHIARLVLS 306
200 GSLMDPNITVETLEAHQLRVSEFTLMNESTHYQILLTSPHMHNSCFEHHNHI----- 252
307 PGVWQDAPCCLPKGVTLQWQAPDQSPCOPLVPRVPOKNAVNEPQDQ-----LVAGH 360
253 -----PAPR-----PEEFHORSNVTLTLRN 272
361 PNLCVOVSTWEKVOLOACSWADSLGPFKDDMLLVEMKTGLNNTSVCLPESGCTPLPSMA 420
273 LKGGCR---HQVQIQ-----PF-----FSSCLND---CLRHSATVSCPEMP 307
421 STRAARLGEELLQDERSHQCMQMLMNDNMGSLMACPMKYIHRRWLVWMLACLLAALF 480
308 DT-----PEPIPDY-----MPLM-----YWFITGISILLVGSYI- 337
481 FELLKKDRRKARGS-----RALLHSADGAGYERLVG 515
338 -LLIVCMTRWLAGPSEKYSDDTKYTDGLPRAADLIPPLKPRKWIITYSADHPILVAVVL 396
516 ALAS-ALSOMPLRAVADLMSRRELSAAGALAMFHHORRRILOGEGVYLLFSPAANAQO 574
397 KFAQFLITACGEVALDLEEGALISEAGVMTWGRQKEWESKTIIVLCSRGTRAKWQ 456
575 QWL-----QLOTVEPGP-HDALAAMLSCVLPDLQGRATGRVGVYFDGILLHDSVSP 627
457 ALLGRGAPVRLRCHGKRVGDLFTAAAMNILLDFKRPACFGTYVVCYFESVSCDGDVPL 516
628 FRVAPFLSLPQLPAF-----LDALOGGCTSSAGRAPRAREVYQ-----A 668
517 FGAAFRPLMDREFEYVTRIDLEMFQPS-----RMHRVGLSGDNYLRSPPGRO 566
669 LRSALD 674
567 LRAALD 572

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SEQUENCE 12

US-09-022-255-10  
Sequence 10, Application US/09022255  
Patent No. 6072033

# GENERAL INFORMATION:

APPLICANT: Yao, Zhengbin  
APPLICANT: Spriggs, Melanie  
APPLICANT: Fanslow, William  
TITLE OF INVENTION: No. 6072033el Receptor That Binds IL-17  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Power Macintosh  
OPERATING SYSTEM: Apple Operating System 7.5.5  
SOFTWARE: Microsoft Word for Apple, Version 6.0.1

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,255
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USN 08/620,694
FILING DATE: 21 MARCH 1996
APPLICATION NUMBER: USN 08/538,765
FILING DATE: 7 AUGUST 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USN 08/410,535
FILING DATE: 23 MARCH 1995
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 866 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-022-255-10

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Query Match 3.98; Score 147.5; DB 3; Length 866;  
Best Local Similarity 19.38; Pred. No. 1.76-06;  
Matches 140; Conservative 78; Mismatches 239; Indels 269; Gaps 32;

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55 SAGP-----YVVP-----TRIQTELYRCQKTDCAIRVVVNLAVHGRABPE 100
10 AVPGPLGLLLLLGLVLAAGSASLRLLDHRALVCSQP---GLNCTVKNSTCLDDSWIHR 66
101 EAGKSDSELOESRNASLQAVVLSF---QAVPIARCALLEVOVPADLVPOGSGVSAVF 156
67 -----NLTPSSPKDLQDLHFPAHTQGGDLFPVAH---IEMTLQTD----- 103
157 DCFEASL-----GAEOVMSYTKPRYOKEINLTQQLPDCRGLEVRDSIQ---SCWVLPMLN 209
104 -----ASILEGAEISV-----LQJLNTNERL---CVREFELSKLRHHRRRFFESH 148
210 VSTDGDNVLLTLDVSEEDFSFLYLRLVPYDALKSLMYKNLTGPONITLNTHTDLYPCLC- 268
149 FVYVDP-----QEYEVYVHNLKPRIPDGDPRNHSKNFLVPCDHAKRKVTPPCMS 199
269 -----IQWLSLEPDSERVEFC-----PREDPGAHNRLMHIARLVLS 306
200 GSLMDPNITVETLEAHQLRVSEFTLMNESTHYQILLTSPHMHNSCFEHHNHI----- 252
307 PGVWQDAPCCLPKGVTLQWQAPDQSPCOPLVPRVPOKNAVNEPQDQ-----LVAGH 360
253 -----PAPR-----PEEFHORSNVTLTLRN 272
361 PNLCVOVSTWEKVOLOACSWADSLGPFKDDMLLVEMKTGLNNTSVCLPESGCTPLPSMA 420
273 LKGGCR---HQVQIQ-----PF-----FSSCLND---CLRHSATVSCPEMP 307
421 STRAARLGEELLQDERSHQCMQMLMNDNMGSLMACPMKYIHRRWLVWMLACLLAALF 480
308 DT-----PEPIPDY-----MPLM-----YWFITGISILLVGSYI- 337
481 FELLKKDRRKARGS-----RALLHSADGAGYERLVG 515
338 -LLIVCMTRWLAGPSEKYSDDTKYTDGLPRAADLIPPLKPRKWIITYSADHPILVAVVL 396
516 ALAS-ALSOMPLRAVADLMSRRELSAAGALAMFHHORRRILOGEGVYLLFSPAANAQO 574
397 KFAQFLITACGEVALDLEEGALISEAGVMTWGRQKEWESKTIIVLCSRGTRAKWQ 456
575 QWL-----QLOTVEPGP-HDALAAMLSCVLPDLQGRATGRVGVYFDGILLHDSVSP 627

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Db 457 ALIGRGAPVRLCDHGRKPVGDLFTFAAMNMLPDKRACGTYVVCSEVSCDGDVDDL 516  
Qy 628 FRVAPLFSLPQLPAF-----IDALOGCSTSGRPRADVERVTO-----A 668  
Db 517 FGAPRYPLMDREFEYVFRIDLEMFQPG-----RMRVGLSGDNYLRSFGGRQ 566  
Qy 669 LRSALD 674  
Db 567 LRAALD 572

RESULT 13  
US-09-022-696-10  
Sequence 10, Application US/09022696  
Patent No. 6072037  
GENERAL INFORMATION:  
APPLICANT: Yao, Zhenobin  
APPLICANT: Spriggs, Melanie  
APPLICANT: Fanslow, William  
TITLE OF INVENTION: No. 6072037e1 Receptor That Binds IL-17  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Power Macintosh  
OPERATING SYSTEM: Apple Operating System 7.5.5  
SOFTWARE: Microsoft Word for Apple, Version 6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/022,696  
FILING DATE:

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/620,694  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/410,535  
FILING DATE: 23 MARCH 1995

ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia Anne  
REGISTRATION NUMBER: 34,695  
REFERENCE/DOCKET NUMBER: 2617-B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 866 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-022-696-10

Query Match 3.9%; Score 147.5; DB 3; Length 866;  
Best Local Similarity 19.3%; Pred. No. 1.7e-06;  
Matches 140; Conservative 78; Mismatches 239; Indels 269; Gaps 32;

Qy 55 SARP-----VLVP-----TRLOTELVLRCPKTDKALRVVVVHLAVHGAEP 100  
Db 10 AVPGPLGLLLILGLVLAFGASLRILDRALVCSQP-----GLNCVKNSTCDDSMIHR 66  
Qy 101 EAGKSSSELOESNALSQAVLSF-----QATPLARCALLLEVQVADLVQSGVSAVF 156  
Db 67 -----NLTPSSPKDILQILQHLFAHTQGGDLFPVAH-----IEMTLQTD----- 103

Qy 157 DCEPASTL-----GAEVOIMSTYTKPRYOKELNLTOOLPDCRGLEVRDSIQ---SCWILPMIN 209  
Db 104 -----ASTILEGAEIASL-----LOLNTNERL---CVREFELSKLRHHRMRFTESH 148  
Qy 210 VSTDGNNVLLTLDVSEBODEFELLRLRPVPDLKSLMYKNTLGPONITLNTHTDLVPCIC- 268  
Db 149 FVVDPD-----QREYEVVHLLPKRIPDGDPRHOSKNFLVPCERAKMAYTPPCSS 199  
Qy 269 -----IQWLSLEPDSERVEFC-----PEREDGARNHMLHIAIRLVLS 306  
Db 200 GSLMDPNITVEETLEAHLQVLRVSFTLNMNESTHYQILLTSPHEMNEHSCFEMHHI----- 252  
Qy 307 PGWQOLDAPCCLPGRKVTLCMQAPDQSPCQPLVPPYPOKNAIVNEQDQ-----LVAGH 360  
Db 253 -----PAPR-----PEEFHORSNVTLLRN 272  
Qy 361 PNLGVSTWEKYOLQACSNWADSLGPEKDDMLLVEMKGTGLNNTSVCALEPSCGTFPLPSMA 420  
Db 273 LKCCCR-----HQVQIQ-----FSSCLND-----CLRHSATVSCPEMP 307  
Qy 421 STRARLGEELLODFPSHQCMQIMNDNMGSLMACPMOKYIHRKVLVWACLALAALE 480  
Db 308 DT-----PEPIDY-----MPLM-----VWFITGISILVGSVI- 337  
Qy 481 FFLKKDRKKAARG-----RTALLHSADGAGTERLVG 515  
Db 338 -LIVCMTRNLAPGSEKYSDDTKYTDGLPADLIPPLPKRWKVIYISADHPIVADVLL 396  
Qy 516 ALAS-ALSQMPLRVAVDLMSRRELTAHGLALAFHRRIRLQEGGVLLFSPAVALQOQ 574  
Db 397 KPAQELLTAQGTVALDLEQAISEGVTWGRQDMESKTIYLSRGTBAKQ 456  
Qy 575 QWL-----QLQVTEPGP-HDALAAMLSCVLPDLQGRATRGVYVFGDLHPDSVSP 627  
Db 457 ALIGRGAPVRLCDHGRKPVGDLFTFAAMNMLPDKRACGTYVVCSEVSCDGDVDDL 516

Qy 628 FRVAPLFSLPQLPAF-----IDALOGCSTSGRPRADVERVTO-----A 668  
Db 517 FGAPRYPLMDREFEYVFRIDLEMFQPG-----RMRVGLSGDNYLRSFGGRQ 566  
Qy 669 LRSALD 674  
Db 567 LRAALD 572

RESULT 14  
US-08-978-773-4  
Sequence 4, Application US/08978773  
Patent No. 6083906  
GENERAL INFORMATION:  
APPLICANT: Trout, Anthony  
TITLE OF INVENTION: Method of Regulating Nitric Oxide Production  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple PowerMacintosh  
OPERATING SYSTEM: Apple Operating System 7.5.5  
SOFTWARE: Microsoft Word for PowerMacintosh, Version 6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/978,773  
FILING DATE:  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 60/052,525  
FILING DATE: 27 NOVEMBER 1996



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CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2623-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 866 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
OS-08-978-773-4

Query Match      3.9%; Score 147.5; DB 3; Length 866;
Best Local Similarity 19.3%; Pred. No. 1.7e-06;
Matches 140; Conservative 78; Mismatches 239; Indels 269; Gaps 32;

55 SAPP-----VLVP-----TRLOTETLVRCPOKTDCAIRVRVYVHLAVGHAAEPE 100
10 AVGPRLGLLLLLGLVLA PGASLRILDHRLVCSQP---GLNCYVKNSTCLDDSWIHR 66
101 EAGKSDSELOESRNASIOAOVYLSF---QAYPIARCALLEVOVPADLVOPGOSVSAVF 156
67 -----NLTPSSPKDQLQHLHFHTOOGDLFPVAH---IEWTLQTD----- 103
157 DCFEASL-----GAEOVIMSTYKPRYQKEINLTQOLPDCRGLEVRSDIQ---SCWVLPWLN 209
104 -----ASILYLEGAEISV-----LQLTNTERL--CVREFELSKLRHHRMRFTFSH 148
210 VSTDGDNVLLITLDVSEEDFSFLYLRVPVDALKSIMYKNLTGPONITLNIHDLVPCIC- 268
149 FVVDPD-----DEYEVTVHHLKPIPDGDPNHQSKNFLVPDCEHARMKVTPCCMS 199
269 -----IQWMSLEPDSERERFEC-----PREDDPCAHNMLHIAIRLVLS 306
200 GSLMDPNITVETLEAQLRVSFTLWNSTHYQILITSPHEMNSCFEIMHI----- 252
307 PCWMDADACCLCGKVTYLCQAPQSPCQPLVPPVPOKNATVNEPDQF-----LVAGH 360
253 -----PAPR-----PEERHONSNVITLTNN 272
361 PNLGVQVSTWEKVOLOACSWADSLGPPKDDMLLVEMKTGLNNTSVCALEPSCGTPLPMA 420
273 LKGCCR---HQVOIQ-----PF-----FSSCLND---CLRHSATVSCPEMP 307
421 STRAARLGEELLQDFRSHOCMOLMNDNMGSLMACPMDKYIHRRVYLVWLACLLAALF 480
308 DT-----PEPIPDY-----MPLM-----VYWFITGISILVLGSVI- 337
481 FELLKKDRKKAARG-----RTALLLSADGAGERYLVG 515
338 -LLIVCMTRIRLARGSEKSYDDTKYTGCLRADLIPPLKFRKRWIITISADPLIYDVVL 396
516 ALAS-ALSOMLPLVAVDLMSRRELISAHGALAFWHHRRRILOEGGVVILLSPAAVQCO 574
397 KPAOELITACGTEVALDLLEQOAISEAGVMTWGRKQOEYENSKIIIVLCSGRRAKQ 456
575 QWL-----OLQTVRGP- HDALAAMLSCVLPDLOGRATRYGVYVDGLHPISVSP 627
457 ALLGKAPVRLRCDHGRKPVGDLTFTAAANNMILLPKRPACFCFTYVVCSEVSCDDVDPL 516
628 FVAVPLFSPTQLPAF-----LDALOGGCSGTSAGRPADRYERYTQ-----A 668
517 FCAAPRYPLMDREERYFYRIQDLEMPQPG-----RHRVGEISGDNVLSPPGGRQ 566
669 LRSALD 674
567 LRAALD 572

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RESULT 15
US-09-022-253-10
: Sequence 10, Application us/09022253
: Patent No. 6096305
GENERAL INFORMATION:
APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 6096305el Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESS: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,253
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/620,694
FILING DATE: 21-MARCH-1996
APPLICATION NUMBER: USSN 08/538,765
FILING DATE: 7 AUGUST 1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 866 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-022-253-10

Query Match      3.9%; Score 147.5; DB 3; Length 866;
Best Local Similarity 19.3%; Pred. No. 1.7e-06;
Matches 140; Conservative 78; Mismatches 239; Indels 269; Gaps 32;

55 SAPP-----VLVP-----TRLOTETLVRCPOKTDCAIRVRVYVHLAVGHAAEPE 100
10 AVGPRLGLLLLLGLVLA PGASLRILDHRLVCSQP---GLNCYVKNSTCLDDSWIHR 66
101 EAGKSDSELOESRNASIOAOVYLSF---QAYPIARCALLEVOVPADLVOPGOSVSAVF 156
67 -----NLTPSSPKDQLQHLHFHTOOGDLFPVAH---IEWTLQTD----- 103
157 DCFEASL-----GAEOVIMSTYKPRYQKEINLTQOLPDCRGLEVRSDIQ---SCWVLPWLN 209
104 -----ASILYLEGAEISV-----LQLTNTERL--CVREFELSKLRHHRMRFTFSH 148
210 VSTDGDNVLLITLDVSEEDFSFLYLRVPVDALKSIMYKNLTGPONITLNIHDLVPCIC- 268
149 FVVDPD-----DEYEVTVHHLKPIPDGDPNHQSKNFLVPDCEHARMKVTPCCMS 199

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OY 269 -----IOWSLPEPDSRVERFC-----PREDPGAHRNLMHIALRVLS 306
DB 200 GSLMDPNITVETLEHAHOLVRSTFLMNESTHYOILLTSFPHMENSCEFHMHI-----252
OY 307 PGWQOLDAFCLPGKVTLCMOAPDQSPCQPLVPVPQKNATVNEPODQ-----LVAGH 360
DB 253 -----PAPR-----PEEFHORSNVTITLRN 272
OY 361 PNLGVQVSTWKEVQLOQACSMADSLGPFKDDMLVEMKTGILNNTSVQALPEPGCTPLPSMA 420
DB 273 LKGCCR---HOVOIQ-----PF-----FSSCLND---CLRHSATVSCPEMP 307
OY 421 STRARIGEELLODFRSHQOQJLNDNDMNGSLMACPMKYIHRRVLVWLACLILLAALF 480
DB 308 DT-----PEPIPDY-----MPLW-----VYWFITGISILLVGSVI- 337
OY 481 FFLILKKORRRKARGS-----RTALLHSADGAGYERLVG 515
DB 338 -LIVCMTWMLAGSGSEKYSDDTKYTDGLPAADLIPPLKPRKRWIITSADHPLLYDVVL 396
OY 516 ALAS-ALSQMLRYAVDUMSRRELSAHGALAFHHQRRRIQEGGVVILFSPAAYAOQ 574
DB 397 KFAQFLITACGTEVALDLLEQATSEAGVMTWVGROKQOMVESNSKIIVLCSSRGTRAKWQ 456
OY 575 QWL-----OLQVVEPGP-HDALAAMLSCVLPDLQGRATGRYGVYFDGLHPDSVPSP 627
DB 457 ALGRGAPVRLRCDHGKPVGDLFTAAAMNMLPDKRPACFGTYVVCYFSEVSCDGOVPL 516
OY 628 FRVAPLESLEPTOLPAF-----LDALOGGCSSTSAGRPAADRVERTO-----A 668
DB 517 FGAAPRYPLMDREFEYTFRIODLEMFOPG-----RMHRVGEISGDNYLRSFGGRQ 566
OY 669 LRSALD 674
DB 567 LRAALD 572

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About: Results were produced by the GenCore software, version 4.5,  
Copyright (c) 1993-2000 Compugen Ltd.

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ID AA518132 standard; cDNA: 2314 BP.  
AA518132;  
26-MAR-2002 (first entry)  
Mouse DNAX cytokine receptor subunit 7 (DCRS7) cDNA.  
Mouse; DNAX cytokine receptor subunit 7; DCRS7; phosphate labelling; ss;  
gene therapy; protein therapy; immunological disorder.  
Mus musculus.  
Key Location/Qualifiers  
CDS 199..2295  
FT /\*tag= a  
FT /product= "Mouse DCRS7"  
W0200190358-A2.  
29-NOV-2001.  
23-MAY-2001: 2001MO-US16767.  
24-MAY-2000: 2000US-206862P.  
(SCHE ) SCHERING CORP.  
Gorman DW;  
WPI: 2002-106198/14.  
P-PSDB; AAU11354.  
Isolated antigenic human or mouse DNAX receptor subunit-1like  
polypeptide useful for detecting antibodies generated in response to  
presence of increased protein levels or immunological disorders -  
Disclosure; Page 17-20; 148pp; English.

The invention relates to primate and rodent DNAX cytokine receptor  
subunit (DCRS) polypeptides and the polynucleotides encoding them. The  
receptors, or their portions may be useful as phosphate labelling enzymes  
to label general or specific substrates. The subunits may also be  
functional immunogens to elicit recognising antibodies, or antigens  
capable of binding antibodies. A combination, e.g., including a DCRS can  
be used as an immunogen for the production of antisera or antibodies  
capable of distinguishing between other cytokine receptor family members.  
A purified DCRS can also be used as a reagent to detect antibodies  
generated in response to the presence of elevated levels of expression,  
or immunological disorders which lead to antibody production to the  
endogenous receptor. This sequence represents cDNA encoding the mouse  
DCRS7 polypeptide.

Sequence 2314 BP; 411 A; 725 C; 705 G; 473 T; 0 other;

## alignment\_scores:

Quality: 3565.00 Length: 698  
Ratio: 5.305 Gaps: 1  
Percent Similarity: 96.275 Percent Identity: 96.132

## alignment\_block:

US-09-899-471-2 x AA518132

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249	GCTGCTCTCTCTGGAGAGACTGATGGAGCTTCAGAGACACTCAGCTGCT	298
34	erLeuGlyLeuSerCysHisLeuTrrAspGlyAspValLeuCysLeuPro	50
299	CTTATGAGCCTCTCCAGCCACCTCTGGGATGGTGAAGTCTGCTGCTGCT	348
51	GlySerLeuGlnSerAlaProGlyProValLeuValProThrArgLeuGlu	67
349	GGAAAGCCCTCACTGTCCGCCAGCCCTGTGCTAGTGCCTACCCGCTGCA	398
67	nThrGluLeuValLeuArgCysProGlnLysTrrAspCysAlaLeuArg	84
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84	AlaArgValValValHisLeuAlaValHisGlyHisTrrPalaGluProGlu	100
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599	CCCGTGTGAGGTCCAGGTGCCCGCTGACTGGTGCAGCCGTGTCACTGC	648
151	ValGlySerAlaValPheAspCysPheGluAlaSerLeuGlyAlaGluVal	167
649	GTGGGTCTCTGGGTATTGACTGTTTCGAGGCTATGCTTGGGGCTGAGCT	698
167	IglnIleTrrSerTrrThrLysProArgTrrGlyIbLysGluLeuAsnLeuT	184
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243	uCysIleGlnValTrrSerLeuGluProAspSerGlyArgValGluPheC	260
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1849	CGAGCGCGGTATCTTCGACGAGAGGTGGCGGTAAATCTTCTTCTTCGCC	1898
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seq\_documentation\_block:  
 AA18133 standard; CDNA; 2094 BP.

AA18133;

26-MAR-2002 (first entry)

Mouse DCRS7 reverse translation generic cDNA.

Mouse; DNA cytokine receptor subunit 7; DCRS7; phosphate labelling; ss;  
 gene therapy; protein therapy; immunological disorder.

Mus musculus.

MO200190358-A2.

29-NOV-2001.

23-MAY-2001; 2001WO-US16767.

24-MAY-2000; 2000US-206862P.

(SCHE ) SCHERING CORP.

Gorman DM;

MP1; 2002-106198/14.

Isolated antigenic human or mouse DNA receptor subunit-like  
 polypeptide useful for detecting antibodies generated in response to  
 presence of increased protein levels or immunological disorders -  
 disclosure; Page 20-21; 148pp; English.

The invention relates to primate and rodent DNA cytokine receptor  
 subunit (DCRS) polypeptides and the polynucleotides encoding them. The  
 receptors, or their portions may be useful as phosphate labelling enzymes  
 to label general or specific substrates. The subunits may also be  
 functional immunogens to elicit recognising antibodies, or antigens  
 capable of binding antibodies. A combination, e.g., including a DCRS can  
 be used as an immunogen for the production of antisera or antibodies  
 capable of distinguishing between other cytokine receptor family members.  
 A purified DCRS can also be used as a reagent to detect antibodies  
 generated in response to the presence of elevated levels of expression,  
 or immunological disorders which lead to antibody production to the  
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 US-09-899-471-2 x AA18133 ..

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 210 YrLeuArgProValProAspAlaLeuLysSerLeuTyrTyrLysAsnLeu 226  
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XX DT 08-MAY-2001 (first entry)	
XX DE Human cytokine receptor zcytor14 encoding cDNA.	
XX KW Cytokine receptor; zcytor14; human; inflammation; rheumatoid arthritis;	
XX KM antiinflammatory; gene therapy; vaccine; ss.	
XX OS Homo sapiens.	
XX FH Key Location/Qualifiers	
FT CDS 3..2232	
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XX XX /product= "Zcytor14"	
PW MO200104304-A1.	
PD 18-JAN-2001.	
PF 30-JUN-2000; 2000MO-USI8383.	
PR 07-JUL-1999; 99US-0348854.	
PA (ZYMO ) ZYMOGENETICS INC.	
PI Presnell SR, Burkhead SK, Powder SL;	
DR WPI: 2001-112618/12.	
DR P-PDB: AAB61880.	
XX New polypeptide encoding a human cytokine receptor zcytor14, for	
527 ArgAtArgIl eLeuGInGluGlyValAlValIIeLeuHeSerP 543	
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560 roGLyProHIsaspaLaLeuaAlaITrPLeuSerCyvalLeuproasp 576	
1751 CNGGNCNCAYGAYGCNTYNGCGCNTGTMTGSNTGTYNTNCCNGAY 1800	
577 PhelEuGIgLyArGaLaThrgYaGtyrValIGlyValTyrrheaspGI 593	
1801 TTYTYTNCARGNGMNGCNACNGNMGTATAGTGGNGTNTAYTYGGYG 1850	
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2001 KGCNTNTMGNWSMGCNTYTNGATYSNTGTACNMSMWSWSGAGCNCNG 2050	
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      AA546223:
      18-DEC-2001 (first entry)
      Human DNA encoding PRO polypeptide sequence #299.
      PRO polypeptide: mammal: tumour: cancer: human: cattle: horse: sheep: ss:
      dog: cat: pig: goat: rabbit: tumour necrosis factor alpha; TNF-alpha;
      blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
      adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder;
      PCR primer.
      Homo sapiens.
      WO200168848-A2.
      20-SEP-2001.
      28-FEB-2001; 2001WO-US06520.

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XX 01-MAR-2000; 2000WO-US05601.
PR 02-MAR-2000; 2000WO-US05841.
PR 03-MAR-2000; 2000US-187202P.
PR 06-MAR-2000; 2000US-186968P.
PR 14-MAR-2000; 2000US-189320P.
PR 14-MAR-2000; 2000US-189328P.
PR 15-MAR-2000; 2000WO-US06884.
PR 21-MAR-2000; 2000US-190828P.
PR 21-MAR-2000; 2000US-191007P.
PR 21-MAR-2000; 2000US-191048P.
PR 21-MAR-2000; 2000US-191314P.
PR 28-MAR-2000; 2000US-192655P.
PR 29-MAR-2000; 2000US-193032P.
PR 29-MAR-2000; 2000US-193053P.
PR 30-MAR-2000; 2000WO-US08439.
PR 04-APR-2000; 2000US-194449P.
PR 04-APR-2000; 2000US-194647P.
PR 11-APR-2000; 2000US-195975P.
PR 11-APR-2000; 2000US-196000P.
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PR 11-APR-2000; 2000US-196820P.
PR 18-APR-2000; 2000US-198121P.
PR 18-APR-2000; 2000US-198585P.
PR 25-APR-2000; 2000US-199397P.
PR 25-APR-2000; 2000US-199550P.
PR 25-APR-2000; 2000US-199654P.
PR 03-MAY-2000; 2000US-201516P.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 05-JUN-2000; 2000US-209832P.
PR 28-JUL-2000; 2000WO-US20710.
PR 22-AUG-2000; 2000US-0644848.
PR 24-AUG-2000; 2000WO-US23338.
PR 08-NOV-2000; 2000WO-US30952.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
XX
XX (GENTH ) GENENTECH INC.
XX
XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
XX WPI; 2001-602746/68.
XX P-PSDB; AA029322.
XX
XX Novel nucleic acids encoding PRO polypeptides, used to diagnose the
XX presence of tumours, such as prostate and breast tumours, in mammals and
XX to screen for modulators of the compounds -
XX
XX Claim 2; Fig 597; 774pp; English.
XX
XX Sequences AA545925-AA546231 represent DNA molecules encoding and PCR
XX primers for PRO polypeptides of the invention. The sequences of the
XX invention can be used to detect the presence of a tumour in a mammal by
XX comparing the level of expression of a PRO polypeptide in a test sample
XX of cells from the animal and a control sample of normal cells, whereby a
XX higher level of expression in the test sample indicates the presence of a
XX tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep,
XX pigs, goats and rabbits but are preferably human. The polypeptides can
XX be used to stimulate tumour necrosis factor (TNF) alpha release from human
XX blood, when contacted with it. A specific polypeptide can be used to
XX stimulate the proliferation or differentiation of chondrocyte cells. The
XX PRO proteins can be used to determine the presence of tumours and also
XX susceptibility to tumour development, particularly adrenal, lung, colon,
XX breast, prostate, cervical, or liver tumours, in mammalian
XX subjects. The oligonucleotide probes specific for the PRO nucleic acids
XX can be used for genetic analysis of individuals with genetic disorders.
XX
XX Sequence 2380 BP; 411 A; 776 C; 743 G; 450 T; 0 other;

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## Alignment scores:

Quality: 2339.00 Length: 692  
 Ratio: 4.118 Gaps: 7  
 Percent Similarity: 82.081 Percent Identity: 66.329

## Alignment block:

US-09-899-471-2 x AAS46223

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17 ValValSerLeuGluArgLeuMetGluProGlnAspThrAlaArgCys 34
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51 GlySerLeuGlnSerAlaProGlyProValLeuValProThrArgLeu 67
383 GGGGACATGCTGCTGCTGCTGCGGCCCTGCTGCGGCTTACGCACTGTA 432
67 nThrGluLeuValLeuArgCysProGlnLysThrAspCysAlaLeuArg 84
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84 AlaArgValValHisLeuAlaValHisGlyHisThrAlaGluProGlu 100
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533 GATGAGGAAAGTTGGAGAGACGAGCTGACGAGGGTGGAGAGCCCTAG 582
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833 GCAGATGTGACAGACGTGATCTGTGTGAATGTCTCTGAGGAGCA 882
204 PheSerPheLeuLeuTyrLeuArgProValProAspAlaLeuLysSerLe 221
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221 eutrTrpTyrLysAsnLeuThrGlyProGlnAsnIleThrLeuAsnHisThr 237
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1532 ...GAGGATGACTTGGAGCGCTATGAGGCTGCTGCTGCTGCTGCTGCT 1579
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557 hValGluPro.....GlyProHisAspAlaLeuAlaAlaTyrleu 570
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1977 TETCCGGCGCGCGGCGGCGACGCGCGGACGAGCGCTTCCGCGCTC 2026
571 SerCysValleuProAspPheLeuGInGlyArGAlaThrGlyArGTYrVa 587
|||||.....|||||.....
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587 IGIyAllyrPheAspGlyLeuLeuHisProAspSerValProserProp 604
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|||||.....|||||.....
2227 AGCGGAGCAAGTGTCCCGGCGCGCTTCAAGCCCTGATGACTACTTCC 2276
653 ..ThrSerSerSerGluAlaProGly 660
2277 ATCCCCGGGAGCTCCCGCGCGGGA 2302

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seq.documentation.block:
AAS09515 standard; cDNA: 2380 BP.
AAS09515:
24-OCT-2001 (first entry)
Human cDNA encoding Interleukin 17 receptor, IL-17RH2.
Human: Interleukin-17 receptor; IL-17RH2; agonist; antagonist; ss;
PRO20040; DNA 164625-2890; systemic lupus erythematosus;
rheumatoid arthritis; osteoarthritis; diabetes mellitus;
allergic disease; asthma; demyelinating disease;
degenerative cartilaginous disorder; transplantation associated disease.
Homo sapiens.
Key Location/Qualifiers
CDS 233..2347
sig.peptide /*tag= a
mat.peptide /*tag= b
/*tag= c
/*tag=
label= Mature_IL_17RH2
MO200146420-A2.
28-JUN-2001.
20-DEC-2000; 2000MO-US34956.
23-DEC-1999; 99US-0172096.
30-DEC-1999; 99MO-US31274.
11-JAN-2000; 2000US-0175481.
18-FEB-2000; 2000MO-US04341.

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PR 02-MAR-2000; 2000MO-US05841.
PR 21-MAR-2000; 2000US-0191007.
PR 21-MAR-2000; 2000MO-US07532.
PR 22-JUN-2000; 2000MO-US15264.
PR 22-JUN-2000; 2000US-0213087.
PR 22-APR-2000; 2000US-0644848.
PR 24-APR-2000; 2000MO-US23328.
PR 24-OCT-2000; 2000US-0242837.
PR 10-NOV-2000; 2000MO-US30873.
PR 28-NOV-2000; 2000US-0253646.
PR 01-DEC-2000; 2000MO-US32678.
PA (GETH ) GENENTECH INC.
XX
XX Chen J, Flivaroff E, Fong S, Goddard A, Godowski PJ, Grimaldi CJ,
PI Gurney AL, Li H, Hillan KJ, Tumas D, Van Lookeren M, Vandlen RU,
PI Matenabe CK, Williams PM, Wood WI, Yansura DG;
XX WPI; 2001-451708/48.
DR P-PSDB; NA004956.
XX
XX Novel PRO polypeptides homologous to interleukin-17, useful for the
PT diagnosis and treatment of immune related disease e.g. rheumatoid
PT arthritis and diabetes -
XX
XX Claim 1; Fig 13; 188bp; English.
XX
PS The sequence (DNA 164625-2890) encodes a PRO polypeptide (PRO20040)
XX which is the human Interleukin 17 receptor, IL-17RH2. A composition
XX containing ant/agonists to the PRO polypeptides or individual components
XX are useful for treating a mammal with an immune related disease, e.g.
XX systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
XX juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an
XX idiopathic inflammatory myopathy, Sjogren's syndrome, systemic
XX vasculitis, sarcoidosis, autoimmune haemolytic anemia, autoimmune
XX thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal
XX disease, contact dermatitis, an allergic disease e.g. food
XX hypersensitivity, asthma, a transplantation associated disease, or a
XX chronic inflammatory demyelinating polyneuropathy. Treating a PRO1031 or
XX PRO1122 polypeptide agonist, or antagonist to the mammal. Numerous
XX examples of the diseases and disorders are given in the specification.
XX
SQ Sequence 2380 BP; 411 A; 776 C; 743 G; 450 T; 0 other;
alignment_scores:
Quality: 2339.00 Length: 692
Ratio: 4.118 Gaps: 7
Percent Similarity: 82.081 Percent Identity: 66.329
alignment_block:
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17 lValValSerleuGlnArGLeuMetGluProGlnAspThrAlaArGcys 34
283 GGTCTTCTCTGAGAGAGCGCTTGTGGCGCTTCAGAGCGTACCTACTGCT 332
34 erleuGlyLeuSerCysHisleuTrpAspGlyAspValleuLeuPro 50
333 CTCGGGCTCTCTCTGCGCGCTTCTGCGAGAGTACATACTCTGCGCT 382
51 GlySerleuGlnSerAlaProGlyProValleuValProThrArGleu 67
383 GGGGACATGCTGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCA 432

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633	CTGCCCGCGTGGCTCCGTGGAGAGTGAATGCTCTGCTGCGCTTGTGAG	682
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683	TTTGTGACGTCTGTGGGCTCTGTGGTATATAGACTGCTTCAGAGCTGCCT	732
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204	pPheSerPheLeuLeuTyrLeuArgProValProAspAlaLeuLysSerL	221
883	CTTGGGCTCTCCCTGTGATGGAATAGGTCACAGGGCCCCCAAAACCCC	932
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490 IGLYAlaLeuAlaSerAlaLeuSerGlnMetProLeuArgValAlaVal 507

1777 GGGCGCCCTGGCGGTGGCGCTGTGCACCTGGCGCGCGCTGGCGCTAG 1826

507 sPLeuTyrSerArgArgGluLeuSerAlaHisGlyAlaLeuAlaTyrPhe 523

1827 ACCTGTGGACCGCGTGAATGACTGACGGCGGAGGGCGCGCTGGCTGT 1876

524 HisHisGlnArgArgArgIleLeuGlnGluGlyValValIleLeu 540

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540 uPheSerProAlaAlaValAlaGlnCysGlnGlnTyrPheGlnLeuGlnT 557

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557 hValGluPro.....GlyProHisAspAlaLeuAlaTyrPleu 570

1977 TGTCGGGGCGCGGGCGGCGGCGGCGGCAAGCGCCGGCGCGCTCGCTC 2026

571 SerCysValLeuProAspPheLeuGlnGlyArgAlaThrGlyTyrVal 587

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587 IGLYAlaTyrPheAspGlyLeuLeuHisProAspSerValProSerPro 604

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604 hArgArgAlaProLeuPheSerLeuProThrGlnLeuProAlaPheLeu 620

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621 AspAlaLeuGlnGluGlyCysSerThrSerAlaGlyArgProAlaAsp 637

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XX	AA18130;
XX	AC
XX	AA18130;
DT	26-MAR-2002 (first entry)
XX	
DE	Human DNA cytokine receptor subunit 7 (DCRS7) cDNA.
XX	
KM	Human; DNA cytokine receptor subunit 7; DCRS7; phosphate labelling; ss;
KW	gene therapy; protein therapy; immunological disorder.
XX	
OS	Homo sapiens.
XX	
XX	
PN	W0200190358-A2.
PD	29-NOV-2001.
XX	
PE	23-MAY-2001; 2001WO-US16767.
XX	
PR	24-MAY-2000; 2000US-206862P.
XX	
PA	(SCHE ) SCHERING CORP.
PI	Gorman DM;
DR	WP1; 2002-106198/14.
XX	P-PDB; AAU1353.
PT	Isolated antigenic human or mouse DNA receptor subunit-like
XX	polypeptide useful for detecting antibodies generated in response to
PS	presence of increased protein levels or immunological disorders -
XX	Disclosure; Page 12-15; 148pp; English.
CC	The invention relates to primate and rodent DNAX cytokine receptor
CC	subunit (DCRS) polypeptides and the polynucleotides encoding them. The
CC	receptors, or their portions may be useful as phosphate labelling
CC	enzymes to label general or specific substrates. The subunits may also be



XX 02-MAY-2000; 2000JP-0183766.  
XX PA (HELI-) HELIX RES INST.  
XX PI Ota T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;  
XX WPI: 2001-093989/11.  
DR P-PSDB; AAB88448.  
XX  
PT Nucleic acids encoding secretory proteins/membrane proteins, useful in  
FT gene therapy or as candidate target molecules in drug development -  
XX  
XX PS Claim 1; SEQ ID 263; 609pp + CD ROM; English.

CC This invention relates to nucleic acid sequences AAF93744 - AAF93916  
CC which encode human secretory or membrane proteins represented by  
CC AAB88317 - AAB88419 included in the invention are primers  
CC AAF93917 - AAF94295 and AAF62232 - AAF62235 which are used to isolate the  
CC cDNA sequences of the invention. The invention also includes methods for  
CC the production of antibodies directed against the proteins, and cDNA  
CC sequences, which can be used in vaccines. The polynucleotide sequences  
CC can be used in gene therapy. The polynucleotide sequences and the  
CC proteins they encode may be used in the prevention, treatment and  
CC diagnosis of diseases associated with inappropriate secretory  
CC protein/membrane protein expression. The nucleic acids and complementary  
CC sequences may also be used as DNA probes in diagnostic assays  
CC (e.g. polymerase chain reactions (PCR)) to detect and quantitate the  
CC presence of similar nucleic acid sequences in samples. They may also be  
CC used to study the expression and function of secretory proteins/membrane  
CC polypeptides and their role in metabolism. The polypeptides may be used  
CC as antigens in the production of antibodies against them and in assays to  
CC identify modulators (agonists and antagonists) of expression and  
CC activity. The antibodies and antagonists may also be used as therapeutic  
CC agents to down regulate expression and activity. The antibodies may also  
CC be used as diagnostic agents for detecting the presence of the  
CC polypeptides in samples (e.g. by enzyme linked immunosorbent assay  
CC (ELISA)). Examples of diseases which may be treated include rheumatoid  
CC arthritis and diabetes.

XX  
SQ Sequence 2499 BP; 418 A; 821 C; 764 G; 496 T; 0 other;

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Quality: 2182.00 Length: 763  
Ratio: 3.974 Gaps: 10  
Percent Similarity: 71.953 Percent Identity: 58.060

alignment\_block:  
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17 ValValSerIleuGluArgLeuMetClnProGlnSprThrAArgGys 34  
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258 GGTCCTTCCTCGAGAAGGCTGTGGGGCTTAGAGCATGCTACCCTACTGCT 307  
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34 etLeuGlyLeuSerGysHisLeuTrpASPGLASpValMetGysLeuPro 50  
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308 CTCGGGGCCCTCTCCGCGCCCTCTGGGAAAGACATACTGCGCGCT 357  
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51 GlySerIleuGlnSerAlaProGlyProValLeuValProThrArgLeuGl 67  
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113 GAsnAspSerLeuGlnAlaGlnValValLeuSerPheGlnAlaTyrProI 130
558 GAATGCTCTCTCCAGGCCCAAGTCGTGCTCTCTCCAGGCCCAACCTTA 607
130 LeuAlaArgCysAlaLeuLeuGlnValGlnValProAlaAspLeuValGln 146
608 CTGCGCCGCTGCGTCTGCTGAGTGCAAGTGCCTGCTGCTGCTGCTGAG 657
147 ProGlnHisSerValGlySerAlaValPheAspCysPheGlnAlaSerLe 163
658 TTTGGTCAGCTGTGGGCTCTGTGGTATGACTGCTTCGAGGGCTCCCT 707
163 uGlnGlnGlnValGlnLeuTyrSerTyrTyrLysProArgTyrGlnLysG 180
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758 AACTCAACACACACAGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCA 807
189 ...AspGlyAspAsnValLeuLeuThrLeuAspValSerGlnGlnAsp 204
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301 CysTyrPheAlaProAspGlnSerProCysGlnProLeuValProProVa 317
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401 AlaArgLeuGlnGlnLeuLeuGlnAspPheArgSerHisGlnCysMe 417
1651 ..... 1651
417 tGlnLeuThrAsnAspAspAsnMetGlySerLeuTyrAlaCysProMetA 434
1652 ....CTATTG...GACGATGACTTGGAGCGCTATGAGGCTGCGCCATGG 1694
434 sPlyTyrIleHisArgArgTyrValLeuValTyrLeuValLysLeuLeu 450
1695 ACAATATCATCACAAGCGCTGGGCCCTCTGCTGCTGCTGCTGCTGCTG 1744
451 LeuAlaAlaAlaLeuPhePhePheLeuLeuLysLysAspArgArgL 467
1745 TTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1794
467 s.....AlaAlaA 470
1795 AGGGTGGCTAGGCTCTTGAACAGAGACCTCGCTGGGGGGCGGCGCA 1844
470 rglLysArgTyrThrAlaLeuLeuHisSerAlaAspGlyAlaGlyTyr 486
1845 GGGGC...CGCGGGCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1891
487 GluArgLeuValGlyAlaLeuAlaSerAlaLeuSerGlnMetProLeuA 503
1892 GACCGCTGTGGGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTG 1941
503 yValAlaValAspLeuThrPserArgArgGlnLeuSerAlaHisGlyAlaL 520
1942 CTGCGCCCTAGACCTGTGAGACCTCGTGAACCTGAGCGCGGCGCGCG 1991
520 euAlaThrPheHisIleGlnArgArgIleLeuGlnGlnGlyAlaL 536
1992 TGGCTTGGTTTCAAGCGCAGCGCGCGCAGACCTGCAAGAGAGCGCGCT 2041
537 ValIleLeuLeuPheSerProAlaAlaValAlaGlnCysGlnGlnTyrLe 553
2042 GTGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2091
553 uGlnLeuGlnThrValGlnPro.....GlyProHisAspAlaLeuA 567
2092 ACAAGATGGGGTCTCGGGCGCGGGGGCGCAGGGCGCGACAGACGCTTCC 2141
567 laAlaTyrPheSerCysValLeuProAspPheLeuGlnGlyArgAlaThr 583
2142 GCGCTGCTCTACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2191
584 GlyArgTyrValGlyValTyrPheAspGlyLeuLeuHisProAspSerVa 600
2192 GGCAGCTAGTGGGGCTGCTCTGACAGGCTGCTCCACCGCGAGCGCGT 2241

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Sep 29 09:32:44 2002

us-09-899-471-2.rng

XQ Sequence 1753 BP; 287 A; 584 C; 548 G; 334 T; 0 other:

Alignment scores: Length: 579  
Quality: 1851.50 Gaps: 7  
Ratio: 4.051  
Percent Similarity: 78.929 Percent Identity: 64.249

Alignment block:  
US-09-899-471-2 x AAC85029

Align seg 1/1 to: AAC85029 from: 1 to: 1753

110 GAGAGCCTAGAGATGCTCTCTCCAGGCCAAGTCGCTCTCTCTCA 51  
2 GAGAGCCTAGAGATGCTCTCTCCAGGCCAAGTCGCTCTCTCTCA 143  
126 GAGAGCCTAGAGATGCTCTCTCCAGGCCAAGTCGCTCTCTCTCA 101  
52 GAGAGCCTAGAGATGCTCTCTCCAGGCCAAGTCGCTCTCTCTCA 159  
143 GAGAGCCTAGAGATGCTCTCTCCAGGCCAAGTCGCTCTCTCTCA 151  
102 GAGAGCCTAGAGATGCTCTCTCCAGGCCAAGTCGCTCTCTCTCA 176  
160 GAGAGCCTAGAGATGCTCTCTCCAGGCCAAGTCGCTCTCTCTCA 201  
152 GAGAGCCTAGAGATGCTCTCTCCAGGCCAAGTCGCTCTCTCTCA 188  
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217 GAGAGCCTAGAGATGCTCTCTCCAGGCCAAGTCGCTCTCTCTCA 401  
352 GAGAGCCTAGAGATGCTCTCTCCAGGCCAAGTCGCTCTCTCTCA 250  
234 GAGAGCCTAGAGATGCTCTCTCCAGGCCAAGTCGCTCTCTCTCA 451  
402 GAGAGCCTAGAGATGCTCTCTCCAGGCCAAGTCGCTCTCTCTCA 267  
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452 GAGAGCCTAGAGATGCTCTCTCCAGGCCAAGTCGCTCTCTCTCA 284  
267 GAGAGCCTAGAGATGCTCTCTCCAGGCCAAGTCGCTCTCTCTCA 551  
502 GAGAGCCTAGAGATGCTCTCTCCAGGCCAAGTCGCTCTCTCTCA 300  
284 GAGAGCCTAGAGATGCTCTCTCCAGGCCAAGTCGCTCTCTCTCA 601  
552 GAGAGCCTAGAGATGCTCTCTCCAGGCCAAGTCGCTCTCTCTCA 317  
301 GAGAGCCTAGAGATGCTCTCTCCAGGCCAAGTCGCTCTCTCTCA 651  
602 GAGAGCCTAGAGATGCTCTCTCCAGGCCAAGTCGCTCTCTCTCA 334  
317 GAGAGCCTAGAGATGCTCTCTCCAGGCCAAGTCGCTCTCTCTCA 676  
652 GAGAGCCTAGAGATGCTCTCTCCAGGCCAAGTCGCTCTCTCTCA 350  
334 GAGAGCCTAGAGATGCTCTCTCCAGGCCAAGTCGCTCTCTCTCA 700  
677 GAGAGCCTAGAGATGCTCTCTCCAGGCCAAGTCGCTCTCTCTCA

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351 LeuGlnAlaIacySSerTrpAlaAspSerLeuGlyProPheLysAspAspMe 367
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701 CTCAGAGAGAGCTTGTGGGCTGACTCCCTGGGGCTCTCAAGACATG 750
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367 tLeuLeuValGlnMetLysThrGlyLeuAsnAsnHisSerValCysAlu 384
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
751 GCTACTTGTGAGACAGAGGCCCCAGACAGACAGATCCCTCTGTGCT 800
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401 AlaArgLeuGlyGluGlnLeuGlnAspPheArgSerHisGlnCysMe 417
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851 GCTGGCTTGGAGAGTACTTACTACAGACCTGACAGCCAGGTCT 900
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417 tGlnLeuTrpAsnAspAsnMetGlySerLeuTrpAlaCysProMet 434
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901 GCAGCTATGG...GACGATGACTTGGAGCGCTATGGCTCCCTCCATG 947
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
434 sPlySTyrIleHisArgTrpValLeuValTrpLeuAlaCysLeu 450
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948 ACAATATCATCCACAGCGCTGGGCGCTGTGGCTGGCTGCCCTACTC 997
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451 LeuAlaAlaAlaLeuPhePhePheLeuLeuLysLysAspArgArgly 467
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998 TTTGCCGCTCGCTTCCCTCATCTCTCTCAAAAAGATCACCGAA 1047
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467 s.....AlaAla 470
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1048 AGGCTGCTAGGCTTGTAAACAGAGCTCCGCGGGGCGCGCGCA 1097
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503 gValAlaValAspLeuTrpSerArgTrpGlnLeuSerAlaHisGlyAla 520
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1195 CGTGGCGCTGAGCTGTGAGCCCTCGAAGCTGAGCGCGAGGGCCGCG 1244
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520 euAlaTrpPheHisHisGlnArgArgIleLeuGlnGlnGlyAla 536
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1245 TGGCTTGGTTTCAAGCGAGCGCGCCAGCCCTGACAGAGGGCGCGT 1294
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537 ValIleLeuLeuPheSerProAlaAlaValAlaGlnCysGlnGlnTrp 553
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553 uGlnLeuGlnThrValGlnPro.....GlyProHisAspAlaLeu 567
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600 lProSerProPheArgValAlaProLeuPheSerLeuProHisGlnLeu 617
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1495 ACCCGGCTTTCGCGACGCGCGCTTTCACACTGCTCCCACTCC 1544
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617 roAlaPheLeuAspAlaLeuGlnGlyCysSerThrSerAlaGlyArg 633
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1545 CAGACTTCTCGGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1594
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634 ProAlaAspArgValGluArgValIleThrGlnAlaLeuArgSerAlaLeu
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1595 CTCACAGAGAGAGCGAGGCAAGTGTCCCGGCTTTCAGCAGCCCTGGG
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650 pSerCys.....ThrSerSerSerGluAlaProGly 660
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1645 TAGCTACTTTCATCCCGGCGGACTCCCGGCGCGGA 1681
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seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NM2000.DAT:AAZ65269

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seq_documentation_block:
ID   AAZ65269 standard; DNA; 1752 BP.
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AC   AAZ65269;
XX
DT   23-MAR-2000 (first entry)
XX
DE   Human secreted protein gene 20.
XX
KW   Human; secreted protein; cancer; tumour; developmental abnormality;
KW   foetal deficiency; blood disorder; immune system disorder; inflammation;
KW   autoimmune disease; allergy; Alzheimer's disease; cognitive disorder;
KW   schizophrenia; arthritis; asthma; psoriasis; sepsis; skin disorder;
KW   atherosclerosis; diabetes; cardiovascular disorder; kidney disorder;
KW   digestive disorder; endocrine disorder; infection; AIDS; leukaemia;
KW   therapy; chromosome 3; ds.
XX
OS   Homo sapiens.
XX
PN   W09958660-A1.
XX
PD   18-NOV-1999.
XX
PF   06-MAY-1999; 99W0-US09847.
XX
PR   12-MAY-1998; 98US-0085093.
PR   12-MAY-1998; 98US-0085094.
PR   12-MAY-1998; 98US-0085105.
PR   12-MAY-1998; 98US-0085180.
PR   18-MAY-1998; 98US-0085906.
PR   18-MAY-1998; 98US-0085920.
PR   18-MAY-1998; 98US-0085921.
PR   18-MAY-1998; 98US-0085922.
PR   18-MAY-1998; 98US-0085923.
PR   18-MAY-1998; 98US-0085924.
PR   18-MAY-1998; 98US-0085925.
PR   18-MAY-1998; 98US-0085925.
PR   18-MAY-1998; 98US-0085927.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Ruben SM, Florence K, Ni J, Rosen CA, Carter KC, Moore PA,
PI   Olsen HS, Shi Y, Young PE, Wei F, Brewer LA, Soppet DR;
PI   Lafleur DW, Endress GA, Edner R;
XX
DR   WPI; 2000-062296/05.
XX
P-SDS; AA76143.
XX

```

New isolated human genes and the secreted polypeptides they encode, useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders

Claim 1; Page 308; 475pp; English.

AAZ65250 to AAZ65350 represent 97 isolated human secreted protein genes. This sequence was found to be present on human chromosome 3.

AA76124 to AA76223 represent the secreted proteins encoded by the 97 human genes. The genes and their corresponding secreted polypeptides are useful for preventing, treating or ameliorating medical conditions, e.g. by protein or gene therapy. Also pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 97 genes, based on which tissues they

are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, tumours, developmental abnormalities and foetal deficiencies, blood disorders, diseases of the immune system, autoimmune diseases, inflammation, allergies, Alzheimer's and cognitive disorders, schizophrenia, arthritis, asthma, psoriasis, sepsis, skin disorders, atherosclerosis, diabetes, cardiovascular disorders, kidney disorders, digestive/endocrine disorders, infections and AIDS. The polypeptides are also useful for identifying their binding partners. The sequences shown in AA76224 to AA76424 represent fragments of the secreted proteins.

Sequence 1752 BP; 324 A; 555 C; 522 G; 347 T; 4 other:

# Alignment scores:

Quality: 1671.00 Length: 496  
Ratio: 4.157 Gaps: 5  
Percent Similarity: 81.048 Percent Identity: 65.726

## Alignment block:

US-09-899-471-2 x AA655269 ..

Align seg 1/1 to: AA655269 from: 1 to: 1752

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1 MetProValSerTrpPheLeuSerLeuSerLeuAlaLeuGlyArgAsnProVal 17
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227 ATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 276
17 ValValSerLeuGluArgLeuMetGluProGlnAspThrAlaArgCys 34
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277 GGTCTTCTCTGAGAGAGCTGTGTGGGCTCAGAGACCTACCTGCT 326
34 LeuGluLeuSerCysHisLeuTrpAspGlyAspValLeuCysLeuPro 50
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327 CTCGGGCGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 376
51 GlySerLeuSerAlaProGlyProGlyProGlyProGlyProGlyProGly 67
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377 GGGGACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 426
67 nThrGluLeuValLeuArgCysProGlnLysThrAspCysAlaLeuArg 84
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427 GACAGAGCTGTGCTGAGTGGCCAGAGAGACCTGCTGCTGCTGCTGCTGCT 476
84 AlaArgValValValHisLeuAlaValHisGlyHisTrpAlaGluProGlu 100
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477 TCGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 526
101 Gln.....AlaGlyLysSerAspSerGluLeuGlnGluSer 113
527 GATGAGCAAAAGTTTGGAGAGACGCTAGCTAGGCTGAGAGAGCTCTG 576
113 GAsnAlaSerLeuGlnAlaGlnValValLeuSerPheGlnAlaTyrPro 130
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577 GATGCTCTCTCCAGGCCAAGCTGCTGCTCTCTCTCCAGGCTACCTCA 626
130 LeuAlaArgCysAlaLeuLeuGluValGlnValProAlaAspLeuValGln 146
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627 CTCGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 676
147 ProGlyLysSerValGlySerAlaValPheAspCysPheGlnAlaSerLe 163
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677 TTTGGTCACTGTGTGGCTGTGTGTATGATGCTGCTGAGGCTGCTGCT 726
163 uGlyAlaGluValGlnIleTrpSerTyrThrLysProArgTyrGlnLys 180
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727 AGGAGTGAAGTACGATGCTGCTTACTACGACCCAGTACGAGAGG 776
180 LeuLeuAsnLeuThrGlnGlnLeuPro..... 188
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777 AAYTCAACACACACAGAGCTGCTGACTGACAGGGGCTCGAAGTCTGG 826
189 .....As 189

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827 AACAGATCCCGAGCTGCTGCGCCCTGCTGCTCAACGTCGTACAGCA 11
189 pGlyAspAsnValLeuLeuThrLeuAspValSerLeuGlnGlnAspPhe 206
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877 TGTGTACACAGCTGATGCTGTGTGATGTCTGTGAGAGAGACCTTGG 926
206 ePheLeuLeuTyrLeuArgProValProAspAlaLeuLysSerLeuTyr 222
927 GCCTCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 976
223 TyrLysAsnLeuThrGlyProGlnAsnIleThrLeuAsnHisThrAsp 239
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977 CACAAAACCTGACTGACCGCAGATCATACCTTGAACACACAGACCT 1026
239 uValProCysLeuCysIleGlnValTrpSerLeuGluProAspSerGlu 256
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1027 GGTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1076
256 rValGluPheCysProPheArgGluAspProGlyAlaHisArgAsnLeu 272
1077 GACG AACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1125
273 TrpHisIleAlaArgLeuArgValLeuSerProGlyValTrpGlnLeu 289
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289 pAlaProCysCysLeuProGlyLysValIleThrLeuCysTrpGlnAlaPro 306
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1226 GTGGGACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1275
323 ThrValAsnGluProGlnAspPheGlnLeuValAlaGlnHisProAsn 339
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339 uCysValGlnValSerThrTrpLysValGlnLeuGlnAlaCysSer 356
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356 rPAlaAspSerLeuGlyProPheLysAspAspMetLeuLeuValGluMet 372
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1376 GGGCTGACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1425
373 LysThrGlyLeuAsnAsnThrSerValCysAlaLeuGluProSerGly 389
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1426 CGAGGCCCCCAGAGACAAAGATCCCTGCTGCTGCTGCTGCTGCTGCTGCT 1475
389 sThrProLeuProSerMetAlaSerThrArgAlaAlaArgLeuGlyGlu 406
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
1476 TACTTCACTACCCAGCAAGCCCTCCACAGAGGCAAGCGCTGAGAGT 1525
406 LeuLeuGlnAspPheArgSerHisGlnCysMetGlnLeuTrpAsp 422
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439 gArgTrpValLeuValTrpLeuAlaCysLeuLeuAlaAlaLeu 456
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1623 GCGTGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1669
456 hE.PhePheLeuLeuLysLysAspArgLys 467
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1797 NTNCCGAYTYYTNCARGNMGCNCNCNGNSNTAYGTNGNCNT 1846
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1847 GYTYGAYMGNNTYNTYNTCCAGTCCNGTNCNCNCNTNTNTYMGNCN 1896
607 ALAProLeuPheSerLeuProThrGlnLeuProAlaPheLeuAspAlaLe 633
1897 GTMCCNCTNTNTYACNTYNTCCMNSNCARITTCNCNGATTTTTCGNCNT 1946
623 uGlnGlyGlyCysSerThrSerAlaGlyArgProAlaAspArgValGln 640
1947 NCARCARCCNMGCNCNCNCNMNSNGMNGNTNCCARGARMGNCGARGC 1996
640 rGValThrGlnAlaLeuArgSerAlaLeuAspSerCys.....ThrSer 654
1997 ARCTNMNSMNGCNYTNCARCCNCNTNGAYMSTAYTTTCAYCCNCNCN 2046
655 SerSerGlnAlaProGly 660
2047 GGNACMNSMNCNCNCNCN 2064
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seq_documentation_block:
AAC85030 standard; cDNA; 1725 BP.

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AAC85030;
08-MAY-2001 (first entry)
Human zcytor14 variant zcytor14-1 degenerate nucleotide sequence.
Cytokine receptor; zcytor14; human; inflammation; rheumatoid arthritis;
antihistaminatory; gene therapy; vaccine; variant; zcytor14-1; ss.
Homo sapiens.
MO200104304-A1.
18-JAN-2001.
30-JUN-2000; 2000MO-US18383.
07-JUL-1999; 99US-0348854.
(ZYMO) ZYMOGENETICS INC.
Presnell SR, Burkhead SK, Powder SL.
MPI: 2001-112618/12.
P-PSDB: AAB61881.
New polypeptide encoding a human cytokine receptor zcytor14, for
treating inflammation e.g. rheumatoid arthritis -
Disclosure; Page 101; 112pp; English.

```

The invention provides a new human cytokine receptor designated zcytor14. zcytor14 can be expressed by standard recombinant methodology. The encoding nucleic acid is useful for detecting the expression of a zcytor14 gene in a biological sample. Anti-zcytor14 antibodies can be used to screen biological samples in vitro for the presence of zcytor14. Proteins, polypeptides and peptides having zcytor14 activity can be administered to a subject who lacks an adequate amount of this polypeptide, for treating inflammation and conditions such as rheumatoid arthritis. In contrast, zcytor14 antagonists (e.g. anti-zcytor14 antibodies) can be used to treat a subject who produces an excess of zcytor14. zcytor14 nucleotide sequences can also be used to provide zcytor14 to a subject. The present sequence represents a degenerate nucleotide sequence of a variant of the human cytokine receptor zcytor14, designated zcytor14-1. The variant is a truncated form of the receptor polypeptide and lacks amino acid residues 1-113 of zcytor14.

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XX      S0      Sequence 1725 BP; 192 A; 226 C; 332 G; 216 T; 759 other;
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  Ratio: 3.628          Gaps: 6
  Percent Similarity: 61.592      Percent Identity: 45.502
alignment_block:
US-09-899-471-2 x AAC85030 ..
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AC	AAH99805;
DT	16-OCT-2001 (first entry)
DE	Human protein encoding cDNA sequence SFG ID NO:640.
XX	Human; cancer; ulcer; HIV infection; human immunodeficiency virus;
XX	antifungal; antifungal; antirheumatic; antiarthritic; immunosuppressive;
XX	antibacterial; endocrine; cardiac; central nervous system; virucide;
XX	anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia;
XX	antiallergic; haemostatic; vulnary; antilucer; osteopathic; eczema;
XX	dermatological; antiallergic; antistimatic; antidiabetic; cytostatic;
XX	neuroprotective; antidepressant; nootropic; antiparkinsonian; infection;
XX	immunostimulant; gene therapy; antisense therapy; vaccine; inflammation;
XX	antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;
XX	cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;
XX	genetic disease; haematopoietic disorder; platelet disorder; asthma;
XX	thrombocytopenia; osteoporosis; severe combined immunodeficiency;
XX	allergic rhinitis; diabetes; multiple sclerosis; depression;
XX	Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
XX	neurological disorder; ss.
XX	Homo sapiens.
OS	WO200153455-A2.
XX	26-JUL-2001.
XX	22-DEC-2000; 2000WO-US35017.
PE	23-DEC-1999; 9905-0471275.
XX	21-JAN-2000; 2000US-0488725.
PR	25-APR-2000; 2000US-0552317.
XX	(HISE-) HISEQ INC.
PA	Tang YT, Liu C, Drmanac RT;
PI	WPI: 2001-457603/49.
DR	P-PSDB; AAM25864.
XX	Claim 1; Page 659-660; 1217pp; English.
XX	AAH99166 to AAH99904 encode the human proteins given in AAM25225 to
CC	AAH25963. The proteins can have activities based on the tissues and
CC	cells they are expressed in, such as: antineoplastic; antirheumatic;
CC	antiarthritic; immunosuppressive; antibacterial; endocrine; cardiac;
CC	central nervous system; virucide; anti-HIV; fungicide; antimutagen;
CC	cardiovascular; antianaemic; antiallergic; antiallergic; antiallergic;
CC	antilucer; osteopathic; dermatological; antiallergic; antiallergic;
CC	antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic;
CC	antiparkinsonian; and immunostimulant. The proteins and polynucleotides
CC	encoding them can be used in gene therapy, antisense therapy and vaccine
CC	production. The proteins and polynucleotides are useful for screening for
CC	agonists or antagonists of a protein and for the treatment and diagnosis
CC	of disorders associated with the activity of a protein e.g. inflammation,
CC	rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,



neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal infections, autoimmunity, genetic diseases, haematopoietic disorders, anaemia, platelet disorders, thrombocytopaenia, wounds, ulcers, osteoporosis, severe combined immunodeficiency, eczema, allergic rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression, Alzheimer's disease, Parkinson's disease, neurodegenerative and neurological disorders.

Sequence 1210 BP; 227 A; 377 C; 352 G; 254 T; 0 other;

# Alignment\_scores:

Quality: 843.50 Length: 330  
Ratio: 3.749 Gaps: 7  
Percent Similarity: 68.182 Percent Identity: 55.152

## Alignment\_block:

US-09-899-471-2 x AAH99805

Align seg 1/1 to: AAH99805 from: 1 to: 1210

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34 erLeuGlyLeuSerCysHisLeuTrpAspClnAspValLeuGlyLeuPro 50
299 CTCCGGGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 348
51 GlySerLeuGlnSerAlaProGlyProValLeuValProThrArgLeuG 67
349 GGGGACATCGCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 398
67 nThrGluLeuValLeuArgCysProGlnTrpAspCysAlaLeuArgV 84
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101 Glu.....AlaGlyLysSerAspSerGluLeuGlnGlnUserAr 113
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599 CTGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 648
147 ProGlyGlnSerValGlySerAlaValPheAspCysPheGlnAlaSerLe 163
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699 AGGAGTAGAGTACGAATCTGCTTACTCTAGCCAGCTAGCAGAGAGG 748
180 luleuAsnLeuThrGlnGlnLeuPro.....As 188
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189 .....As 189
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AC AA102817
XX
DT 21-NOV-2001 (first entry)
XX
DE Human reproductive system related antigen DNA SEQ ID NO: 5505.
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KW Human; reproductive system related antigen; reproductive system disorder;
KW cancer; gene therapy; ds.
XX
OS Homo sapiens.
XX
PN W0200155320-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01339.
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PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
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PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
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Date: Sep 29, 2002 1:01 AM

About: Results were produced by the Gencore software, version 4.5,  
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Command line parameters:

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Search information block:

Query: US-09-899-471-2

Query length: 674

Database sequences: 1797656

Database length: 187333701

Search time (sec): 11857.370000

More lists:

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DEFINITION Sequence 10 from Patent WO0190358.

ACCESSION AX350976

VERSION AX350976.1 GI:18616352

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

SOURCE

CDS

mat\_peptide

BASE COUNT

ORIGIN

alignment\_scores:

Percent Similarity:

Percent Identity:

alignment\_block:

US-09-899-471-2 x AX350976

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 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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 1 (bases 1 to 2015)  
 DIRECT SUBMISSION  
 SUBMITTED (21-MAR-2001) National Institutes of Health, Mammalian  
 Gene Collection (MGC), Cancer Genomics Office, National Cancer  
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
 USA  
 NIH-MGC Project URL: http://mgc.nci.nih.gov  
 CONTACT: MGC help desk  
 EMAIL: cgaps-rt@mail.nih.gov  
 Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.  
 CDNA Library Preparation: Life Technologies, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Baylor College of Medicine Human Genome  
 Sequencing Center  
 Center code: BCM-HGSC  
 Web site: http://www.hgsc.bcm.tmc.edu/cdna/  
 Contact: villalobos@bcm.tmc.edu.  
 Villalobos, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garcia,  
 A.M., Holloway, M., Telford, B., Hodgson, A., Bouck, J., Yu, W.,  
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ORGANISM unidentified.
REFERENCE 1 (sites)
AUTHORS Gorman,D.M.
TITLE Minimalian receptor proteins; related reagents and methods
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SCHERING CORPORATION (US)
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 ZymoGenetics, Inc. (US)  
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VERSION AX092430.1 GI:13444529
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1 (bases 1 to 2380)
Eaton,D.L., Filvaroff,E., Gerritsen,M.E., Goddard,A.,
Godowski,P.J., Grimaldi,C.J., Gurney,A.L., Watanabe,C.K. and
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DEFINITION  Sequence 13 from Patent WO0146420.
ACCESSION   AX180776
VERSION     AX180776.1 GI:15132622
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            Chen,Y., Filvaroff,E., Fong,S., Goddard,A., Godowski,P.J.,
            Grimaldi,C.J., Gurney,A.L., Li,H., Hillan,K.J., Tumas,D., van
            Lookeren,M., Vanden,R.L., Watanabe,C.K., Williams,P.M., Wood,W.I.
            and Yansura,D.G.
            IL-17 and IL-17r homologous polypeptides and therapeutic uses
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            Patent: WO 0146420-A 13 28-JUN-2001;
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VERSION BC006411.1 GI:13623590

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AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE 1 (bases 1 to 2507)
JOURNAL Strausberg, R.
Direct Submission
Submitted (09-Apr-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2550,
USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgapbs-rt@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
Info@bcgsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Buterfeld,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Jetticia Hsiao, Martin Krzyzinski, Keta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Ness, Pawan Pandoh, Anna-Lisa Prabhu, Parvaneh Saeedi, Jacqueline
Schein, Duane Smalins, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.

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DEFINITION Sequence 7 from Patent WO0190358.
ACCESSION AX350973
VERSION AX350973.1 GI:18616349
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (sites)
AUTHORS Gorman,D.M.
TITLE Mammalian receptor proteins: related reagents and methods
JOURNAL SCHERING CORPORATION (US)
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 1 (bases 1 to 2499)  
 AUTHORS Ota,T., Iwagaki,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and  
 Hayashi,K.  
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 JOURNAL Patent: EP 1067182-A 263 10-JAN-2001;  
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DEFINITION Sequence 3 from Patent WO0104304.
ACCESSION AX073995
VERSION AX073995.1 GI:12710227
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
artificial sequence.
REFERENCE
1 (bases 1 to 2076)
AUTHORS
Presnell,S.R., Burkhead,S.K. and Pownder,S.L.
TITLE
Human cytokine receptor
JOURNAL
Patent: WO 0104304-A 3 18-JAN-2001;
ZymoGenetics, Inc. (US)
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 seq\_documentation\_block:  
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 DEFINITION Sequence 6 from Patent WO0104304.

1725 bp DNA linear PAT 06-FEB-2001

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ACCESSION AX073998
VERSION AX073998.1 GI:12710230
KEYWORDS
SOURCE
ORGANISM synthetic construct.
REFERENCE
AUTHORS Presnell,S.R., Burkhead,S.K. and Pownder,S.L.
TITLE Human cytokine receptor
JOURNAL Patent: WO 0104304-A 6 18-JAN-2001;
ZymoGenetics, Inc. (US)
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variation
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US-09-899-471-2 x AX073998
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 SEQUENCE, 22 unordered pieces.  
 ACCESSION AC024612  
 VERSION AC024612.2 GI:9929740  
 KEYWORDS HTG; HTGS; PHASE1; HTGS\_DRAFT.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 1 (bases 1 to 166620)  
 Birtten,B., Linton,L., Nusbaum,C. and Lander,E.  
 Homo sapiens chromosome 3, clone RP11-481H17  
 Unpublished  
 2 (bases 1 to 166620)  
 Birtten,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,  
 Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,  
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 Klein,J., Lacombe,K., Lamazares,R., Landers,T., Lehotzky,J.,  
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 Young,G., Zainoun,D., Zimmer,A. and Zody,M.  
 Direct Submission  
 TITLE JOURNAL  
 COMMENT submitted (01-MAR-2000) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 On Aug 26, 2000 this sequence version replaced gi:7132995.  
 All repeats were identified using RepeatMasker.



Smt. A.F.A. & Green, P. (1996:1997)  
<http://ftp.genome.washington.edu/RW/RepeatMasker.html>

Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)

Project Information

Center Project name: L1857

Center Clone name: 481.H\_17

Summary Statistics

Sequencing vector: M13; M7815; 95% of reads

Sequencing vector: Plasmid; n/a; %0.1% of reads

5.03173463177115Chemistry: Dye-terminator Big Dye; 100% of

reads

Assembly program: Phrap; version 0.960731

Consensus quality: 156366 bases at least Q40

Consensus quality: 161786 bases at least Q30

Consensus quality: 163606 bases at least Q20

Insert size: 156000; agarose-fp

Insert size: 164520; sum-of-contigs

Quality coverage: 4.9 in Q20 bases; agarose-fp

Quality co.

\* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 22 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

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Sun Sep 29 09:32:43 2002

us-09-899-471-2.rge

Page 25

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657 uAlaProGly 660

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seq\_documentation\_block:

Sequence 1, Application US/08620694A

Patent No. 5869286

GENERAL INFORMATION:

APPLICANT: Spriggs, Melanie

APPLICANT: Fanslow, William

TITLE OF INVENTION: No. 5869286el Receptor That Binds IL-17

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunex Corporation

STREET: 51 University Street

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: Apple Power Macintosh

SOFTWARE: Microsoft Word for Apple, Version 6.0.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/620,694A

FILING DATE: 21 MARCH 1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: USSN 08/538,765

FILING DATE: 7 AUGUST 1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: USSN 08/410,535

FILING DATE: 23 MARCH 1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia Anne

REGISTRATION NUMBER: 34,695

REFERENCE/DOCKET NUMBER: 2617-B

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206)587-0430

TELEFAX: (206)587-0430

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 3288 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA to mRNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Mouse

STRAIN: HVS13 receptor

FEATURE:

NAME/KEY: CDS

LOCATION: 121..2715

US-08-620-694A-1

alignment\_scores: Quality: 174.50

Length: 582

Ratio: 0.687 Gaps: 28  
Percent similarity: 43.643 Percent identity: 20.619

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seq\_name: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq:us-09-022-255-1

## seq\_documentation\_block:

Sequence 1, Application US/09022255  
Patent No. 6072033

## GENERAL INFORMATION:

APPLICANT: Yao, Zhenbin  
APPLICANT: Spriggs, Melanie  
APPLICANT: Fanslow, William  
TITLE OF INVENTION: No. 6072033el Receptor That Binds IL-17  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Power Macintosh  
OPERATING SYSTEM: Apple Operating System 7.5.5  
SOFTWARE: Microsoft Word for Apple, Version 6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/022,255

## FILING DATE:

## CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/620,694  
FILING DATE: 21 MARCH 1996  
APPLICATION NUMBER: USSN 08/538,765  
FILING DATE: 7 AUGUST 1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/410,535  
FILING DATE: 23 MARCH 1995

## ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia Anne  
REGISTRATION NUMBER: 34,695  
REFERENCE/DOCKET NUMBER: 2617-B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)

## INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:  
LENGTH: 3288 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
HYPOTHEetical: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Mouse  
STRAIN: HVS13 receptor  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 121..2715  
US-09-022-255-1

## alignment\_scores:

Quality: 174.50 Length: 582  
Ratio: 0.687 Gaps: 28  
Percent Similarity: 43.643 Percent Identity: 20.619

## alignment\_block:

US-09-899-471-2 x US-09-022-255-1

Align seg 1/1 to: US-09-022-255-1 from: 1 to: 3288

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seq documentation_block:
Sequence 1, Application US/09022696
Patent No. 6072037
GENERAL INFORMATION:
APPLICANT: Yao, Zhengbin

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APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 6072037el Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,696
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/620,694
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/620,694
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3288 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Mouse
STRAIN: HVS13 receptor
FEATURE:
NAME/KEY: CDS
LOCATION: 121..2715
US-09-022-696-1
alignment_scores:
Quality: 174.50 Length: 582
Ratio: 0.687 Gaps: 28
Percent Similarity: 43.643 Percent Identity: 20.619
alignment_block:
US-09-899-471-2 x US-09-022-696-1 ..
Align seg 1/1 to: US-09-022-696-1 from: 1 to: 3288
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 seq.name: /cgn2.6/ptodata/2/lna/6A.COMB.seq: us-08-978-773-1  
 seq.documentation\_block:  
 : Sequence 1, Application US/08978773  
 : Patent No. 6083906  
 : GENERAL INFORMATION:  
 : APPLICANT: Trout, Anthony  
 : TITLE OF INVENTION: Method of Regulating Nitric Oxide Production  
 : NUMBER OF SEQUENCES: 4  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: Immunex Corporation  
 : STREET: 51 University Street  
 : CITY: Seattle  
 : STATE: WA  
 : COUNTRY: USA  
 : ZIP: 98101

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
 COMPUTER: Apple PowerMacintosh  
 OPERATING SYSTEM: Apple Operating System 7.5.5  
 SOFTWARE: Microsoft Word for PowerMacintosh, Version 6.0.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/978,773  
 FILING DATE:  
 CLASSIFICATION: 530  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: USSN 60/052,525  
 FILING DATE: 27 NOVEMBER 1996  
 CLASSIFICATION: 530  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Perkins, Patricia Anne  
 REGISTRATION NUMBER: 34,693  
 REFERENCE/DOCKET NUMBER: 2623-A  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (206)587-0430  
 TELEFAX: (206)  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 3288 base pairs  
 TYPE: nucleic acid  
 TOPOLOGY: linear  
 STRANDEDNESS: single  
 MOLECULE TYPE: cDNA to mRNA  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 ORIGINAL SOURCE:  
 ORGANISM: Mouse  
 IMMEDIATE SOURCE:  
 CLONE: IL-17 receptor  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 121..2712  
 US-08-978-773-1

Alignment scores:  
 Quality: 174.50 Length: 582  
 Ratio: 0.687 Gaps: 28  
 Percent Similarity: 43.643 Percent Identity: 20.619

alignment block:  
 US-09-899-471-2 x US-08-978-773-1 ..

Align seg 1/1 to: US-08-978-773-1 from: 1 to: 3288

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590 TyrPheAspGlyLeuLeuInIshProAspSerValProSerProPheArg 606
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623 leuGIn.....GlyGlyCysSer.....Th 629
1736 TCCAGAGCCTGGAGATGTTTACCCGCGGATGATCACCATGTCAGAGAG 1785
629 rSerAlaGlyArgProAlaAspArgValGlyValThrGInAlaLeuAla 646
1786 CTCACAGGGGACAACTTACCTCAGAGCCCTAGTGGCCGCGACCTCAAGA 1835
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seq_name: /c9n2_6/ptodata/2/lna/6A_COMB.seq:us-09-022-253-1
seq_documentation_block:
Sequence 1, Application US/09022253
Patent No. 6096305
GENERAL INFORMATION:
APPLICANT: Yao, Zhengbin
APPLICANT: Fanliow, William
TITLE OF INVENTION: No. 6096305el Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSER: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,253
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/620,694
FILING DATE: 21-MARCH-1996

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APPLICATION NUMBER: USSN 08/538,765
FILING DATE: 7 AUGUST 1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3288 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Mouse
STRAIN: HVS13 receptor
FEATURE:
NAME/KEY: CDS
LOCATION: 121..2715
US-09-022-253-1

alignment_scores:
Quality: 174.50 Length: 582
Ratio: 0.687 Gaps: 28
Percent Similarity: 43.643 Percent Identity: 20.619
alignment_block:
US-09-899-471-2 x US-09-022-253-1 ..
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316 AAAAACTGACCCCGCTCTTCCCAAAAAATCATATCAATCTTAGTGT 365
236 .....HistnAspLeuValProCysLeuGlyIleGlnValT 248
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248 rPserLeuGluProAsp..... 253
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278 euArg.....ValleuSerProGlyValTyrGlnleuAspAlaProCys 293
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556 nThrValGluProGlyProHisAspAlaLeuAlaAlaTrpLeuSerCys 573
1546 .....AAGCTGCT...GGGACCTTTTCACTGACGACCATGAACATGA 1585
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606 lAlaProLeuPheSerLeuPro...ThrGlnLeuProAlaPheLeuAspAla 622
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623 LeuGln.....GlyGlyCysSer.....Th 629
1736 TCCAGACCTGAGATGTTGAACCCGCGGATGACCATGTGAGAG 1785
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; Sequence 1, Application US/09022260
; Patent No. 6100235
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; TITLE OF INVENTION: No. 6100235el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Apple Power Macintosh
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,260
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/620,694
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/410,535
; FILING DATE: 23 MARCH 1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne

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[illegible][illegible]





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402 ArgLeuGlyYGLuGluLeuGlnAspPheArgSerHisGlnCysMetGly 418
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1586 TCTCTGCAACTTCAAGAGCCAGCTGCTGCGACCTACGTTGTTGC 1635
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1636 TACTTCAGTGGCATCTGTAGTGAGAGGATGTCCCGACCTCTTCAACT 1685
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seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-09-022-257-1

seq_documentation_block:
: Sequence 1, Application US/09022257
: Patent No. 6197525
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: GENERAL INFORMATION:
: APPLICANT: Yao, Zhengbin
: APPLICANT: Spriggs, Melanie
: APPLICANT: Fanslow, William
: TITLE OF INVENTION: No. 6197525el Receptor That Binds IL-17
: NUMBER OF SEQUENCES: 10
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Immunex Corporation
: STREET: 51 University Street
: CITY: Seattle
: STATE: WA
: COUNTRY: USA
: ZIP: 98101
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: Apple Power Macintosh
: OPERATING SYSTEM: Apple Operating System 7.5.5
: SOFTWARE: Microsoft Word for Apple, Version 6.0.1
:
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/022, 257
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/620, 694
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/620, 694
: FILING DATE:
: APPLICATION DATA:
: APPLICATION NUMBER: USSN 08/410, 535
: FILING DATE: 23 MARCH 1995
: ATTORNEY/AGENT INFORMATION:
: NAME: Perkins, Patricia Anne
: REGISTRATION NUMBER: 34,695
: REFERENCE/DOCKET NUMBER: 2617-B
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (206)587-0430
: TELEFAX: (206)
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 3288 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA to mRNA
: HYPOTHEICAL: NO
: ANTI-SENSE: NO
: ORIGINAL SOURCE:
: ORGANISM: Mouse
: STRAIN: HVS13 receptor
: FEATURE:

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NAME/KEY: CDS  
LOCATION: 121..2715  
US-09-022-257-1

Alignment\_scores:  
Quality: 174.50 Length: 582  
Ratio: 0.687 Gaps: 28  
Percent Similarity: 43.643 Percent Identity: 20.619

Alignment\_block:  
US-09-899-471-2 x US-09-022-257-1 ..

Align seg 1/1 to: US-09-022-257-1 from: 1 to: 3288

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366 TTCCTGTACCCAGACGAGGAAATTAGTCCCTGTGTTCATGTTGAG..T 412
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413 GGACCTGACAGACAGATGCCACATCTCTACTGACGAGGTGCAGAGCTG 462
254 .....SerGluArg.....ValGluPhcCysPr 261
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463 TCCGCTCTGACGCTGAACACCAATGAGCGCTGTGTCAAGTTC...CA 509
261 oPheArgGluAspProGlyAlaHisArgAsnLeuThrPheHisIleAlaArgL 278
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291 .AMCGTAGCCCTCTCCGCCCAAGGAGCTGAGATCCAGCTGCACCTTG 339
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340 CCGACAGCCCAACAAGAGAGACTGTTCCCGTGGCTCAC.....ATC 380
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252 oAspSerGlnArgValGlnPheCys..... 260
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490 ValGlyAlaLeuAlaSer...AlaLeuSerGlnMetProLeuArgValAl 505
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582 AlArTrpGlyArgTrpValGlyValTrpPheAspGlyLeuLeuHisProAs 598
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seq_documentation_block:
; Sequence 9, Application US/09022255
; Patent No. 6072033
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Springs, Melanie
; TITLE OF INVENTION: No. 6072033el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Apple Macintosh
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022.255
; FILING DATE:
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US98 08/620,694
; FILING DATE: 21 MARCH 1996
; APPLICATION NUMBER: US98 08/538,765
; FILING DATE: 7 AUGUST 1995
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US98 08/410,535
; FILING DATE: 23 MARCH 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne

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REGISTRATION NUMBER: 34,695  
REFERENCE/DOCKET NUMBER: 2617-B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430

TELEFAX: (206)  
INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:  
LENGTH: 3223 base pairs

TYPE: nucleic acid  
STRANDEDNESS: single

TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA

HYPOTHETICAL: NO  
ANTI-SENSE: NO

ORIGINAL SOURCE:  
ORGANISM: Human

FEATURE:  
STRAIN: IL-17 R (hCTLA8 receptor)

NAME/KEY: CDS  
LOCATION: 93..2693

US-09-022-255-9

# Alignment scores:

Quality: 154.00 Length: 732  
Ratio: 0.552 Gaps: 33  
Percent Similarity: 38.115 Percent Identity: 19.399

Alignment block:  
US-09-899-471-2 x US-09-022-255-9

Align seg 1/1 to: US-09-022-255-9 from: 1 to: 3223

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61 uValPro.....ThArgLeuInThrGluLeuValLeuArg 74  
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74 ySPGlnLysThrAspCysAlaLeuArgValArgValValHisLeu 90  
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91 AlaValHisGlyHisThrAlaGluProGluGluValGlyLysSerAsp 107  
261 TGCTGATGACAGCTGGATTCACCTCGA..... 290  
107 GlnLeuGlnLysSerArgAsnAlaSerLeuGlnAlaGlnValLeu 124  
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340 CCCACACCCCAAGAGAGAGCTGTCCTCCGCGCTCAC.....ATC 380  
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215 oASP.....AlaLeu 219  
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seq_name: /cgn2_6/ptodata/2/lna/6A_COMB.seq:us-US-09-022-696-9
seq_documentation_block:
? Sequence 9, Application US/09022696
? Patent No. 6072037
? GENERAL INFORMATION:
? APPLICANT: Yao, Zhenqin
? APPLICANT: Spriggs, Melanie
? APPLICANT: Fanson, William
? TITLE OF INVENTION: NO. 6072037e1 Receptor That Binds IL-17

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1 NUMBER OF SEQUENCES: 10
2 CORRESPONDENCE ADDRESS:
3 ADDRESSEE: Immunex Corporation
4 STREET: 51 University Street
5 CITY: Seattle
6 STATE: WA
7 COUNTRY: USA
8 ZIP: 98101
9
10 COMPUTER READABLE FORM:
11 MEDIUM TYPE: Floppy disk
12 COMPUTER: Apple Power Macintosh
13 OPERATING SYSTEM: Apple Operating System 7.5.5
14 SOFTWARE: Microsoft Word for Apple, Version 6.0.1
15 CURRENT APPLICATION DATA:
16 FILING DATE: US/09/022,696
17 CLASSIFICATION:
18 PRIOR APPLICATION DATA:
19 APPLICATION NUMBER: 08/620,694
20 FILING DATE:
21 CLASSIFICATION:
22 PRIOR APPLICATION DATA:
23 APPLICATION NUMBER: 08/620,694
24 FILING DATE:
25 CLASSIFICATION:
26 PRIOR APPLICATION DATA:
27 APPLICATION NUMBER: USSN 08/410,535
28 FILING DATE: 23 MARCH 1995
29 CLASSIFICATION:
30 ATTORNEY/AGENT INFORMATION:
31 NAME: Perkins, Patricia Anne
32 REGISTRATION NUMBER: 34,695
33 REFERENCE/DOCKET NUMBER: 2617-B
34 TELECOMMUNICATION INFORMATION:
35 TELEPHONE: (206)587-0430
36 TELEFAX: (206)
37 INFORMATION FOR SEQ ID NO: 9:
38 SEQUENCE CHARACTERISTICS:
39 LENGTH: 3223 base pairs
40 TYPE: nucleic acid
41 STRANDEDNESS: single
42 TOPOLOGY: linear
43 MOLECULE TYPE: cDNA to mRNA
44 HYPOTHEetical: NO
45 ANTI-SENSE: NO
46 ORIGINAL SOURCE:
47 ORGANISM: Human
48 STRAIN: IL-17 R (MCTLA8 receptor)
49 FEATURE:
50 NAME/KEY: CDS
51 LOCATION: 93..2693
52 US-09-022-696-9
53
54 Alignment_scores:
55 Quality: 154.00 Length: 732
56 Ratio: 0.552 Gaps: 33
57 Percent Similarity: 38.115 Percent Identity: 19.399
58 alignment_block:
59 US-09-899-471-2 x US-09-022-696-9 ..
60 Align seg 1/1 to: US-09-022-696-9 from: 1 to: 3223
61
62 55 SerAlaProLysPro.....Valle 61
63 :::::CCCCCCCCCCCCCGTGGGCTGCTCCTGCCTCCCTGGCGCTGTCT 169
64 120 GGCTGCCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 169
65 61 ValPro.....TharGlauGlnThrGluLeuValIleuArgc 74
66 I::::II IIIII ::::::::::I
67 170 GGGCCCCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 74
68 74 ysfRoSlglnlystRhpAspCySAlaLeuArGValaRgValaValaIHsl 90
69 II IIII ::::IIIIII III
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71 AlavAlHslGlnlystRpAlaGlnProGluGlnAlaGlnLySerAspse 107

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1375 GGGTGGCGGCTGAGAGAGAGATGAGTGGAGAGCACTCTATATATATC 1424
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alignment_block:
US-09-899-471-2 x US-08-978-773-3 ..
Percent Similarity: 38.115 Percent Identity: 19.399

Quality: 154.00 Length: 732
Ratio: 0.552 Gaps: 33

Align seg 1/1 to: US-08-978-773-3 from: 1 to: 3223

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US-108-978-773-3

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009-899-471-2 x US-08-978-773-3
align seg 1/1 to: US-08-978-773-3 from: 1 to: 3223

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632 GlyArgProAlaAspArgValGluArgValThrGlnAlaLeuArgSera 648
1668 ..... ATGACAGGTTCAGAGAGGTGTACTTCCGATCCAGACGCT 1708
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; Patent No. 6096305
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6096305el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,253
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/620,694
; FILING DATE: 21-MARCH-1996
; APPLICATION NUMBER: USSN 08/538,765
; FILING DATE: 7 AUGUST 1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:

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APPLICATION NUMBER: USSN 08/410,535

FILING DATE: 23 MARCH 1995

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia Anne

REGISTRATION NUMBER: 34,695

REFERENCE/DOCKET NUMBER: 2617-B

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206)587-0430

TELEFAX: (206)

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 3223 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Human

FEATURE: IL-17 R (IL17A receptor)

NAME/KEY: CDS

LOCATION: 93..2693

US-09-022-253-9

alignment\_scores:

Quality: 154.00

Ratio: 0.552

Percent Similarity: 38.115

Percent Identity: 19.399

Gaps: 33

Length: 732

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261 .....ProPheArgGluAspProGlyAlaHisArg 270

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287 nLeuAspValProCysCysLeuProGlyLysValThrLeuCysTyrPola 304

848 ..... 848

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patent No. 6100235



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:::|||||::: ||| :::||||| ::: |||
1625 CGACGTCCCGCACCTGTTCGGCGCGCGCGGTACCCGCTC..... 1667
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Ratio: 5.330 Gaps: 1  
Percent Similarity: 99.138 Percent Identity: 98.707

Alignment block:  
US-09-899-471-2 x B1332055

Align seg 1/1 to: B1332055 from: 1 to: 697

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seq\_documentation\_block:

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DEFINITION 602832412F1 NCI\_CGAP\_Co24 Mus musculus cDNA clone IMAGE:4987035 5',  
ACCESSION BG968034  
VERSION BG968034.1 GI:14355671  
KEYWORDS EST.

SOURCE house mouse.  
ORGANISM Mus musculus

REFERENCE Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 784)  
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)  
Tissue Procurement: Jeffrey E. Green, M.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLAM10997 row: 9 column: 04  
High quality sequence stop: 646.  
Location/Qualifiers

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Average insert size 1.6 kb. Constructed by Life  
Technologies. Note: this is a NCI\_CGAP Library."  
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ORIGIN

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Quality: 1187.00 Length: 254  
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Percent Similarity: 92.520 Percent Identity: 89.370

alignment\_block:  
US-09-899-471-2 x BG968034

Align seg 1/1 to: BG968034 from: 1 to: 784

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253 TCCCCAGAGAAAGCCACTGTGATGAGCCACACAGATTCAGTGGTGG 302
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 SOURCE house mouse.  
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 1 (bases 1 to 1006)  
 AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.,  
 Hiramoto,K., Horii,F., Ishii,Y., Ito,M., Kawai,U., Konno,H., Kouda,  
 M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,  
 Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,  
 D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,  
 Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toyata,T.,  
 Muramatsu,M. and Hayashizaki,Y.  
 RIKEN Mouse ESTs (Arakawa,T., et al. 2001)  
 Unpublished (2001)  
 COMMENT  
 TITLE Laboratory for Genome Exploration Research Group, RIKEN Genomic  
 Sciences Center(GSC), Yokohama Institute  
 The Institute of Physical and Chemical Research (RIKEN)  
 1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan  
 Tel: 81-45-503-9212  
 Fax: 81-45-503-9216  
 Email: genome-res@gs.riken.go.jp/  
 URL:http://genome.gsc.riken.go.jp/  
 Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh  
 M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.  
 Normalization and subtraction of cap-trapper-selected cDNAs to  
 prepare full-length cDNA libraries for rapid discovery of new  
 genes. Genome Res. 10 (10), 1617-1630 (2000)

wagi,K., Fujisake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,  
 Natabiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura  
 S., Kawai,U., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and  
 Hayashizaki,Y.  
 RIKEN integrated sequence analysis (RISA) system-384-format  
 sequencing pipeline with 384 multichipillary sequencer. Genome Res.  
 10 (11), 1757-1771 (2000)  
 Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara  
 K. and Hayashizaki,Y.  
 Computer-based methods for the mouse full-length cDNA  
 encyclopedia: real-time sequence clustering for construction of a  
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
 Konno,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa  
 K., Fukuda,S., Hara,A., Itoh,M., Kawai,U., Shibata,K. and  
 Hayashizaki,Y.  
 Computational Analysis of Full-length Mouse cDNAs Compared with  
 Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)  
 Please visit our web site (<http://genome.gsc.riken.go.jp>) for  
 further details.

#### FEATURES

Location/Qualifiers  
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 /organism="Mus musculus"  
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 Project of Genome Exploration Research Group in Riken  
 Genomic Sciences Center and Genome Science Laboratory in  
 RIKEN. Division of Experimental Animal Research in Riken  
 contributed to prepare mouse tissues. 1st strand cDNA was  
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 Ratio: 4.227 Gaps: 12  
 Percent Similarity: 76.989 Percent Identity: 69.886

alignment\_block:  
 US-09-899-471-2 x BB609618 ..

Align seg 1/1 to: BB609618 from: 1 to: 1006.

123 leuseRphcgnalatyRProilleaIaRgysAlaLeuLeuGluValAla 139  
 14 CTCTCCTTCAGNCTACCCATCCCGCGCTGCTCTCTCGAGAGTCCA 63  
 139 nvalProlaaspLeuValAlaInProGlyInServalGlySeralVala 156  
 64 GGTCCCGCTGACCTGCTGCA.CCTGGTCAGTCCGTGGCTTCGCGGTAT 112  
 156 heaspCysPheGlnAlaSerleuglyAlaGluValGlnletrPserTy 172  
 113 TTGACTGTTTGGAGCTAGTCTTGGGCTGAGGTACAGTGTGGTCTTAC 162  
 173 ThrLySPArgTyrglnLysgluLeuasnleutrhrglnleuPro.. 188  
 163 ACGAAGCCAGGTACGAAAGAGAGCTCAACCTCACACAGCACTGCTTA 212  
 188 .....



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103 AGTGTCTGCAAGACTTCCGATCACCACAGTGTATGACAGCTGTGACAGCAT 152
423 ASPASmetGlySerLeuTrpAlaCysProMetAspLysTrpIleHisar 439
153 GACACATGATGATCGCTATGGCGCTGCCATG.GACACATGATCACCACAG 201
439 GATGTTPValLeuValTrpLeuAlaCysLeuLeuLeuAlaAlaLeuP 456
202 GCGCTGGGCTCTAGTATGGCTGGCTGCTACTCTTGGCTGGCGGCTTT 251
456 hePhePheLeuLeuLeuLysLysAspArgArgLysAlaAlaArgLys 472
252 TCTTCTCTCTCTCTTAAAGAGACCGAGAAAGGCGCCGCTGCTCC 301
473 ArgPheAlaLeuLeuLeuHisSerAlaAspGlyAlaGlyTrpGluArgLe 489
302 CCGACAGCGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 351
489 uValAlaLeuAlaSerAlaLeuSerGlnMetProLeuArgValAlaV 506
352 GGTGGGAGACATGGCGCTCCGCTTGAGCCAGATGCCACTGCGCTGGCG 401
506 AlAspLeuTrpSerArgArgGluLeuSerAlaHisGlyAlaLeuAlaTrp 522
402 TGGACCTGTGAGCCCGCGAGCTGAGCCGACGAGCCCTAGCCTGG 451
523 PheHisGlnArgArgArgGluLeuGlnGlyValValAlaIlele 539
452 TTACACACACACAGCGCGCTATCTGACAGAGGCTGCGCTGTAATCT 501
539 uLeuPheSerProAlaAlaValAlaGlnGlnGlnGlnTrpLeuGlnLeu 556
502 TCTCTTCTGCGCGCGCGCGCTGGGAGGTGTACAGCACTGCTGAGCTCC 551
556 ltrhValGluProGlyProHisAspAlaLeuAlaAlaTrpLeuSerCys 572
552 AGACAGTTGAGCCCGCGCGCATGAGCCCTCGCTGCTGCTGCTGCTGCTG 601
573 ValLeuProAspPheLeuGlnGlnArgAlaTrpGlyArgGlyValGly 589
602 GTGCTTACCGATTTTCTGCAAGC.CGGGCGACCGTTAAACCGTGGGGGT 650
589 lTyrPheAspGlyLeuLeuHisProAspSerValProSerProPheArg 606
651 CTACTTCACAGCGCGCTGCGCAACCAACTGTGTCTCTCTCTCTCTCTCT 700
606 AlAlaProLeuPheSerLeuProTrpGlnLeuProAlaPheLeuAspAla 622
701 GTGGCCCGTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 750
623 LeuGlnGlyGlyCysSerThrSer 630
751 CTTAAGGGAAGGTGATCAATTTCG 774

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Seq name: gb_est2.BF237179
Seq documentation block:
LOCUS BF237179 722 bp mRNA linear EST 14-NOV-2000
DEFINITION 60208133F1 NCL_CGAP_L19 Mus musculus cDNA clone IMAGE:4163217 5',

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ACCESSION BF237179 mRNA sequence.
VERSION BF237179.1 GI:11151096
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus.

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REFERENCE 1 (bases 1 to 722)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)

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COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-femail.nih.gov

```

Tissue Procurement: Jeffrey E. Green, M.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.jnl.gov>  
 Plate: L1AM9447 row: a column: 10  
 High quality sequence stop: 584.  
 Location/Qualifiers  
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 /organism="Mus musculus"  
 /strain="FVB/N"  
 /db\_xref="taxon:10090"  
 /clone\_id="NCL\_CGAP\_L19"  
 /lab\_host="DH10B (T1 phage-resistant)"  
 /note="Organ: Liver; Vector: pCMV-SPORE6; Site\_1: NotI;  
 Site\_2: SalI; Cloned unidirectionally. Primer: Oligo dT.  
 Average insert size 1.9 kb. Constructed by Life  
 Technologies. Note: this is a NCL\_CGAP Library."

BASE COUNT  
 ORIGIN  
 128 a 238 c 255 g 101 t

alignment\_scores:  
 Quality: 1058.00 Length: 207  
 Ratio: 5.161 Gaps: 0  
 Percent Similarity: 99.034 Percent Identity: 97.585

alignment\_block:  
 US-09-899-471-2 x BF237179/rev ..  
 Align seg 1/1 to reverse of: BF237179 from: 1 to: 722

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468 AlAlaArgGlySerArgTrpAlaLeuLeuHisSerAlaAspGlyAl 484
629 GCGCGCGGTGCTCCGCGACAGCTGCTCTCTCTCTCTCTCTCTCTCT 580
484 aglyTrpGluArgLeuValGlyAlaLeuAlaSerAlaLeuSerGlnMet 501
579 GGGCTACGAGCGTCTGTGGAGACACTGCGCTCGCTTACAGCCAGATC 530
501 roleuArgValAlaValAspLeuTrpSerArgArgGluLeuSerAlaHis 517
529 CACTGCGCTGGCGCTGAGCACTGTGAGCCGCGCGAGCTGAGCGCCAC 480
518 GlyAlaLeuAlaTrpPheHisGlnArgArgGluLeuGlnGln 534
479 GAGGCGCTAGCTGCTTCCACACACAGCGCGCGATCTCTGACAGAGG 430
534 yGlyValValIleLeuLeuPheSerProAlaAlaValAlaGlnCysGln 551
429 TGGCGGTGTAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 380
551 ltrPheGlnLeuGlnTrpValGluProGlyProHisAspAlaLeuAla 567
379 AGTGGCTGAGCTCCAGACAGTGGAGCCCGCGCGCTGACGCCCTGGCC 330
568 AlATrPheSerCysValLeuProAspPheLeuGlnGlyArgAlaTrpG 584
329 GCGTGGCTAGCTGCTGCTACCCGATTTCTCTCAAGGCGCGGAGCCG 280
584 yArgTrpValGlyValTyrPheAspGlyLeuLeuHisProAspSerValP 601
279 CCGGTACGTGCGGGGTCTACTTGGAGGGGTGCGACCCAGACTCTGTGC 230
601 roSerProPheArgValAlaProLeuPheSerLeuProTrpGlnLeuPro 617
229 CCTCCCGCTTCCGCGCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCG 180
618 AlApeLeuAspAlaLeuGlnGlyGlyCysSerThrSerAlaGlyArgPr 634

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OCUS BB625706 643 bp mRNA linear EST 26-OCT-2001

ECUTION BB625706 RIKEN full-length enriched, adult male diencephalon mus

CCESION BB625706 musculus cDNA clone 9330110N14 5', mRNA sequence.

ERSION BB625706.1 GI:16463928

WORD EST.

ORCE house mouse.

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 643)

AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Kono,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasakita,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Mukemitsu,M. and Hayashizaki,Y.

RIKEN Mouse ESTs (Arakawa,T., et al. 2001)

JOURNAL Unpublished (2001)

COMMENT Contact: Yoshihide Hayashizaki

KIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. *Genome Res.* 10 (11), 1757-1771 (2000)

Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y., and Hayashizaki, Y.

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. *Genome Res.* 11 (2), 281-288 (2001)

Kondo, S., Shinagawa, A., Saito, T., Kiyosaka, H., Yamanaoka, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K., and Hayashizaki, Y.

Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences. *Mamm. Genome* 12, 673-677 (2001)

Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

/organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone\_1id="Riken full-length enriched, adult male  
 diencephalon"  
 /sex="male"  
 /tissue\_type="dienecephalon"  
 /dev\_stage="adult"  
 /lab\_host="DH10B"  
 /note="Site 1: Sali; Site 2: BamHI: cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer 15'  
 GAGGACGAGAGCATCCACAGCGCTTTTATTTTTTTTAAATTAATTC  
 GAGGACGAGAGCATCCACAGCGCTTTTATTTTTTTTAAATTAATTC  
 prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 185.0. Second strand cDNA was prepared with the primer adapter of sequence 15' GAGGACGAGATTCGAGTAAATTAATTAATTC  
 3'. cDNA was cloned into the XhoI and BamHI sites.  
 Vector: a modified pluescript KS(+) after bulk exsition from Lambda PLC I. Cloning sites, 5' end: Sali; 3' end:  
 BamHI"



268 GCCCTCCCGCTCCGCGCCGCGCTCTTCCTCCCTGCGCCGACCTGC 219  
 617 roAlaPheLeuAspAlaLeuGlnGlyGlyCysSerThrSerAlaGlyArg 633  
 218 CGGCTTTCCTGATGACTGCAGGAGAGCTGCTCCACTCCGCGGAGCA 169  
 634 ProAlaAspArgValGlyArgValThrGlnAlaLeuArgSerAlaLeuAs 650  
 168 CCCCGGAGACCGGCTGGAGACAGTACCCAGCGCGCTGCGCCCTGGA 119  
 650 pSerCysThrSerSerGlnAlaProGlyCysGlnGluTrpAspL 667  
 118 CAGCTGACTCTTACGCTCGGAAGCCCGGCTGCTCGAGATGGGACC 69  
 667 euGlyProCysThrThrLeuGlu 674  
 68 TGGGACCCCTGCACCTACACTAGCA 46

seq\_name: gb\_est2:BE290565

seq\_documentation\_block:

LOCUS BE290565 562 bp mRNA linear EST 26-OCT-2000  
 DEFINITION 601089427F1 NCI\_CGAP\_Mam5 Mus musculus cDNA clone IMAGE:3484038 5',  
 mRNA sequence.

ACCESSION BE290565  
 VERSION BE290565.1 GI:9171696

KEYWORDS EST.  
 SOURCE house mouse.

ORGANISM

Mus musculus.  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NIH-MGC http://mgi.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgaabs-r@mail.nih.gov  
 Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys  
 cDNA Library Preparation: Life Technologies, Inc.  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LHAM8516 row: f column: 07  
 High quality sequence stop: 562.

# FEATURES

SOURCE

1. 562  
 Location/Qualifiers  
 /organism="Mus musculus"  
 /strain="C57/B6"  
 /db\_xref="taxon:10090"  
 /clone\_lib="NCI\_CGAP\_Mam5"  
 /clone\_image="3484038"  
 /tissue\_type="tumor, gross tissue"  
 /dev\_stage="7 months"  
 /lab\_host="DH10B"  
 /note="Organ: mammary; Vector: pCMV-SPORT6; Site\_1: SalI;  
 Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dt.  
 Library constructed by Life Technologies. Investigators  
 providing samples: Lothar Hennighausen/Robin Humphreys,  
 NIH"

BASE COUNT 86 a 190 c 180 g 106 t

ORIGIN

Alignment\_scores:

Quality: 999.00 Length: 187  
 Ratio: 5.342 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

Alignment\_block:

US-09-899-471-2 x BE290565

Align seg 1/1 to: BE290565 from: 1 to: 562

414 HisGlnCysMetGlnLeuTrpAsnAspAspAsnMetGlySerLeuTrpAl 430  
 2 CACCAAGTGTATCAGCTGTGGAACGATGACACATGATGATGATGGGC 51  
 430 acYSPrometAspLysTyrLleHisArgArgTrpValLeuValTrpLeu 447  
 52 CTGCCCATAGGCAACACTACATCCACAGGCGCTGGTCTTGATGGCTGG 101  
 447 laCysLeuLeuLeuAlaAlaAlaLeuPhePheLeuLeuLysLys 463  
 102 CCGCTACTCTTGGCTGGCGGCTTTCTTCTTCCCTCCTTAATAAAG 151  
 464 AspAlaGlyGlyAlaAlaAlaArgLysArgTrpAlaLeuLeuHisSe 480  
 152 GACCCGAGGAAAGCGGCCGCTGCTCCGACGCGCTTCTCCCTCCACTC 201  
 480 rAlaAspGlyAlaGlyTyrGlnArgLeuValGlyAlaLeuAlaSerAla 497  
 202 CCGCAAGAGGAGCGGCTACGAGCGTCTGGTGGAGCACTGGCTCCGCT 251  
 497 euSerGlnMetProLeuArgValAlaValAspLeuTrpSerArgArgGlu 513  
 252 TGAGCCAGATGCCACTCGCGCGTGGCGCTGGACCTGTGGACCCGCGGAG 301  
 514 LeuSerAlaHisGlyAlaLeuAlaTrpPheHisGlnArgArgGlu 530  
 302 CTGACGCGGCGACGAGCCCTAGCCTGTTCACACACAGGAGCGCCGTAT 351  
 530 elenGlnGlnGlyGlyValValIleLeuLeuPheSerProAlaAlaVal 547  
 352 CTGGAGGAGGGGTGGGTGTAATCTTCTCTTCTGCGCCGCGCGCTGG 401  
 547 laGlnCysGlnGlnTrpLeuGlnLeuGlnThrValGluProGlyProHis 563  
 402 CGCACTGTACGACAGTGGCTGCACCTCCACAGAGTGGAGCCGCGGCAT 451  
 564 AspAlaLeuAlaAlaTrpLeuSerCysValLeuProAspPheLeuGln 580  
 452 GACGCGCTCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 501  
 580 yArgAlaThrGlyArgTyrValGlyValIleTrpPheAspGlyLeuLeuHis 597  
 502 CCGGCGAGCGGCGCGCTACGTGGGGTCTACTTCGAGGCGGCTGTCAC 551  
 597 roAspSerVal 600  
 552 CAGACTCTGTG 562

seq\_name: gb\_est2:BF160122

seq\_documentation\_block:

LOCUS BF160122 635 bp mRNA linear EST 30-OCT-2000  
 DEFINITION 601767822F1 NCI\_CGAP\_Lu29 Mus musculus cDNA clone IMAGE:3984149 5',  
 mRNA sequence.  
 ACCESSION BF160122  
 VERSION BF160122.1 GI:11040229  
 KEYWORDS EST.  
 SOURCE house mouse.  
 ORGANISM Mus musculus.  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NIH-MGC http://mgi.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgaabs-r@mail.nih.gov  
 Tissue Procurement: Gilbert Smith, Ph.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov  
 Plate: LLAM9185 row: 1 column: 06  
 High quality sequence start: 2  
 High quality sequence stop: 632.  
 Location/Qualifiers

# FEATURES

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 /clone\_1ib="IMAGE:3984149"  
 /tissue\_type="spontaneous tumor, metastatic to mammary."  
 Stem cell origin:  
 /lab\_host="DH10B"  
 /note="Organ: lung; Vector: pCMV-SPORT6; Site: 1: SalI; Site: 2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"

BASE COUNT 92 a 229 c 204 g 110 t

ORIGIN

Alignment\_scores:  
 Quality: 975.00 Length: 207  
 Ratio: 4.924 Gaps: 4  
 Percent Similarity: 95.652 Percent Identity: 93.237

Alignment\_block:  
 US-09-899-471-2 x BF160122

Align seg 1/1 to: BF160122 from: 1 to: 635

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2 CGTGGCGCCGCGACGCGCTGCTCCACATCCGCGACGAGCGGCGCTA 51
486 rguArLeuValGlyAlaLeuAlaSerAlaLeuSerGlnMetProLeu 503
52 CGAGCGCTGTGTAGGACACTGCGCTCCGCTGTGAGCCAGATGCCACTGC 101
503 rGValAlaValAlaSerLeuTrpSerArgGluLeuSerAlaHisGlyAla 519
102 GCGGCGCGCGTGTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 151
520 LeuAlaTrpPheHisHisGlnArgArgGlyLeuGlnGlyGlyVal 536
152 CTAGCGCTGTGTCCACGACGCGCGCGCGCTGTGCGAGAGATGGCGCT 201
536 lValAlaLeuLeuPheSerProAlaAlaValAlaGlnGlnGlnGlnTrp 553
202 GGTATATCTTCTCTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 251
553 eugLeuGlnThrValGlnProGlyProHisAspAlaLeuAlaTrp 569
252 TGCAGCTCCAGACAGTGGAGCGCGCTCCGATGACGCCCTCCCTGG 301
570 LeuSerCysValLeuProAspPheLeuGlnGlyArgAlaTrpGlyArg 586
302 CTCAGCTGTGTGTACCGATTCCTGCAAGCGCGCGCGCGCGCGCTA 351
586 rValGlyValTyrPheAspGlyLeuLeuHisProAspSerValProSer 603
352 CGTGGCGCGTGTGTGAGCGCGCGCGCGCGCGCGCGCGCGCGCTCC 401
603 rPheArgValAlaProLeuPheSerLeuProThrGlnLeuProAlaPhe 619
402 CGTTCGCGCGCGCGCGCTCTCTCTCTGCGCGCGCGCGCGCGCGCTTC 451
620 LeuAspAlaLeuGlnGlyGlyCysSerThrSerAlaGlyArgProAla 636
452 CTGGATGCACTGCAAGGAGGCTGTCTCAGCGTCCCGGGGCGAGCGCGGA 500

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636 SPARGValGluArgValThrGlnAlaLeuArgSerAlaLeuAspSerCys 652
501 ..CGGTGGAGACGAGTGGCGCGCTGC...AGTCCGCTGTGACACTG 545
652 sThrSerSerSerGluAlaProGlyCysGlnGlnGlnTrpAspLeuGly 669
546 TACTCTGACTGTGAGAGCCGCGCTGTGCGAGATGAGTGGACCTGGAC 595
669 rOCysThrThrLeuGlu 674
596 CCGTGCACCTACACTAGCA 612

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seq\_name: gb\_est2:BI251117

seq\_documentation\_block:

LOCUS BI251117 839 bp mRNA linear EST 17-JUL-2001  
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 mRNA sequence.  
 ACCESSION BI251117 GI:14800198  
 VERSION BI251117.1 GI:14800198  
 KEYWORDS EST.  
 SOURCE house mouse.  
 ORGANISM Mus musculus

REFERENCE  
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgaps-remail.nih.gov  
 Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys  
 CDNA Library Preparation: Life Technologies, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLAM1371 row: m column: 03  
 High quality sequence stop: 836.  
 Location/Qualifiers

# FEATURES

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 /dev\_stage="7 months"  
 /lab\_host="DH10B"  
 /note="Organ: mammary; Vector: pCMV-SPORT6; Site: 1: SalI; Site: 2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys, NIH"

BASE COUNT 146 a 248 c 268 g 177 t

ORIGIN

alignment\_scores:  
 Quality: 967.50 Length: 211  
 Ratio: 5.013 Gaps: 2  
 Percent Similarity: 91.469 Percent Identity: 91.469

alignment\_block:

US-09-899-471-2 x BI251117

Align seg 1/1 to: BI251117 from: 1 to: 839

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1 MetProValSerTrpPheLeuLeuSerLeuAlaLeuGlyArgAspProVal 17
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199 ATGCTGTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 248

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17 lvalvalserleuGluArgleuMetGluProGlnAspThrAlaArgCys 34  
 249 GGTCGCTCTCTGAGAGACTGATGAGCCCTCAGACACTCAGCTCT 298  
 34 erleuGlyLeuSerCysHisLeuTrpAspGlyAspValLeuCysLeuPro 50  
 299 CTCCTAGCCCTCTCTGACCTCTGGAGTGGTGAAGCTGTGCTGCT 348  
 51 GlySerLeuGlnSerAlaProGlyProValLeuValProThrArgLeuG1 67  
 349 GGAAGCTCCAGTCTGCCAGGCCCTGTCTACTGCTTACCCTGCTGA 398  
 67 nThrGluLeuValLeuArgCysProGlnLysThrAspCysAlaLeuArg 84  
 399 GACGAGCTGCTGCTGAGTGTCCACAGAACAGATGGCCCTCTGTG 448  
 84 AlArgValValValHisLeuAlaValHisGlyHisThrAlaGluProGlu 100  
 449 TCCGTGTGTGCTGCACCTTGGCCGTGATGGCAGCTGGCAGAGCTGA 498  
 101 GluAlaGlyLysSerAspSerGluLeuGlnGluSerArgAsnAlaSerle 117  
 499 GAAAGCTGGAAGTCTGATTCAGAACTCCAGAGTCTAGGAAGCTCTCT 548  
 117 uGlnAlaGlnValValLeuSerPheGlnAlaTyrProIleAlaArgCysA 134  
 549 CAGAGCCAGTGTGCTCTCTCCAGGCCCTACCCATGCCCGCTGTG 598  
 134 lAlaLeuGlnValAlaGlnValProAlaAspLeuValGlnProGlyLys 150  
 599 CCTGTGTGAGGTCCAGTCCCGCTACCTGTGTCAGCTGTGTCAGTCC 648  
 151 ValGlySerAlaValPheAspCysPheGlnAlaSerLeuGlnAlaGlu 167  
 649 GTGGTCTGCGGTATTTGACTGTTTCGAGGCTAGTCTTGGGCTGAGGT 698  
 167 lGlnIleTyrPser.TyrThrLysProArgTyrGlnLysGluLeuAsnLeu 183  
 699 ACAGATCTGTCTTACACGAGCCAGTACACGAAAGACTCAACTC 748  
 184 ThrGlnGluLeuProAsp..... 189  
 749 ACACACACACTGCTCTGACTGACAGGCTTGAAGTCCGGACAGCATCCAG 798  
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Seq\_name: gb\_est2.BG761977

Seq documentation block:  
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 DEFINITION M2721892881 NIH\_MGC\_49 Homo sapiens cDNA clone IMAGE:4858806 5',  
 mRNA sequence.  
 ACCESSION BG761977  
 VERSION BG761977.1 GI:14072630  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 935)  
 NIH-MGC http://mhc.nci.nih.gov/  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: ATCC/DCFD/DTF  
 cDNA Library Preparation: Ling Hong/Rubin Laboratory  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:  
 http://image.lnl.gov  
 Plate: LNCM713 row: h column: 07  
 High quality sequence stop: 813.  
 Location/Qualifiers  
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 /db\_xref="taxon:9606"  
 /clone="IMAGE:4858806"  
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 /tissue\_type="melanotic melanoma, high MDR (cell line)"  
 /lab\_host="DH10B (phage-resistant)"  
 /note="Organ: skin; Vector: pOTB7; Site: 1: XhoI; Site: 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAACAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

BASE COUNT 154 a 301 c 291 g 189 t

ORIGIN

alignment\_scores:  
 Quality: 912.50 Length: 307  
 Ratio: 3.755 Gaps: 8  
 Percent Similarity: 79.153 Percent Identity: 62.866

alignment\_block:  
 US-09-899-471-2 x BG761977

Align seg 1/1 to: BG761977 from: 1 to: 935

237 ThrAspLeuValProCysLeuGlnIleGlnValTrpSerLeuGluProAs 253  
 2 ACAGACTGTGTTCCCTGCTCTGTATTCAGTGTGCGCCCTGGAACCTGA 51  
 253 pSerGluArgValGluPheCysProPheArg.GluAspProGlyLysHis 269  
 52 CTCCTTAGAGACGAACATCTGCCCTTCAGGAGAGACCCCGCGCACAC 101  
 270 ArgAsnLeuTrpHisIleAlaArgLeuArgValLeuSerProGlyValTr 286  
 102 CAGAACCTCTGCGAAGCCGCCGACTGACTGACTGACCTGCAGAGCTG 151  
 286 pGlnLeuAspAlaProCysCysLeuProGlyLysValThrLeuCysTrpG 303  
 152 GCTGCTGGAGCAGCAGTCTGCTGCTGCCCGCAGACAGCGGACGTGCTGC 201  
 303 lAlaLProAspGlnSerProCysGlnProLeuValProProValProGln 319  
 202 GGGCTCCGGGGGGAGCCCTGCCAGCACACTGCTCCAGCCCTTTCCTGG 251  
 320 LysAsnAlaThrValAsnGluProGlnAspPheGlnLeuValAlaGlyTr 336  
 252 GAGATGTCTACTGTG...GACCTTCTCGAGTTCCTCTCTAAAGGCCA 298  
 336 sProAsnLeuCysValGlnValSerThrTrpLysValGlnLeuGlnA 353  
 299 CCTTACCTCTGTGTGAGTGAAGACAGCTCGGAGAAGCTGAGCTGACAG 348  
 353 lAcysSerTrpAlaAspSerLeuGlyProPheLysAspAspMetLeuLeu 369  
 349 AGTCTGTGTGGCTGACTCCCTGGGGCCTCTCAAAAGACATGTGCTACG 398  
 370 ValGluMetLysThrGlyLeuAsnAsnThrSerValCysAlaLeuGlnTr 386  
 399 TTGAGACACAGAGGCCCGCAGACACAGATCTCTGTGCTTGGAAAC 448  
 386 oSerGlyCysThrProLeuProSerMetAlaSerThrArgAlaAlaArgL 403



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449 CAGTGGCTTACTTACTACCAACGCAAGCCCTCCAGAGGCGACCTCGCC 498
403 euGlygluLeuLeuGlnAspPheArgSerHisGlnCysMetGlnLeu 419
499 TTGGAGAGTACTTACTACAGACCTGCAAGGCGACGTGCTGACAGTA 548
420 TTPAsuAspAspMetGlySerLeuTIPAlaCysPrometAspLysTyr 436
549 TGG...GACGATGACTTGGAGCGCTATGGCGCTCCCGCATGACAAATA 595
436 rllhAsArgArgTIPValLeuValTIPLeuAlaCysLeuLeuAla 453
596 CMTCCACAAGCCCTGGGCGCTGTGGCTGCGCTCTACTCTTTCGGC 645
453 lAlaLeuPhePhePheLeuLeuLysAspArg... 466
646 CTGGCTTCCCTCATCTCTCTCTCAAAAAGATCACCGGAAAGGTT 695
467 .....LysAlaAlaArgGly.....Se 472
696 GCGTTGAGGCTCTGAACACAGACGCTCCGCGGCGCGCCCGCCAG 745
472 rArgTrAlaLeuLeuHisSerAlaAspGlyAlaGlyTyrGlnArgL 489
746 GCGCGCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 795
489 euVal.GlyAlaLeuAlaSerAla.LeuSerGlnMetProLeuArgVal 505
796 TGGTGGGCGCGCTGCG...TCGCTGTCCGACGCTTCCGCTGCGCTG 842
505 lAvAlaPleuTIPSerArgArgGluLeuSerAlaHisGlyAlaLeuAla 521
843 CCGTACACTGTTGACCGCGTGTGACTGACGCGCA.GGGGCGCTGGCT 891
522 TTPheHisGln 526
892 TGGTTCCGCGCGAG 906

Seq.name: gb_est2:BI282622

Seq_documentation_block:
LOCUS BI282622 619 bp mRNA linear EST 19-JUL-2001
DEFINITION UI-R-CW05-ccd-b-11-0-UI-s1 UI-R-CW05 Rattus norvegicus cDNA clone
ACCESSION BI282622
VERSION BI282622.1 GI:14933575
KEYWORDS EST.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 619)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 9704447
COMMENT Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@iuiw.uow.edu
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. The sequence tag present in the cDNA between the NotI site
and the oligo-dT track served to identify it as a clone from the
non-normalized rat aorta pool library cDNA library Preparation:
M.B. Soares Lab Clone distribution: clones will be available
through Research Genetics (www.resgen.com)

```

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Seq primer: MJ3 Forward
POLYA=Yes.
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                /clone_1lb="UI-R-CW05"
                /dev_stage="ADULT"
                /lab_host="DH10B (Life Technologies)"
                /note="Vector: pT7TD-Pac (Pharmacia) with a modified
                polylinker. Site.1: Not I. Site.2: Eco RI. The UI-R-CW05
                library is a non-normalized library constructed from the
                following rat aorta tissues: embryonic day 19, embryonic
                day 21, adult day 1, adult day 12, adult day 75, adult day
                200. For a detailed description of the library from which
                this clone was derived, please visit our web site at
                ratest.eng.uiowa.edu. The subtraction has been previously
                described in (Bonaldo, Lennon and Soares, Genome Research
                6:791-806, 1996)
                TAG_L1B=UI-R-CW05
                TAG_TISSUE=rat aorta pool
                TAG_SEQ=CTGTAGATC"
BASE COUNT 105 a 197 c 211 g 106 t
ORIGIN

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    Percent Similarity: 94.301 Percent Identity: 89.119

alignment_block:
US-09-899-471-2 x BI282622/rev ..
Align seg 1/1 to reverse of: BI282622 from: 1 to: 619

482 AspGlyAlaGlyTyrGluArgLeuValGlyAlaLeuAlaSerAlaLeu 498
619 GATGAGACATACATACAGACGCTGTGGCGCTGCGGCTGAG 570
498 rGlnMetProLeuArgValAlaValAspLeuTIPSerArgArgGluLeu 515
569 CCAGATGCACCTGGCGCTGCGGTGGACCTGTGGAGCGCGCGAGTGA 520
515 eAlaHisGlyAlaLeuAlaTIPheHisGlnArgArgGlyLeu 531
519 CCGCGACGAGCGCTGCGCTGCTCCACACAGACGCGCGGACCTG 470
532 GlnGluGlyValValIleLeuLeuPheSerProAlaAlaValAlaG1 548
469 CAGGAGATGGCGGTGCATCTCTCTCTCTCTCTCTCTCTCTCTCT 420
548 ncysGlnGlnTIPLeuGlnLeuGlnThValGluProGlyProHisAsp 565
419 GTGTGACAGTGGCTGCAGCTCCAGACGCTGAGCGCGGGGATGAG 370
565 lAlaValAlaTIPLeuSerCysValLeuProAspPheGlnGlnArg 581
369 CTGTGGCGCGCTGCTGACGCTGCTGCTGCTGCTGCTGCTGCTG 320
582 AlAThrGlyArgTyrValGlyValTyrPheAspGlyLeuHisAsp 598
319 GCGACGCGCGCTGACGCTGCTGCTGCTGCTGCTGCTGCTGCTG 270
598 pSerValProSerProPheArgValAlaProLeuPheSerLeuProthrg 615
269 CACTGTACCGCGCTGTTCGCGCGCGCGCTCTCTCTCTCTCTCT 220
615 lIneuProAlaPheLeuAspAlaLeuGlnGlyGlyCysSerThSerAla 631
219 AGCTGGCGCTTCTCTGATGACTGAGGAGACAGCTCCAGTCCGCC 170

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REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
1 (bases 1 to 702)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)  
Tissue Procurement: DCTD/DRP  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.lnl.gov>  
Plate: LNCM1922 row: c column: 05  
High quality sequence stop: 697.  
Location/Qualifiers

## FEATURES

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1. 702  
/organism="Homo sapiens"  
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/issue\_type="amelanotic melanoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: skin; Vector: pOTB7; Site\_1: XhoI; Site\_2:  
EcoRI; cDNA made by oligo-dT priming. Directionally cloned  
into EcoRI/XhoI sites using the following 5' adaptor:  
GGCAGCAG(G). Library constructed by Ling Hong in the  
laboratory of Gerald M. Rubin (University of California,  
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and  
Superscript II RT (Life Technologies). Note: this is a  
NIH-MGC library."

BASE COUNT 118 a 218 c 222 g 144 t  
ORIGIN

## alignment\_scores:

Quality: 872.50 Length: 232  
Ratio: 4.256 Gaps: 1  
Percent Similarity: 88.362 Percent Identity: 71.983

## alignment\_block:

us-09-899-471-2 x BM009552 ..

Align seg 1/1 to: BM009552 from: 1 to: 702

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323 ThrValasngluproglInaspPheglIneuValaIaIyHIsProasne 339
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6 ACTGTGACAAAGTTCTCGAGTTCACATGCTGCAAGGCCACCTAACT 55
339 uCyValaIglInValSerThrTrpGluLysValaIglIneuGlnaIaCysSert 356
|||||.....:|||||
56 CTGTGTTCAGGTGTAACAGCTCGAAGAGCTGCAGAGTGCCTTGT 105
356 rPaIaAspSerleuGlyProphelysAspAspMetleuLeuValaIuMet 372
|||||.....:|||||
106 GGCCTGCTCCTCTGGGCTCTCAAGACGAGTCTACTCTGTGGAGACA 155
373 LysThrclLysLeuAsnThrSerValaCysAlaLeuGluProSerGlyCY 389
|||.....:|||||
156 CGAGGCCCCAGGACAAACAGATCCCTGTGCTTGGAAACCCAGTGGCTG 205
389 sThrProleuProserMetAlaSerThrArgAlaIaArgleuGlyIug 406
|||||.....:|||||
206 TACTTCACTACCAAGCCCTCAGAGGCGCAGCTCCCTTGGAGAGT 255
406 lueLeuGlnaAspPheArgSerHisGlnCysMetGlnLeuTrpAsnsp 422
|||||.....:|||||
256 ACTTACTACAAAGACTGACAGTCCAGGCAAGTCTGACACTATGG...GAC 302
423 AspAsnMetclLysSerleuTrpAlaCysProMetAspLysTyrIleHisAr 439
|||||.....:|||||

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303 GATGACTTGGAGAGCGCTATGGCGCTGCCCATATGACAAATACATCCACAA 352
439 GARGTrpAlleuValaTrpLeuAlaCysleuLeuAlaAlaAlaLeuP 456
|||||.....:|||||
353 GCGCTGGGCGCTCGTGTGGCTGCTGCTTCTTGGCGGCTGCGCTT 402
456 hepPheLeuLeuLeuLysLysAspArgArgLysAlaAlaArgGlySer 472
|||.....:|||||
403 CCTTATCTCTCTTCAAAAAGATCAGCGCAAGCGGCCGAGGGGC 452
473 ArgThrAlaLeuLeuLeuHisSerAlaAspGlyAlaGlyTyrGluArgle 489
|||||.....:|||||
453 GCGCGGCTCTGCTCTCTACACAGCGGATGACTCGGGTTTCCAGCCCT 502
489 uValaIglAlaLeuAlaSerAlaLeuSerGlnMetProLeuArgValaIay 506
|||||.....:|||||
503 GGTGGGCGCCCTGCGGCTCGGCTGTGCAAGTCCGCTCGCGCTGCGG 552
506 AlAspLeuTrpSerArgArgGluLeuSerAlaHisGlyAlaLeuAlaTrp 522
|||||.....:|||||
553 TAGACCTGTGAGCCGTCGTGAACGTAGCGCGCAGGGCGCGGTGG 602
523 PheHisLysGlnArgArgArgIleLeuGlnGlyValaValaIlele 539
|||||.....:|||||
603 TTTCACGCGGACGCGGCCAGAACTGCAAGAGGCGGCGTGGTCTT 652
539 uLeuPheSerProAlaAlaValaIaGlnCysGlnGlnTrpLeuGln 554
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653 GCTCTTCTCTCCCGGTGGCGGTGGCTGTGACAGCAAGTGGCTTACAG 698

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OM of: US-09-899-471-2\_COPY\_21\_440 to: GenEmbl:\* out\_format: pfs

Date: Sep 29, 2002 1:03 AM

About: Results were produced by the GenCore software, version 4.5,  
Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:

-MODEL=ifam+pan.model -DEV=x1h  
-O=/cgn2.1/USPTO.spool/US09899471/runat\_27092002\_142439\_17908/app-query.fasta.1.2519  
-DB=GenEmbl -OFMT=fastap -SUFFIX=rge -GAPOP=12.000 -GAPEXT=4.000  
-MINMATCH=0.100 -LOOPEC=0.000 -LOOPEXT=0.000 -OCAPOP=4.500  
-OGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -FCAPOP=6.000  
-FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELAP=6.000  
-DELXT=7.000 -START=1 -MATRIX=blomsun62 -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR\_SCORE=pcr -THR\_MAX=100 -THR\_MIN=0  
-ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -HEAPSIZE=500  
-MINLEN=0 -MAXLEN=2000000000 -USER=US09899471@cgn1.1.11274  
-NCPI=6 -ICPU=3 -LONGLOG -DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30  
-NO\_XLPMX -WAIT -THREDS=1

Search information block:

Query: US-09-899-471-2\_COPY\_21\_440  
Query length: 420  
Database: GenEmbl:\*  
Database sequences: 1797656  
Database length: 187333701  
Search time (sec): 11857.370000

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b.ro:BC004759	+	2240.00	3193.34	1.7e-169	2015
b.pat:AX350976	+	2240.00	3192.10	1.9e-169	2214
b.pat:AX350978	+	1729.00	2461.29	9.9e-129	2094
b.pat:AX073993	+	1554.00	2210.05	9.7e-115	2255
b.pat:AX092430	+	1554.00	2209.56	1.0e-114	2380
b.pat:AX180776	+	1554.00	2209.56	1.0e-114	2380
b.pat:BC006411	+	1554.00	2209.10	1.1e-114	2507
b.pat:AX350973	+	1465.00	2082.40	1.3e-107	2308
b.pat:AX136541	+	1397.00	1984.33	3.6e-102	2499
b.pat:AX073996	+	1154.50	1640.26	5.3e-83	2076
b.pat:AX350975	+	1148.00	1629.43	2.1e-82	2109
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b.pat:AX073998	+	852.50	1207.96	6.4e-59	1725
b.pat:AX136589	+	464.00	659.82	2.2e-28	694
b.pat:AX026196	+	316.00	337.57	8.8e-14	191834
b.pat:AX018809	+	316.00	336.47	1.0e-13	216905
b.pat:AX024612	+	310.00	390.24	2.3e-13	166620
b.pat:AC007783	+	310.00	390.13	2.3e-13	168665
b.pat:AC022007	+	310.00	389.86	2.4e-13	173765
b.pat:AC026685	+	309.50	380.74	2.4e-13	145435
b.pat:AC024612	+	307.50	366.66	3.6e-13	166620
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b.pat:AF130972	+	123.00	169.46	0.4474	1206
b.pat:AC093548	+	124.00	136.12	32.17	42559
b.pat:AC093540	+	123.50	120.99	224.16	213045
b.pat:AC092466	+	123.00	120.85	228.22	216408
b.pat:AC010973	+	123.50	120.59	235.74	222605
b.pat:AF19049	+	122.50	163.92	0.9096	1500
b.ro:RRE65	+	122.50	160.30	1.45	2249
b.ro:AF333983	+	122.50	159.16	1.68	2554
b.pat:AC007603	+	122.00	119.54	269.74	196924

gb.ro:AF206720 + 120.00 155.42 2.71 2601 AF206720 Mus musculus Fe65  
gb.htg:AC103308 + 120.00 117.57 347.58 178349 AC103308 Rattus norvegicus  
gb.htg:AC060230 + 119.00 110.57 852.22 331909 AC060230 Homo sapiens chr  
gb.htg:AC073808 + 118.50 116.98 374.51 149727 AC073808 Mus musculus c1c  
gb.pr:AC073957 - 118.50 114.56 510.83 196204 AC073957 Homo sapiens BAC

seq\_name: gb.ro:BC004759

seq\_documentation\_block:

LOCUS BC004759 2015 bp mRNA linear ROD 12-JUL-2001  
DEFINITION Mus musculus, clone MGC:6973 IMAGE:3154616, mRNA, complete cds.  
ACCESSION BC004759  
VERSION BC004759.1 GI:13435809  
KEYWORDS MGC.  
SOURCE house mouse.  
ORGANISM Mus musculus.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 2015)

REFERENCE 1 (bases 1 to 2015)

AUTHORS Strausberg, R.

JOURNAL Direct Submission

Submitted (21-MAR-2001) National Institutes of Health, Mammalian  
Gene Collection (MGC), Cancer Genomics Office, National Cancer  
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
USA

REMARK  
COMMENT NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
Contact: MGC help desk  
Email: [cgabbs-remail.nih.gov](mailto:cgabbs-remail.nih.gov)

Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)

DNA Sequencing by: Baylor College of Medicine Human Genome  
Sequencing Center

Center code: BCM-HGSC  
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>  
Contact: [villalob@bcm.tmc.edu](mailto:villalob@bcm.tmc.edu)

Villalob, D.R., Luna, R.A., Hale, S.M., Huylk, S., Lu, X., Garcia,  
A.M., Holloway, M., Telford, B., Hodgson, A., Bouck, J., Yu, W.,  
Mizny, D.M., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found  
through the I.M.A.G.E. Consortium/LIML at: <http://image.liml.gov>  
Series: IRAC Plate: 6 Row: 3 Column: 3.

FEATURES  
source location/Qualifiers

1..2015  
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/clone="MGC:6973 IMAGE:3154616"  
/tissue\_type="Mammary tumor. Breast./EL: MMTV-Cre model. 10  
months old, gross tissue."  
/clone\_lib="NCI CGAP Mam3"  
/lab\_host="DH10B"  
/note="Vector: pCMV-SPORT6"  
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/db\_xref="GI:13435810"

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ASGAEVQINSYTPRROKELNITQDLDCRQLEVRDLSIOSCVLPLWLVSDGVNL  
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CDS  
379 a 616 c 595 g 425 t

BASE COUNT  
ORIGIN

## alignment\_scores:

Quality: 2240.00 Length: 444  
 Ratio: 5.359 Gaps: 1  
 Percent Similarity: 94.144 Percent Identity: 94.144

## alignment\_block:

US-09-899-471-2\_COPY\_21\_440 x BC004759

Align seg 1/1 to: BC004759 from: 1 to: 2015

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1 LeuGluaRgleuMetGluProGlnAspThrAlaArgCysSerLeuGlyLeu 17
237 CTGAGAGAACTGATGAGAGCTCAGAGACTGACAGCGCTGCTTGAAGCCT 286
17 uSerCysHisLeuTrpAspGlyAspValLeuCysLeuProGlySerLeu 34
287 CTCTGCGCAGCTGAGAGTGTGAGCTGCTGCTGCTGAGAGCCTCC 336
34 InSerAlaProGlyProValLeuValProThrArgLeuGlnThrGluLeu 50
337 AGTGTGCCCCAGGCCCTGTGCTAGTGCCTACCCGCTGACAGAGAGCTG 386
51 ValLeuArgCysProGlnLysThrAspCysAlaLeuArgValArgVala 67
387 GTGCTGAGGTGTCCACAGAGAGATTGCGCCCTGTGCTGCTGCTGCTG 436
67 lValHisLeuAlaValHisGlyHisThrAlaGluProGluGluAlaGly 84
437 GGTCCACTGGCCCGTCAGTGGGCGAGCTGGGCGAGAGCTGAAGAGCTGG 486
84 ySerAspSerGluLeuGlnLysArgAspAlaSerLeuGlnAlaGln 100
487 AGCTGATTCAGAACTCCAGAGAGTGTAGAGAGCCCTCTCTCCAGGCCAG 536
101 ValValLeuSerPheGlnAlaTyrProIleAlaArgCysAlaLeuLeu 117
537 GTGCTGCTCTCTCCAGGCCATCCAGCCGCTGCTGCTGCTGCTGCTG 586
117 uValGlnValProAlaAspLeuValGlnProGlyLysSerValGlySer 134
587 GGTCCAGAGTCCCGCTGACCTGAGCTGAGCTGCTGCTGCTGCTGCTG 636
134 lValAlaPheAspCysPheGlnAlaSerLeuGlyAlaGluValGlnIle 150
637 CGGATTTGAGCTGTTTGAAGGCTACTCTTGGGGCGTACAGATCTGG 686
151 SerTyrThrLysProArgTyrGlnLysLeuLeuAsnLeuThrGlnIle 167
687 TCCATACAGAGAGCCAGCTACAGAGAGCTCAACTCAGACAGAGAGCT 736
167 uPro..... 168
737 GCTGAGCTGCGAGGGGCTTGAAGTCCGGGAGAGATCCAGAGCTGCTGG 786
169 .....AspGlyAspAsnValLeuLeuThr 176
787 TCTGCGCCTGGCTCAATGTGTCTACAGATGAGATCTCTTCTGACACA 836
177 LeuAspValSerGluGluGlnAspPheSerPheLeuLeuTyrLeuArg 193
837 CTGATATCTCTGAGAGAGAGCTTACTTACTTACTTACTTACTTACTT 886
193 oValProAspAlaLeuLysSerLeuTrpTyrLysAsnLeuThrGlyPro 210
887 AGTCCCGAGAGCTCTCAATCTTGTGTACAAAAAAGCTGAGTGGAGCT 936
210 lAsnAlaLeuThrLeuAsnHisThrAspLeuValProCysLeuCysIle 226
937 AGAACAATTACTTAAACACACAGAGCTGTTCTCTGCTGCTGCTGCTG 986
227 ValTyrSerLeuGluProAspSerGluArgValGluPheCysProPhe 243
987 GTGGTGTGCTAGAGCAGACTGTGAGAGGCTGCAATCTGCGCCCTTCG 1036

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DEFINITION Sequence 10 from Patent WO0190358.

ACCESSION AX350976

VERSION AX350976.1 GI:18616352

KEYWORDS

SOURCE unidentified.

ORGANISM unidentified.

REFERENCE 1 (sites)

AUTHORS Gorman, D.M.

TITLE Mammalian receptor proteins; reagents and methods

JOURNAL Patent: WO 0190358-A 10 29-NOV-2001;

SCHERING CORPORATION (US)

FEATURES

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 VERSION AX350978.1 GI:18616354  
 KEYWORDS  
 SOURCE unidentified.  
 ORGANISM unidentified.  
 unclassified.

REFERENCE 1 (sites)  
 AUTHORS Gorman, D.M.  
 TITLE Mammalian receptor proteins: related reagents and methods  
 JOURNAL Patent: WO 0190358-A 12-29-NOV-2001;  
 SCHERING CORPORATION (US)  
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 VERSION AX073993.1 GI:12710225  
 KEYWORDS  
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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 REFERENCE 1 (bases 1 to 2255)  
 Presnell, S.R., Burkhead, S.K. and Powder, S.L.

TITLE Human cytokine receptor  
JOURNAL Patent: WO 0104304-A 18-JAN-2001;  
ZymoGenetics, Inc. (US)

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 REFERENCE 1 (bases 1 to 2380)  
 Eaton, D.L., Filvaroff, E., Gerritsen, M.E., Goddard, A.,  
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 Wood, W.I.  
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 Genentech, Inc. (US)  
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## KEYWORDS

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

## REFERENCE

1 (bases 1 to 2380)

Chen, J., Filvaroff, E., Fong, S., Goddard, A., Godowski, P. J., Grimaldi, C. J., Gunney, A. L., Li, H., Hillan, K. J., Tumas, D., van Lookeren, M., Vandlen, R. L., Watanabe, C. K., Williams, P. M., Wood, W. I.

11-17 and 11-17r homologous polypeptides and therapeutic uses thereof

Patent: WO 0146420-A 13 28-JUN-2001.

## JOURNAL

Genentech, Inc. (US)

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## REFERENCE

1 (sites)  
 Gorman, D.M.

## AUTHORS

JOURNAL Mammalian receptor proteins: related reagents and methods

PATENT: WO 0190358-A 7 29-NOV-2001;  
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DEFINITION Sequence 4 from Patent WO0104304.
ACCESSION AX073996
VERSION AX073996.1 GI:12710228
KEYWORDS
SOURCE
ORGANISM human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 1753)
AUTHORS Presnell,S.R., Burthead,S.K. and Pownder,S.L.
TITLE Human cytokine receptor
JOURNAL Patent: WO 0104304-A 4 18-JAN-2001;
Zymogenetics, Inc. (US)
FEATURES
location/Qualifiers
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COLPLVAVLDMRSRELSAGPVAMFHAQRQTYOEGGVVLLFSPGAVALCSERLQD
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Percent Similarity: 79.706 Percent Identity: 65.588
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2 GAGAGCGCTAGAGATGCTCTCTCCAGGCCCAAGTCGTCTCTCTCCA 51
106 nAlaTyrProIleAlaArgCysAlaLeuLeuGlnValGlnValProAla 123
52 GGCCTACCTTACTCCCGCTGCTCTCTGAGAGGTCAAGTGGCTGTG 101
123 spleuValGlnProGlyGlnSerValGlySerAlaValPheAspCysPhe 139
102 CCGTGTGCACTTGGTGTGCTGTGGGCTCTGTGTATATACGTCTTC 151
140 GluAlaSerLeuGlnAlaGlnValGlnIleTyrPheTyrLysProArg 156
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156 gTyrGlnLysGlnLeuAsnLeuThrGlnGlnLeuPro..... 168
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169 .....AspGlyAspAsnValLeuLeuThrLeuAspValSer 180
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214 euAsnHisThrAspLeuValProCysLeuCysIleGlnValTrpSerLeu 230
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LOCUS AX073995 2076 bp DNA linear PAT 06-FEB-2001
DEFINITION Sequence 3 from Patent WO0104304.
ACCESSION AX073995
VERSION AX073995.1 GI:12710227
KEYWORDS
SOURCE
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 2076)
AUTHORS Presnell,S.R., Burkhead,S.K. and Powder,S.L.
TITLE Human cytokine receptor

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JOURNAL Patent: WO 0104304-A 3 18-JAN-2001;
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variation
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BASE COUNT 232 a 273 c 399 g 265 t 907 others
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18 rCysHisLeuTrpAspGlyAspValLeuCysLeuProGlySerLeuGln 35
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364 CARCCNARGTNGTNTYTMNSNTTYCARCNCNTAYCCNACNGCNGNGTNGT 413
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seq_documentation block:
LOCUS AX073998 1725 bp DNA linear PAT 06-FEB-2001
DEFINITION Sequence 6 from Patent WO0104304.
ACCESSION AX073998
VERSION AX073998.1 GI:12710230
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
artificial sequence.
REFERENCE
1 (bases 1 to 1725)
AUTHORS Presnell,S.R., Burkhead,S.K. and Powder,S.L.
TITLE Human cytokine receptor
JOURNAL Patent: WO 0104304-A 6 18-JAN-2001;
ZymoGenetics, Inc. (US)
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 DEFINITION Sequence 511 from Patent EP1067182.  
 ACCESSION AX136589  
 VERSION AX136589.1 GI:14272993

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 694)  
 Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and  
 Hayashi,K.

TITLE Secretory protein or membrane protein  
 JOURNAL Patent: EP 1067182-A 511 10-JAN-2001;  
 Helix Research Institute (JP)

FEATURES

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 Location/Qualifiers

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 Ratio: 3.803 Gaps: 1  
 Percent Similarity: 85.915 Percent Identity: 69.014

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 568 CTCACGAGCCCAAGTCTGCTCTCTTACAG.CCCTACCTACTGCCCCGCTG 616  
 113 sAlaLeuLeuGluValGlnValProAlaAspLeuValGlnProGlyLns 130  
 617 CTTCTGCTGTGANGTCAAGTCCCTGCTG.CCTGTGCAATTGGNCAAT 665  
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 DEFINITION Homo sapiens chromosome 3 clone RP11-474F16 map 3p, WORKING DRAFT  
 SEQUENCE, 22 unordered pieces.  
 ACCESSION AC026196  
 VERSION AC026196.3 GI:8101230

KEYWORDS

HTG; HTGS\_PHASE1; HTGS\_DRAFT.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 191834)  
 Cai,T., Dong,X., Gao,Q., Gu,J., Gong,J., He,F., Kang,N., Lu,T.,  
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TITLE Chromosome 3p genomic sequence  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 191834)

AUTHORS

Wang,R., Hu,S., Dong,W., Wang,J., Zhang,Y., Zhang,H., Liu,B.,  
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 and Yang,H.

TITLE

JOURNAL

REFERENCE

AUTHORS

Direct Submission  
 Submitted (21-MAR-2000) Human Genomic Center, Institute of  
 Genetics, Chinese Academy of Sciences, Datun Road, Beijing, Beijing  
 100101, P.R.China  
 On May 29, 2000 this sequence version replaced gi:8050894.

Genome Center

COMMENT

\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 22 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
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DT 26-MAR-2002 (first entry)  
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DE Mouse DNAX cytokine receptor subunit 7 (DCRS7) CDNA.  
XX  
KW Mouse; DNAX cytokine receptor subunit 7; DCRS7; phosphate labelling; ss;  
KM gene therapy; protein therapy; immunological disorder.  
XX  
OS Mus musculus.  
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XX  
PD 29-NOV-2001.  
XX  
PE 23-MAY-2001; 2001MO-US16767.  
XX  
PR 24-MAY-2000; 2000US-206862P.  
XX  
PA (SCHE ) SCHERING CORP.  
XX  
PI Gorman DK;  
XX  
DR WPI: 2002-106198/14.  
XX  
DR P-PSDB: AA011354.  
XX  
PT Isolated antigenic human or mouse DNAX receptor subunit-like  
PT polypeptide useful for detecting antibodies generated in response to  
PT presence of increased protein levels or immunological disorders -  
XX  
XX Disclosure: Page 17-20; 148pp; English.  
XX  
PS The invention relates to primate and rodent DNAX cytokine receptor  
PS subunit (DCRS) polypeptides and the polynucleotides encoding them. The  
CC subunit (DCRS) polypeptides and the polynucleotides encoding them. The  
CC receptors, or their portions may be useful as phosphate labelling enzymes  
CC to label general or specific substrates. The subunits may also be  
CC functional immunogens to elicit recognising antibodies, or antigens  
CC capable of binding antibodies. A combination, e.g., including a DCRS can  
CC be used as an immunogen for the production of antisera or antibodies  
CC capable of distinguishing between other cytokine receptor family members.  
CC A purified DCRS can also be used as a reagent to detect antibodies  
CC generated in response to the presence of elevated levels of expression,  
CC or immunological disorders which lead to antibody production to the  
CC endogenous receptor. This sequence represents CDNA encoding the mouse  
XX DCRS7 polypeptide.  
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AC AAS18133;
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DE Mouse DCRS7 reverse translation generic cDNA.
KW Mouse; DNAX cytokine receptor subunit 7; DCRS7; phosphate labelling; ss;
KW gene therapy; protein therapy; immunological disorder.
OS Mus musculus.
PN MO200190358-A2.
PD 29-NOV-2001.
PE 23-MAY-2001; 2001MO-US16767.
PF 24-MAY-2000; 2000US-206862P.
PR (SCHE ) SCHERING CORP.
PA Gorman DM;
PI
XX WPI; 2002-106198/14.
XX Isolated antigenic human or mouse DNAX receptor subunit-1-like
XX polypeptide useful for detecting antibodies generated in response to
XX presence of increased protein levels or immunological disorders -
XX Disclosure; Page 20-21; 148pp; English.
PS
XX

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CC The invention relates to primate and rodent DNA cytokine receptor  
 CC subunit (DCRS) polypeptides and the polynucleotides encoding them. The  
 CC receptor, or their portions may be useful as phosphate labelling enzymes  
 CC to label general or specific substrates. The subunits may also be  
 CC functional immunogens to elicit recognising antibodies, or antigens  
 CC capable of binding antibodies. A combination, e.g., including a DCRS can  
 CC be used as an immunogen for the production of antisera or antibodies  
 CC capable of distinguishing between other cytokine receptor family members.  
 CC A purified DCRS can also be used as a reagent to detect antibodies  
 CC generated in response to the presence of elevated levels of expression,  
 CC or immunological disorders which lead to antibody production to the  
 CC endogenous receptor. This sequence represents mouse DCRS7 reverse  
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211  snLThrLeuAsnHisThrAspLeuValProCysLeuCysIleGlnVal 227
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
764  AYTHACNTNTAAAYCAACNGAYTCNGTNCNTGTYTNTGATATHCARGTN 813
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
228  TrpSerLeuGluProAspSerGluArgValGluLeuPheCysProPheArg 244
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
814  TGGWSNTNTNGARCCNGAYWSNGARMGNTNGARTTYTGCCNTTYTMGNGA 863
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
244  uAspProGlyAlaHisArgAsnLeuTyrPheHisIleAlaArgLeuArgVal 261
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
864  RGAYCCNGCNGCNCAYMGNAATYTTTGCAATATHCNMGNTNMGNGTNY 913
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
914  TWSNCCNGCNGTNTGCGCARTNGAYGNCNCNTGYTGYYTNCNCGNAR 963
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
278  ValThrLeuCysTrpGlnAlaProAspGlnSerProCysGlnProLeuVal 294
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
964  GTNACNTNTNTGTCGARGCNGCNGAYCARMSNCCNTGYTCARCCNTYTGT 1013
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
294  LProProValProGlnLysAsnAlaThrValAsnGluProGlnAspPheG 311
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1014  NCNCCNGTNCNCARARARAYGNCNACNGTNAATGARGCNCARARAYTTC 1063
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
311  LLeuValAlaGlyHisProAsnLeuCysValGlnValSerThrTrpGlu 327
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1064  ARYTNTGNCNGCNGCAYCCNAAYTNTGYTNCARGTWSNACNTGGGAR 1113
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1164  RGAYGAYATGTYTNTNTNGARATGARGARACNGGNTTNAAYATACMSNG 1213
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1214  TMTGYCANTYNGARCCNWSNGNTGYACNCCNTYTNCCNWSNATGCGMSN 1263
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378  ThrArgAlaAlaArgLeuGlyGluGluLeuLeuGlnAspPheArgSerH 394
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1264  ACNMGNGCNGCNGNNTYNGNGARGARTYTNTCARGATYTTTGMWSNCA 1313
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
394  sGlnCysMetGlnLeuTyrPAsnAspAspAspMetGlySerLeuTrpAlaC 411
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1314  YCARGTATATGCAATYTNCGAAYGAYATATGAGNNSYTTNTGGCGTNT 1363
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
411  ySPrometAspLysTyrIleHis 418
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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seq\_documentation\_block:

ID AAC85027 standard; cDNA; 2255 BP.

AC AAC85027;

DT 08-MAY-2001 (first entry)

DE Human cytokine receptor zcytor1a encoding cDNA.

XX

Cytokine receptor; Zcytor14; human; inflammation; rheumatoid arthritis;  
antiinflammatory; gene therapy; vaccine; ss.

Homo sapiens.  
Key Location/Qualifiers  
CDS 3..2232  
T //tag- a  
T /product= "Zcytor14"

MO200104304-A1.

18-JAN-2001.

30-JUN-2000; 2000MO-US18383.

07-JUL-1999; 99US-0348854.

(Zymo) ZYMOGENETICS INC.

Presnell SR, Burkhead SK, Powder SL;

WPI; 2001-112618/12.

P-PSDB; AAB61880.

New polypeptide encoding a human cytokine receptor zcytor14, for  
treating inflammation e.g. rheumatoid arthritis -

Claim 8; Page 87-91; 112pp; English.

The invention provides a new human cytokine receptor designated zcytor14.  
Zcytor14 can be expressed by standard recombinant methodology. The  
encoding nucleic acid is useful for detecting the expression of a  
Zcytor14 gene in a biological sample. Anti-Zcytor14 antibodies can be  
used to screen biological samples in vitro for the presence of Zcytor14.  
Proteins, polypeptides and peptides having Zcytor14 activity can be  
administered to a subject who lacks an adequate amount of this  
polypeptide, for treating inflammation and conditions such as rheumatoid  
arthritis. In contrast, Zcytor14 antagonists (e.g. anti-Zcytor14  
antibodies) can be used to treat a subject who produces an excess of  
Zcytor14. Zcytor14 nucleotide sequences can also be used to provide  
Zcytor14 to a subject. The present sequence represents a cDNA encoding  
the human cytokine receptor zcytor14.

Sequence 2255 BP; 369 A; 748 C; 703 G; 435 T; 0 other;

Alignment scores:

Quality: 1554.00 Length: 433  
Ratio: 4.281 Gaps: 3  
Percent Similarity: 83.834 Percent Identity: 67.667

Alignment block:  
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Align seg 1/1 to: AAC85027 from: 1 to: 2255

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214 CTGAGAGGCTGTGGGCTCAGACGCTACCCACTGCTCCGGGCT 263  
17 UserCysHisLeuTrpAspGlyAspValLeuLysLeuProGlySerLeu 34  
|||||.....  
264 CTCTGCGGCTCTGGGACAGTACATCTGCTGCTGGGGACATCG 313  
34 InSerAlaProGlyProValLeuValProThrArgLeuGlnThrGluLeu 50  
|||||.....  
314 TGCTGCTCCGGGCCCCGTGCTGGCGCTACGACCTGACAGAGAGCTG 363  
51 ValLeuArgCysProGlnLysThrAspGlyAlaLeuArgValArgVal 67  
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364 GTGCTGAGGTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 413

67 ValHisLeuAlaValHisGlyHisTrpAlaGluProGluLys..... 81  
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414 TGTCACCTTGGCCGTGCTGAGGCTGGAGAGAGCTGAAAGATGAGAGAA 463  
82 ....AlaGlyLysSerAspSerGluLeuGlnGlnSerArgAsnAlaSer 96  
:|||||.....  
464 AGTTGGAG 513  
97 LeuGlnAlaGlnValValLeuSerPheGlnAlaTrpProIleAlaArgC 113  
|||||.....  
514 CTCCAGGCCCAAGTCTGCTGCTCCAGGCTTACCTTACCTGCGCCGCTG 563  
113 salAlaLeuGlnValGlnValProAlaAspLeuValGlnProGlyGln 130  
:|||||.....  
564 GGTCTGCTGGAGAGCTGCAAGTCTGCTGCTGCTGCTGCTGCTGCTGCT 613  
130 exValGlySerAlaValAlaPheAspCysPheGlnAlaSerLeuGlyAla 146  
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614 CTGTGGCTCTGTGTRATGATGCTGCTTCCAGGCTGCTGCTGCTGCTG 663  
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664 GTACGATCTGTGCTATACTACAGCCAGGTACAGAGAGAGAGAGAGAG 713  
163 urhGlnGlnLeuPro.....AspGly 171  
|||||.....  
714 CACAGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 763  
171 sPaValLeuLeuThrLeuAspValSerGlnGlnGlnAspPheSerPhe 187  
|||||.....  
764 ACACGCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 813  
188 LeuLeuTrpLeuArgProValProAspAlaLeuLysSerLeuTrpTyr 204  
|||||.....  
814 TCCCTGATCTGATGATGATGATGATGATGATGATGATGATGATGAT 863  
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1064 GGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1113  
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:|||||.....  
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:|||||.....  
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321 aGlnValSerThrTrpGluLysValGlnLeuGlnAlaCysSerTrpAla 337  
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338 AspSerLeuGlyProPheLysAspAspMetLeuLeuValGlnLysTrp 354  
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1314 CCCCCAGGACACAGATCCCTGTCCTTGGAACCCAGTGGCTGACTT 1363
371 roleProserMetalaserThrArgAlaAlaArgLeuGluGluLeu 387
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388 LeuGlnAspPheArgSerHisGlnCysMetGlnLeuTrpAsnAspAsp 404
1414 CTACAGAGACCTCAGTACAGGACGCTGTGCAGCTATGG...GACGATGA 1460
404 nMeClySerLeuTrpAlaCysProMetAspLysTrpLeuHisArgArg 420
1461 CTGGGAGCGCTATGGGCTGCCCTGGACCAATAATCATCCACAAGCCG 1509

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eq_documentation_block:
D AAS46223 standard; cDNA: 2380 BP.
X
X AAS46223:
X
X 18-DEC-2001 (first entry)
X
X Human DNA encoding PRO polypeptide sequence #299.
X
X PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; sw;
X dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
X blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
X adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder;
X PCR primer.
X
X Homo sapiens.
X
X WO200168848-A2.
X
X 20-SEP-2001.
X
X
X 28-FEB-2001; 2001MO-US06520.
X
X 01-MAR-2000; 2000MO-US05801.
X 02-MAR-2000; 2000MO-US05861.
X 03-MAR-2000; 2000US-187202P.
X 06-MAR-2000; 2000US-186968P.
X 14-MAR-2000; 2000US-189320P.
X 14-MAR-2000; 2000US-189328P.
X 15-MAR-2000; 2000MO-US06884.
X 21-MAR-2000; 2000US-190828P.
X 21-MAR-2000; 2000US-191007P.
X 21-MAR-2000; 2000US-191048P.
X 21-MAR-2000; 2000US-191314P.
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X 29-MAR-2000; 2000US-193032P.
X 29-MAR-2000; 2000US-193053P.
X 30-MAR-2000; 2000MO-US08439.
X 04-APR-2000; 2000US-194447P.
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X 11-APR-2000; 2000US-196187P.
X 11-APR-2000; 2000US-196690P.
X 11-APR-2000; 2000US-196820P.
X 18-APR-2000; 2000US-198121P.
X 18-APR-2000; 2000US-198585P.
X 25-APR-2000; 2000US-199397P.
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X 03-MAY-2000; 2000US-201516P.
X 17-MAY-2000; 2000MO-US13705.
X 22-MAY-2000; 2000MO-US14042.
X 30-MAY-2000; 2000MO-US14941.
X 02-JUN-2000; 2000MO-US15264.
X 05-JUN-2000; 2000US-2098332P.

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PR 28-JUL-2000; 2000MO-US20710.
PR 22-AUG-2000; 2000US-0644848.
PR 24-AUG-2000; 2000MO-US23328.
PR 08-NOV-2000; 2000MO-US30952.
PR 01-DEC-2000; 2000MO-US32678.
PR 20-DEC-2000; 2000MO-US34956.
XX
XX (GETH ) GENENTECH INC.
XX
XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL,
XX Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
XX WPI; 2001-602746/68.
XX P-PSDB; AAU29322.
XX
XX Novel nucleic acids encoding PRO polypeptides, used to diagnose the
XX presence of tumours, such as prostate and breast tumours, in mammals and
XX to screen for modulators of the compounds -
XX
XX Claim 2; Fig 597; 774pp; English.
XX
XX Sequences AAS45925-AAS46231 represent DNA molecules encoding and PCR
XX primers for PRO polypeptides of the invention. The sequences of the
XX invention can be used to detect the presence of a tumour in a mammal by
XX comparing the level of expression of a PRO polypeptide in a test sample
XX of cells from the animal and a control sample of normal cells, whereby a
XX higher level of expression in the test sample indicates the presence of a
XX tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep,
XX pigs, goats and rabbits but are preferably human. The polypeptides can be
XX used to stimulate tumour necrosis factor (TNF) alpha release from human
XX blood, when contacted with it. A specific polypeptide can be used to
XX stimulate the proliferation or differentiation of chondrocyte cells. The
XX PRO proteins can be used to determine the presence of tumours and also
XX susceptibility to tumour development, particularly adrenal, lung, colon,
XX breast, prostate, rectal, cervical, or liver tumours, in mammalian
XX subjects. The oligonucleotide probes specific for the PRO nucleic acids
XX can be used for genetic analysis of individuals with genetic disorders.
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XX Sequence 2380 BP; 411 A; 776 C; 743 G; 450 T; 0 other;
XX
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XX alignment_scores:
XX      Quality: 1554.00      Length: 433
XX      Ratio: 4.281          Gaps: 3
XX      Percent Similarity: 83.834      Percent Identity: 67.667
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XX alignment_block:
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XX
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XX
XX 34 InsertAlaProGlyProValLeuValProThrArgLeuGlnThrGluLeu 50
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XX 67 ValHisLeuAlaValHisGlyHisTrpAlaGluProGluGlu..... 81
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XX 493 TGTCCACTTGGCGGCTGATGGGAGAGAGAGAGAGAGAGAGAGAGAGAG 542
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XX 82 .....AlaGlyLysSerAspSerGluLeuGlnGluSerArgAsnAlaSer 96
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543 AGTTGAGAGACAGCTGACTCAGGGGTGAGAGACCTAGAAATGCTCT 592  
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 1393 CCCCAGAGACAAAGATCTCTGTGCTGTGAGACCACTGCTGACTT 1442  
 371 rOleuProSerMetAlaSerThrArgAlaAlaArgLeuGlyGluLeu 387  
 1443 CACTAACCCAGAAAGCTTCACAGAGGCGAGTCTGCTGAGAGTACTTA 1492

388 LeuGlnAspPheArgSerHisGlnCysMetGlnLeuThrPasnAspAspAs 404  
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 AC AA09515;  
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 DT 24-OCT-2001 (first entry)  
 XX  
 DE Human cDNA encoding Interleukin 17 receptor, IL-17RH2.  
 XX  
 KW Human; Interleukin-17 receptor; IL-17RH2; agonist; antagonist; ss;  
 KW PRO20040; DNA 164625-2890; systemic lupus erythematosus;  
 KW rheumatoid arthritis; osteoarthritis; diabetes mellitus;  
 KW allergic disease; asthma; demyelinating disease;  
 KW degenerative cartilaginous disorder; transplantation associated disease.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
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 FT mat\_peptide 293..2344  
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 PN W0200146420-A2.  
 XX  
 PD 28-JUN-2001.  
 XX  
 PE 20-DEC-2000; 2000WO-US34956.  
 XX  
 PR 23-DEC-1999; 99US-0172096.  
 PR 30-DEC-1999; 99WO-US31274.  
 PR 11-JAN-2000; 2000US-0175481.  
 PR 18-FEB-2000; 2000WO-US04341.  
 PR 02-MAR-2000; 2000WO-US05841.  
 PR 21-MAR-2000; 2000US-0191007.  
 PR 21-MAR-2000; 2000WO-US07532.  
 PR 02-JUN-2000; 2000WO-US15264.  
 PR 22-JUN-2000; 2000US-0213087.  
 PR 22-AUG-2000; 2000US-0644848.  
 PR 24-AUG-2000; 2000WO-US33328.  
 PR 24-OCT-2000; 2000US-0242837.  
 PR 10-NOV-2000; 2000WO-US30873.  
 PR 28-NOV-2000; 2000US-0253646.  
 PR 01-DEC-2000; 2000WO-US32678.  
 XX  
 PA (GENTECH ) GENENTECH INC.  
 XX  
 PI Chen J, Filvaroff E, Fong S, Goddard A, Godowski PJ, Grimaldi CJ,  
 PI Gurney AL, Li H, Hillan KJ, Tamas D, Van Lookeren M, Vandlen RJ,  
 PI Watanabe CK, Williams PM, Wood WI, Yansura DG;  
 DR WPI: 2001-451708/48.  
 DR P-PSDB: AA004956.  
 XX  
 PT Novel PRO polypeptides homologous to interleukin-17, useful for the  
 PT diagnosis and treatment of immune related disease e.g. rheumatoid  
 PT arthritis and diabetes -  
 XX

PS Claim 1; Fig 13; 188bp; English.

XX The sequence (DNA 164625-2890) encodes a PRO polypeptide (PRO20040) which is the human Interleukin 17 receptor, IL-17R2. A composition containing ant/agonists to the PRO polypeptides or individual components are useful for treating a mammal with an immune related disease, e.g. systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, an idiopathic chronic arthritis, a spondyloarthropathy, systemic sclerosis, vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, a demyelinating disease, an autoimmune or immune-mediated skin disease, contact dermatitis, an allergic disease e.g. food hypersensitivity, asthma, a transplantation associated disease, or a chronic inflammatory demyelinating polyneuropathy. Treating a degenerative cartilaginous disorder comprises administering a PRO1031 or PRO1122 polypeptide agonist, or antagonist to the mammal. Numerous examples of the diseases and disorders are given in the specification.

Sequence 2380 BP; 411 A; 776 C; 743 G; 450 T; 0 other;

Alignment\_scores:  
Quality: 1554.00 Length: 433  
Ratio: 4.281 Gaps: 3  
Percent Similarity: 83.834 Percent Identity: 67.667

Alignment\_block:  
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Align seg 1/1 to: AAS09515 from: 1 to: 2380

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17 uSerCysHisLeuTrpAspGlyAspValLeuCysLeuProGlySerLeu 34
343 CTCTGCGCGCTCTGGGACAGTACATCTGCTGCTGCGGAGACATCG 392
34 InSerAlaProGlyProValLeuValProThrArgLeuGlnThiGluLeu 50
393 TGCCTGCTCCGGGCCCCGCTGCTGGCGCTACGACCTGCTGCTGCTG 442
51 ValLeuArgCysProGlnLysThrAspCysAlaLeuArgValArgVala 67
443 GTGCGAGGTGCGCAGAGAGACCGACTGACCTGCTGCTGCTGCTGCTG 492
67 lValHisLeuAlaValHisGlyHisTrpAlaGluProGluGlu..... 81
493 TGTCACCTGGCGCTGACATGGGCACTGGAGAGCGTGAAGATGAGGAA 542
82 ....AlaGlyLysSerAspSerGluLeuGlnLysSerArgAsnAlaSer 96
543 AGTTGGAGGACGACCTGACTCAGGGGTGAGAGAGCTTAGAATGCTCT 592
97 LeuGlnAlaGlnValValLeuSerPheGlnAlaTyrProIleAlaArgC 113
593 CTCACGGCCCAAGTGTGCTCTCTCTCCAGGCTTACCTTACCTGCGCTG 642
113 sAlaLeuLeuGlnValGlnValProAlaAspLeuValGlnProGlyGln 130
643 CGTCCCTGCTGGAGTGACAGTGGCTGCTGCTGCTGCTGCTGCTGCTG 692
130 eValGlySerLysAlaValPheAspCysPheGlnAlaSerLeuGlyAla 146
693 CTGTGGGCTCTGTGTATATATGACTGCTTGGAGGCTGCTGCTGCTG 742
147 ValGlnIleTrpSerTyrThrLysProArgTyrGlnLysGluLeuAsn 163
743 GTAGCAATCTGCTCTATATCTCAGCCAGGTACGAGAGAGACTCAACA 792
163 uThrGlnGlnLeuPro.....AspGlyA 171

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793 CACACAGACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 842
171 sPAsnValLeuLeuThrLeuAspValSerGluGlnGlnAspPheSerPhe 187
843 ACAACGCAATCTGTGTGTATATGACTGCTTGGAGGCTGCTGCTGCTG 892
188 LeuLeuTyrLeuArgProValProAspAlaLeuLysSerLeuTyrTyr 204
893 TCCTGTACAGCAATATCAGTGTCCAGGCCCCCAAAACCCGCTGACAA 942
204 sAsnLeuThrGlyProGlnAsnIleThrLeuAsnHisThrAspLeuVal 221
943 AAACCTGACAGGAGCCGACATCATCTGATACCAACACACAGACTGTTC 992
221 rOCysCysLeuGlnValTyrPheSerLeuGlnProAspSerGluArgVal 237
993 CTTGCTCTTATTCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1042
238 GluPheCysProPheArgGluAspProGlyValHisArgAsnLeuTrp 254
1043 AACATGCCCCCTTCAGAGGAGGACCCCGCCACACCAACCTGTGCA 1092
254 sIleAlaArgLeuArgValLeuSerProGlyValTyrPheLeuAspAla 271
1093 AGCGCCGCACTGCGACTGCTGACCTTCAGAGTGGCTGTGGAGCGAC 1142
271 rOCysCysLeuProGlyLysValThrLeuCysTyrPheAlaProAspGln 287
1143 CGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1192
288 SerProCysGlnProLeuValProProValProGlnLysAsnAlaTyr 304
1193 GACCCCTGCCAGCCACTGTGTCACCGCTTCTCCGGGAGAACCTACTGT 1242
304 lAsnGluProGlnAspPheGlnLeuValAlaGlyHisProAsnLeuCys 321
1243 GGAACAAGTCTTCGAGTTCATGTTGTAAGGCCACCTTAACCTCTGTG 1292
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354 rGlyLeuAsnAsnThrSerValCysAlaLeuGluProSerGlyCysTrp 371
1393 CCCCAGAGAACAGATCCCTGTGCTGCTTGGAAACCCAGTGTACTT 1442
371 rOLeuProSerMetAlaSerThrArgAlaAlaArgLeuGlyGlnLeu 387
1443 CACTACCCACAAAGCTCCACAGAGGACAGCTCGCTGGAGAGTACTTA 1492
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1493 CTACAAGACCTGCAGTCAAGGCACTGTCTGCAAGGCTG...GACGAGA 1539
404 mMetGlySerLeuTrpAlaCysProMetAspLysTyrIleHisArgArg 420
1540 CTTGGGAGCGCTATGGGCTGCCCCATGAGCAATATCATCAACAAGCC 1588
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seq_documentation_block:
ID AAF92138 standard; cDNA: 2380 BP.
XX AAF92138:
AC
XX
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XX
DT 15-MAY-2001 (first entry)
XX
DE Human PRO20040 cDNA.

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KM Human; PRO protein; mapping; ss.  
KS Homo sapiens.  
KN WO200116318-A2.  
KD 08-MAR-2001.  
KF 24-AUG-2000; 200OMO-US23328.  
KX 01-SEP-1999; 99MO-US20111.  
KR 15-SEP-1999; 99MO-US21090.  
KR 07-DEC-1999; 99DS-0169495.  
KR 09-DEC-1999; 99DS-0170262.  
KR 11-JAN-2000; 200OMS-0175431.  
KR 18-FEB-2000; 200OMO-US04341.  
KR 18-FEB-2000; 200OMO-US04342.  
KR 22-FEB-2000; 200OMO-US04414.  
KR 01-MAR-2000; 200OMO-US05601.  
KR 03-MAR-2000; 200OMS-0187202.  
KR 25-APR-2000; 200OMS-0199397.  
KR 22-MAY-2000; 200OMO-US14042.  
KR 05-JUN-2000; 200OMS-0209832.  
KA (GETH ) GENENTECH INC.  
KI Eaton DL, Flyvareff E, Gerritsen ME, Goddard A, Godowski PJ,  
KI Grimaldi CJ, Gurney AL, Watanabe CK, Wood WI;  
KI MPI: 2001-183260/18.  
KI P-PSTB; AAB87606.  
KT Eighty four nucleic acids encoding PRO polypeptides, useful in  
KT molecular biology, including use as hybridization probes, and in  
KT chromosome and gene mapping.  
KU Claim 2; Fig 161; 27bp; English.  
KV The present sequence is the coding sequence for a human PRO polypeptide  
KV (secreted and transmembrane). The PRO protein, and PRO agonists PRO  
KV antagonists or anti-PRO antibodies are useful for preparation of a  
KV medicament useful in the treatment of a condition which is responsive to  
KV the PRO protein, agonists, antagonists or anti-PRO antibodies. The PRO  
KV protein may also be employed as molecular weight markers for protein  
KV electrophoresis. The PRO coding sequence has applications in molecular  
KV biology, including use as hybridisation probes, and in chromosome and  
KV gene mapping.

X Sequence 2380 BP; 411 A; 776 C; 743 G; 450 T; 0 other;

Alignment\_scores:  
Quality: 1554.00 Length: 433  
Ratio: 4.281 Gaps: 3  
Percent Similarity: 83.834 Percent Identity: 67.667

Alignment\_block:  
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293 CTGGAGAGCGCTTGTGGGGCCTCAGAGACGCTACCAACACTGCTCCGGGCT 342  
  
17 uSeCYHisLeuTrpaspGlyaspValIeuCysLeuProGlySerIeu 34  
|||||::: |||||::: |||||  
343 CTCCTGCAGCGCTCTGGGACATGACATACACTGCTGCCCTGGGGACATCG 392  
  
34 InseRalaproGlyProValIeuValProthrArGLeuGIInThrGluLeu 50  
|||||::: |||||::: |||||  
393 TGCGTGCTCCGGGGCCCCGCTGCGGCTACGACACCTGCAGACAGACACTG 442

51	ValIeuAaYgCyPProGlnIysTrpAspCysAlaIleuArGVala	67
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443	GTGGAGAGTGGCAGAGAGAGACCGATGTGACTGTGTCTGGCTGTGGC	492
67	IValHisIleuAlaValHisGlyHisTrpAlaGlnProGlnIu	81
493	TGTGCACCTGGCCGTGCATACGGCAGCTGGAGAGCCTGAATATGAGAA	542
82	.... AlaGlyIysSerAspSerGlnIleuGlnIuSerArGAsnAlaSer	96
543	AGTTGGAGAGACACTGTACTAGGGGTGGAGAGCGCTAGAAATGCCCT	592
97	IeuGlnAlaGlnValIleuSerPheGlnAlaTrpProIleAlaGcy	113
593	CTCCAGGCCCAAGTGGTGTCTCTCCACAGCCCTACCTACTGGCCGCTG	642
113	sAlaIleuIeuGlnValGlnValProIlaAspIleuValGlnProGlyGlns	130
643	CGTCTGCTGGAGGTGCACAGTGCCTCTGCTCCCTGTGTGCAGTTGGTCA	692
130	eValGlySerAlaValPheAspCysPheGlnAlaSerIleuGlyAlaIu	146
693	CTGGGGCTGTGTGATATGACTGCTTCAGAGCTGCCCTTAGGGAGTAG	742
147	ValGlnIleTrpSerTrpThrIysProArGTrGlnIysGlnIleuAsnIe	163
743	GTAGAAATCTGGTCTATCTACTACGCCAGGTAGCAGAAAGAACTCAACA	792
163	uThrGlnGlnIeuPro..... AspGlyA	171
793	CACACAGAGCTGCTGCTGCCCTGGCTCAACGTGTACGACAAATGTG	842
171	sPasnValIleuIleuThrIleuAspValSerGlnIuGlnIAspPheSerPhe	187
843	ACAACGGTCACTGGTCTTGCAATGTCTGAGAGACAGCACTTGGCCCTC	892
188	IeuIleuTrpIleuArGProValProAspAlaIleuIysSerIleuTrpYrly	204
893	TCCCTGTACTGAAATCAGGTCCAGGGCCCCCAAAACCCGGTGGCACAA	942
204	sAsnIleuThrGlyProGlnIAsnIlePheIleuAsnHisThrAspIleuValP	221
943	AAACCTGACTGACGCGACATCATTAACCTTGAACCAACACAGACTGTGTC	992
221	roCysIleuCysIleGlnAlaTrpSerIleuGlnIuProAspSerGlnArVal	237
993	CTGCGCTGTATTTCAGGTGTGGCTCTGGAACTGACTCGGTATGAGACG	1042
238	GlnPheCysProPheArGlnAspProGlyAlaHisArGAsnIeuTrpHI	254
1043	AACATCTGCCCTTCAGGAGAGACCCCCCGCACACAGAAACCTTGGA	1092
254	sIleAlaArgIleuArGValIleuSerProGlyAlaTrGlnIleuAspAlaP	271
1093	AGCGCCCGATGGACATGCTGACCCCTGCAGACACTGGCTGCTGGACACAC	1142
271	roCysCysIleProGlyIuYsValThrIleuCysTrGlnAlaProAspGln	287
1143	CGTGTGCTGCTGCCCGCAGAGCGGCACTGTGCTGGCGGCTCTCCGGGTGG	1192
288	SerProCysGlnProIleuValProProValProGlnIlysAsnAlaTrpVa	304
1193	GACCCCTGCCAGCACATGTCACCGCTTCTCTGGAGAAACGTCACTGT	1242
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1243	GGACAAAGTTCTGAGATGCCATTGCTGAAAGGCCACCTTAACCTGTGTG	1292
321	AlaIleuValSerTrpIleuIuYsValGlnIleuGlnAlaCysSerTrpAla	337
1293	TTTACGTGAAACAGCTCGAGAAAGCTGCAAGCTCAAGAGATGTGTGTGGCT	1342

338 AspSerLeuGlyProPheLysAspAspMetLeuValGluMetLysTh 354  
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 354 rGlyLeuAsnThrSerValLysAlaLeuGluProSerGlyCysThp 371  
 1393 CCCCCAGACACAGATCCCTCTGTGGTGTGACCCAGTGGCTACTT 1442  
 371 rGluProSerMetAlaSerThrArgAlaAlaArgLeuGlyGluLeu 387  
 1443 CACTACCCACCAAGCCTCCAGGAGGAGCTCCCTTGGAGAGACTTA 1492  
 388 LeuGlnAspPheArgSerHisGlnCysMetGlnLeuTrpAsnAspAsp 404  
 1493 CTCAAGACCTGACAGTCCAGCCAGTGTCTGACAGTATG...GACGATGA 1539  
 404 nMetGlySerLeuTrpAlaCysProMetAspLysTrpIleHisAlaArg 420  
 1540 CTGGGAGGCGCTATGGGCTGGCCCATGACAAATACATCCACCAAGCCG 1588  
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seq\_documentation\_block:  
 AA265269 standard; DNA; 1752 BP.

AA265269;

23-MAR-2000 (first entry)

Human secreted protein gene 20.

Human; secreted protein; cancer; tumour; developmental abnormality;  
 foetal deficiency; blood disorder; immune system disorder; inflammation;  
 autoimmune disease; allergy; Alzheimer's disease; cognitive disorder;  
 schizophrenia; arthritis; asthma; psoriasis; sepsis; skin disorder;  
 atherosclerosis; diabetes; cardiovascular disorder; kidney disorder;  
 digestive disorder; endocrine disorder; infection; AIDS; leukaemia;  
 therapy; chromosome 3; ds.

Homo sapiens.

WO9958660-A1.

18-NOV-1999.

06-MAY-1999; 99MO-US09847.

12-MAY-1998; 98US-0085093.  
 12-MAY-1998; 98US-0085094.  
 12-MAY-1998; 98US-0085105.  
 12-MAY-1998; 98US-0085180.  
 18-MAY-1998; 98US-0085906.  
 18-MAY-1998; 98US-0085920.  
 18-MAY-1998; 98US-0085921.  
 18-MAY-1998; 98US-0085922.  
 18-MAY-1998; 98US-0085923.  
 18-MAY-1998; 98US-0085924.  
 18-MAY-1998; 98US-0085928.  
 18-MAY-1998; 98US-0085925.  
 18-MAY-1998; 98US-0085927.

(HUMA-) HUMAN GENOME SCI INC.

Ruben SM, Florence K, Ni J, Rosen CA, Carter KC, Moore PA;  
 Olsen HS, Shi Y, Young PE, Wei F, Brewer LA, Soppet DR;  
 Latleur DW, Endress GA, Edner R;

MP1; 2000-062296/05.  
 P-PSDB; AAY76143.

New isolated human genes and the secreted polypeptides they encode,  
 useful for diagnosis and treatment of e.g. cancers, neurological  
 disorders, immune diseases, inflammation or blood disorders

XX Claim 1; Page 308; 475pp; English.  
 PS This sequence was found to be present on human chromosome 3.  
 XX AA265269 to AA265350 represent 97 isolated human secreted protein genes.  
 CC This sequence was found to be present on human chromosome 3.  
 CC AA265269 to AA265350 represent the secreted proteins encoded by the 97  
 CC human genes. The genes and their corresponding secreted polypeptides are  
 CC useful for preventing, treating or ameliorating medical conditions,  
 CC e.g. by protein or gene therapy. Also pathological conditions can be  
 CC diagnosed by determining the amount of the new polypeptides in a sample  
 CC or by determining the presence of mutations in the new genes. Specific  
 CC uses are described for each of the 97 genes, based on which tissues they  
 CC are most highly expressed in, and include developing products for the  
 CC diagnosis or treatment of cancer, tumours, developmental abnormalities  
 CC and foetal deficiencies, blood disorders, diseases of the immune system,  
 CC autoimmune diseases, inflammation, allergies, Alzheimer's and cognitive  
 CC disorders, schizophrenia, arthritis, asthma, psoriasis, sepsis, skin  
 CC disorders, atherosclerosis, diabetes, cardiovascular disorders, kidney  
 CC disorders, digestive/endocrine disorders, infections and AIDS. The  
 CC polypeptides are also useful for identifying their binding partners.  
 CC The sequences shown in AA265269 to AA265350 represent fragments of the  
 CC secreted proteins.  
 SQ Sequence 1752 BP; 324 A; 555 C; 522 G; 347 T; 4 other;

alignment\_scores:  
 Quality: 1505.50 Length: 448  
 Ratio: 4.205 Gaps: 3  
 Percent Similarity: 79.911 Percent Identity: 64.732

alignment\_block:

US-09-899-471-2\_COPY\_21\_440 x AA265269

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 17 uSerCysHisLeuTrpAspGlyAspValLeuGlySerProGlySerLeuG 34  
 337 CTCTGCGCCCTCTGTGGACATGACATGACATGACATGACATGACATG 386  
 34 InsErAlaProGlyProValLeuAlaProThrArgLeuGlnThrGluLeu 50  
 387 TGCTGCTCGGGCCCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 436  
 51 ValLeuArgCysProGlnLysThrAspCysAlaLeuArgValAla 67  
 437 GTGCGAGGTGCGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 486  
 67 ValHisLeuAlaValHisGlyHisTrpAlaGluProGluGlu..... 81  
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 82 ....AlaGlyLysSerAspSerGluLeuGlnGlnGlnGlnGlnGlnGln 96  
 537 AGTTTGGAGGAGCAGCTGACTTAGGGGTGGAGGAGGAGGAGGAGGAGCT 586  
 97 LeuGlnAlaGlnValValLeuSerPheGlnAlaTyrProPheAlaArgC 113  
 587 CTCACAGCCCAAGTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 636  
 113 SalAlaLeuGluValGlnValProAlaAspLeuValGlnProGlyGlns 130  
 637 GCTCTGCTGTGAGGTGCAAGTCCCTCTCTCTCTCTCTCTCTCTCTCTCT 686  
 130 eValGlySerAlaValAlaPheAspCysPheGlnAlaSerLeuGlyValG 146  
 687 CTGTGGGCTGTGGGTATAGTCTGCTGAGGCTGCTGAGGAGGAGGAGGAG 736  
 147 ValGlnIleTrpSerTyrThrLysProArgTyrGlnLysGluLeuAsnLe 163



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291 CTCGCGCCGCTGTGGAGACATGACTCTGCTGCTGGGACATCG 340
34 InsertAlaProGlyProValLeuValProThrArgLeuGlnThrGluLeu 50
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341 TGCCGCTGCTGGGCCCCGCTGCTGGCCCTACGACATCGACAGACAGCTG 390
51 ValLeuArgCysProGlnIlyThrAspCysAlaLeuArgValArgVala 67
|||||
391 GTGCGAGGTGCCAGAGAGACAGACCTGACTGTGCTGCTGCTGCTGCTG 440
67 ValHisLeuAlaValHisGlyHisThrPalaGluProGluGlu..... 81
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441 TGTCCACTGGCCGCTGATGCGATGCGAGGAGAGCCGTAAGATGAGGAAA 490
82 .....AlaGlyLysSerAspSerGluLeuGlnGlnIlySerArgAsnAlaSer 96
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941 TGACGAGACCGGACATCACTTGAACACACAGACCTGCTGCTGCTGCTG 990
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|||||
991 CTTCTGATTCAGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1040
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|||||
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323 ValSerThrTrpGluLysValGlnLeuGlnAlaCysSerThrPalaAspSe 339
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339 rLeuGlyProPheLysAspAspMetLeuValGlnLeuLysThrGlyL 356
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1290 CTTGGGCTCTCTCAAGACGATGTGCTACTGTGTGAGACAGAGGCCCCCC 1339
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389 naSpPheArgSerHisGlnCysMetGlnLeuThrPnaSpAspAsnMetG 406
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seq_documentation_block:
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AC AAF93875;
XX
XX
XX 23-MAY-2001 (first entry)
XX
XX Human cDNA encoding a membrane or secretory protein clone PSEC0233.
XX
XX Human; secretory protein; membrane protein; vaccine; gene therapy;
XX rheumatoid arthritis; diabetes; ss.
XX
XX Homo sapiens.
XX
XX EP1067182-A2.
XX
XX 10-JAN-2001.
XX
XX PD
XX 07-JUL-2000; 2000EP-0114090.
XX
XX PF
XX 08-JUL-1999; 99JP-0194179.
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XX PR 11-JAN-2000; 2000JP-0118775.
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XX PR 02-MAY-2000; 2000JP-0183766.
XX
XX PA
XX (HELI-) HELIX RES INST.
XX
XX PI
XX Ota T, Isogai T, Nishikawa T, Kawachi T, Sugiyama T, Hayashi K;
XX WPI: 2001-093989/11.
XX DR P-PSDB; AAB88448.
XX
XX Nucleic acids encoding secretory proteins/membrane proteins, useful in
XX gene therapy or as candidate target molecules in drug development -
XX
XX Claim 1: SEQ ID 263; 609pp + CD ROM; English.
XX
XX PS
XX
XX This invention relates to nucleic acid sequences AAF93744 - AAF93916
XX which encode human secretory or membrane proteins represented by
XX AAB88317 - AAB88419. Included in the invention are primers
XX AAF93917 - AAF94295 and AAF62232 - AAF62235 which are used to isolate the
XX cDNA sequences of the invention. The invention also includes methods for
XX the production of antibodies directed against the proteins, and cDNA

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CC sequences, which can be used in vaccines. The polynucleotide sequences  
 CC can be used in gene therapy. The polynucleotide sequences and the  
 CC proteins they encode may be used in the prevention, treatment and  
 CC diagnosis of diseases associated with inappropriate secretory  
 CC protein/membrane protein expression. The nucleic acids and complementary  
 CC sequences may also be used as DNA probes in diagnostic assays  
 CC (e.g. polymerase chain reactions (PCR)) to detect and quantify the  
 CC presence of similar nucleic acid sequences in samples. They may also be  
 CC used to study the expression and function of secretory proteins/membrane  
 CC polypeptides and their role in metabolism. The polypeptides may be used  
 CC as antigens in the production of antibodies against them and in assays to  
 CC identify modulators (agonists and antagonists) of expression and  
 CC activity. The antibodies and antagonists may also be used as therapeutic  
 CC agents to down regulate expression and activity. The antibodies may also  
 CC be used as diagnostic agents for detecting the presence of the  
 CC polypeptides in samples (e.g. by enzyme linked immunosorbant assay  
 CC (ELISA)). Examples of diseases which may be treated include rheumatoid  
 CC arthritis and diabetes.

XX Sequence 2499 BP: 418 A; 821 C; 764 G; 496 T; 0 other;

# alignment\_scores:

Quality: 1397.00 Length: 504  
 Ratio: 4.061 Gaps: 6  
 Percent Similarity: 68.254 Percent Identity: 54.960

## alignment\_block:

US-09-899-471-2\_COPY\_21\_440 x AAF93875

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 34 InseRAlaProGlyProValLeuValProThrArgLeuGlnThrGluLeu 50  
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 51 ValLeuArgCysProGlnLysThrAspCysAlaLeuArgValAlaArgVal 67  
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 82 .....AlaGlyLysSerAspSerGluLeuGlnGluSerArgAsnAlaSer 96  
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 97 LeuGlnAlaGlnValValLeuSerPheGlnAlaTrpProIleAlaArgCys 113  
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 568 CTCACAGGCCCAAGTGTCTCTCTTCACAGGCTTACCTTACCTGCGGCTG 617  
 113 AlaLeuLeuGlnValValGlnValProAlaAspLeuValGlnProGlyGln 130  
 |||||  
 618 CTTCTCTGTGAGGTGCAAGTGCCTGTGCTGCTTGTGCACTTGTGCTG 667  
 130 eTrValGlySerAlaValAlaPheAspCysPheGlnAlaSerLeuGlnAla 146  
 |||||  
 668 CTGAGGCTCTGTGTATATATGCTTCTGAGGCTGCTTACGAGATGTAG 717  
 147 ValGlnIleTrpSerTrpThrLysProArgTrpGlnLysGluLeuAsnIle 163  
 |||||  
 718 GTAGAGATCTGTCTTACTACAGCCCAAGTACGATGAGAACTCAACA 767  
 163 uThrGlnGlnLeuPro.....AspGlyAla 171

768 CACACAGAGCTGCTGCTGCCCTGCTGCTCAACGTGTACAGAGATGGTG 817  
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 171 sPsnValLeuLeuThrLeuAspValSerGluGlnGlnAspPheSerPhe 187  
 |||||  
 818 ACAACGTGATCTGTGTGTGATGTCTGTAGAGACAGACTTGGGCTC 867  
 188 LeuLeuTrpLeuAlaGlyProValProAlaAlaLeuLysSerLeuTrpTyr 204  
 |||||  
 868 TCCCTGTACTGGAATCAGTCTCAGAGGCCCCCAAAACCCGGTGACANA 917  
 204 sAsn..... 205  
 918 AAACCTGTGAGGCTCCCTCCCTCCCAAGTCATCCACATGTAGCCGA 967  
 205 ..... 205  
 968 TGCCTGTGCAAGAGCAGCAGTCCATATCAGAGAGATCTTGAAGAGA 1017  
 205 ..... 205  
 1018 CTCACCCCAAGCAGGAAATGTGTGGGGAGACTTTCCTCTGCTGTT 1067  
 205 ..... 205  
 1068 TCCCTGACTTTGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1117  
 206.....Leu..ThrGlyProGlnAsnIleThrLeuAsnHisThr 217  
 1118 CCTTATTATTTCACACAGACTGGACCGCAGATCATTTACCTGAAACAC 1167  
 217 rAspLeuValProCysLeuCysIleGlnValTrpSerLeuGlnProAsp 234  
 |||||  
 1168 AGACATAGTTCCTGCTGCTGTATCAGTGTGCTGCTGTGACCTGACT 1217  
 234 eArgLysValGluPheCysProPheArgGlnAspProGlyAlaHisArg 250  
 |||||  
 1218 CCGTTTGGAGACATCTGCCCTTCAGGGAGACCCCGGCGACACACAG 1267  
 251 AsnLeuTrpHisIleAlaArgLeuArgValLeuSerProGlyValTrpG 267  
 |||||  
 1268 AACCTGTGCAACCCCGCCGACTGCGACTGCTGACCTGACAGACTGCT 1317  
 267 nLeuAspAlaProCysCysLeuProGlyLysValThrLeuCysTrpGln 284  
 |||||  
 1318 GCTGGAGCAGCGTGTGCTGCTGCCGCGAAGAGCGCACTGTGCGGG 1367  
 284 lArProAspLysSerProCysGlnProLeuValProProValProGlnLys 300  
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 1368 CTCGGGTGGGACCCCTGCCACCACTGCTCCACCGCTTCTGCGGAG 1417  
 301 AsnAlaThrValAsnGluProGlnAspPheGlnLeuValAlaGlyHisPr 317  
 |||||  
 1418 AACGTCACCTGTGACAGAGGCTTCTGAGTTCCATGTGTGAAAGGCCACC 1467  
 317 oAsnLeuCysValGlnValSerThrTrpGlnLysValGlnLeuGlnAla 334  
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 1468 TAACCTGTGTGACGTGACAGAGCTGCGAGAGAGGACACTGAGAGAGT 1517  
 334 ySerTrpAlaAspSerLeuGlyProPheLysAspPheLeuVal 350  
 |||||  
 1518 CTTTGTGGCTGACTCCCTGGGGCTCTCAAGACGATGTGCTACTGTGT 1567  
 351 GluMetLysThrGlyLeuAsnAsnThrSerValCysAlaLeuGlnProSe 367  
 |||||  
 1568 GAGACAGCAGGCCCCCAGAGCAACAATCCTTGTGCTTGGAAACCCAG 1617  
 367 rGlyCysThrProLeuProSerMetAlaSerThrArgAlaAlaArgLeu 384  
 |||||  
 1618 TGGCTGTACTTCACTAACCCAGCAAAAGCTTCACG..... 1651  
 384 LysGlnGlnLeuLeuGlnAspPheArgSerHisGlnCysMetGlnLeuTrp 400  
 |||||



1652 .....CTATCG 1657  
401 AsnAspAspAsnMetGlySerLeuTrpAlaCysPrometAspLysIle 417  
1658 ...GACGATGACTGTGGAGAGCCTATGGCTCCCTCCATGACAAATATCAT 1704  
417 eHisArgArg 420  
1705 CCACACAGCGC 1714

eq\_name: /STDS1/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT: AAC85029

eq\_documentation\_block:

D AAC85029 standard; cDNA; 1753 BP.

C AAC85029;

T 08-MAY-2001 (first entry)

X Human variant Zcytor14 protein Zcytor14-1 encoding cDNA.

X Cytokine receptor: Zcytor14; human; inflammation; rheumatoid arthritis;  
X antiinflammatory; gene therapy; vaccine; variant; Zcytor14-1; ss.

S Homo sapiens.

X Key Location/Qualifiers

T CDS 2..1179

T /tag= a

T /product= "Zcytor14-1"

X WO200104304-A1.

X 18-JAN-2001.

X 30-JUN-2000; 2000MO-US18383.

X 07-JUL-1999; 99US-0348854.

X (ZYMO ) ZYMOGENETICS INC.

X Presnell SR, Burkhead SK, Powder SL;

X WPI; 2001-112618/12.

X P-PSDB; AAB61881.

X New polypeptide encoding a human cytokine receptor Zcytor14, for  
X treating inflammation e.g. rheumatoid arthritis -

X Disclosure; Page 95-98; 112pp; English.

X The invention provides a new human cytokine receptor designated Zcytor14.  
X Zcytor14 can be expressed by standard recombinant methodology. The  
X encoding nucleic acid is useful for detecting the expression of a  
X Zcytor14 gene in a biological sample. Anti-Zcytor14 antibodies can be  
X used to screen biological samples in vitro for the presence of Zcytor14.  
X Proteins, polypeptides and peptides having Zcytor14 activity can be  
X administered to a subject who lacks an adequate amount of this  
X polypeptide, for treating inflammation and conditions such as rheumatoid  
X arthritis. In contrast, Zcytor14 antagonists (e.g. anti-Zcytor14  
X antibodies) can be used to treat a subject who produces an excess of  
X Zcytor14. Zcytor14 nucleotide sequences can also be used to provide  
X Zcytor14 to a subject. The present sequence represents a cDNA encoding  
X a variant of the human cytokine receptor Zcytor14, designated Zcytor14-1.  
X The variant is a truncated form of the receptor polypeptide and lacks  
X amino acid residues 1-113 of Zcytor14.

X Sequence 1753 BP; 287 A; 584 C; 548 G; 334 T; 0 other;

X Alignment\_scores:

X Quality: 1154.50

X Ratio: 4.260

X Length: 340

X Gaps: 3

Percent Similarity: 79.706 Percent Identity: 65.588

alignment\_block:

us-09-899-471-2\_copy\_21\_440 x AAC85029 ..

Align seg 1/1 to: AAC85029 from: 1 to: 1753

90 GlnGlnSerArgAsnAlaSerLeuGlnAlaGlnValValLeuSerPheGln 106  
:::|||||  
2 GAGGAGCCTAGAAATGCTCTCTCCAGGCCCAAGTCGTCTCTCCCA 51  
106 nAlaTyrProIleAlaArgCysAlaLeuLeuGlnValGlnValProIleA 123  
|||||  
52 GGCCCTACCTACTGCCCGCTGCTGCGAGGAGTCAAGTGCCTCTG 101  
123 sPLeuValGlnProGlnGlnSerValGlySerAlaValPheAspCysPhe 139  
|||||  
102 CCTTGTGCAGTTTGTGTCAGTCTGTGGGCTGTGTGATATGACTGCTTC 151  
140 GlnAlaSerLeuGlnValGlnValGlnIleTrpSerTyrThrLysProAr 156  
|||||  
152 GAGGCTGCCCTAGGAGTGAAGTACGAATGTGCTATACTAGCCAG 201  
156 gTyrGlnLysGlnLeuAsnLeuThrGlnGlnLeuPro..... 168  
202 GTACGAGAAGAACTCAACACACACAGCTGCTGCCCTGCCCTGCC 251  
169 .....AspGlyAspAsnValLeuLeuThrLeuAspValSer 180  
252 TCACGGTGCACACAGATGGTGAACAGTGCATCTGTTGAATGTCCT 301  
181 GlnGlnGlnAspPheSerPheLeuLeuTyrLeuArgProValProAspAl 197  
|||||  
302 GAGGAGCAGCAGCTTGGCTCTCTCTGACTGAATGAGTCCAGGGCCC 351  
197 aLeuLysSerLeuTyrPThrLysAsnLeuThrGlyProGlnAsnIleThrL 214  
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352 CCCAAACCCCGGTGGCACAAAACCTGACTGACCCCAATATCATTA 401  
214 euAsnHisThrAspLeuValProCysLeuLysIleGlnValTrpSerLeu 230  
402 TGAACACACAGACCTGTTCCCTGCTGTATTCAGTGTGGCCCTGTG 451  
231 GlnProAspSerGlnArgValGlnPheCysProPheArgGlnAspProGln 247  
|||||  
452 GAACCTGACTCTGCTTAGAGACAACTGCCCCCTTACGGAGAGACCCCG 501  
247 yAlaHisArgAsnLeuTrpHisIleAlaArgLeuArgValLeuSerProG 264  
|||||  
502 CGCACACCAAGAACTCTGGCAAGCCCGCCAGCTGCCACTGACCTGC 551  
264 lValAlaTrpGlnLeuAspAlaProCysCysLeuProGlnLysValThrLeu 280  
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552 AGAGCTGGCTGCTGGACGACCGCTGCTGCCGCCGAGAGAGGGCAGCTG 601  
281 CysTrpGlnAlaProAspGlnSerProCysGlnProLeuValProProVa 297  
|||||  
602 TGCTGCGCGGCTCCGGGTGGGAGCCCTGCCACCTGTGTCCACCGCT 651  
297 lProGlnLysAsnAlaThrValAsnGlnProGlnAspPheGlnLeuValA 314  
:::|||||  
652 TTCCTGGGAGAACTGCTGTGCAC..... 676  
314 lAlaGlnHisProAsnLeuCysValGlnValSerThrTrpGlnLysValGln 330  
|||||  
677 .....GTACACAGCTCGAGAGAGCTCAG 700  
331 LeuGlnAlaCysSerTrpAlaAspSerLeuGlyProPheLysAspAspMe 347  
|||||  
701 CTGACAGAGATGCTGTGGGCTGACTCCCTGGGCGCTCTCAAAAGCATGT 750  
347 tLeuLeuValGlnMetLysThrGlyLeuAsnAspThrSerValCysAlaL 364  
:|||||  
:::|||||





DE Human Zcyltor14 variant zcyltor14-1 degenerate nucleotide sequence.

XX Cytokine receptor; zcyltor14; human; inflammation; rheumatoid arthritis;

KW antiinflammatory; gene therapy; vaccine; variant; Zcyltor14-1; ss.

XX

OS Homo sapiens.

XX

PN MO200104304-A1.

XX

PD 18-JAN-2001.

XX

PF 30-JUN-2000; 2000MO-USI8383.

XX

PR 07-JUL-1999; 99US-0348854.

XX

PA (ZYMO ) ZYMOGENETICS INC.

XX

PI Presnell SR, Burkhead SK, Powderer SL,

XX WPI; 2001-112618/12.

DR P-PSDB; AAB61881.

XX

PT New polypeptide encoding a human cytokine receptor zcyltor14, for

XX treating inflammation e.g. rheumatoid arthritis -

XX Disclosure; Page 101; 112pp; English.

XX

XX The invention provides a new human cytokine receptor designated Zcyltor14.

CC Zcyltor14 can be expressed by standard recombinant methodology. The

CC encoding nucleic acid is useful for detecting the expression of a

CC Zcyltor14 gene in a biological sample. Anti-Zcyltor14 antibodies can be

CC used to screen biological samples in vitro for the presence of Zcyltor14.

CC Proteins, polypeptides and peptides having Zcyltor14 activity can be

CC administered to a subject who lacks an adequate amount of this

CC polypeptide, for treating inflammation and conditions such as Rheumatoid

CC arthritis. In contrast, Zcyltor14 antagonists (e.g. anti-Zcyltor14

CC antibodies) can be used to treat a subject who produces an excess of

CC Zcyltor14. Zcyltor14 nucleotide sequences can also be used to provide

CC Zcyltor14 to a subject. The present sequence represents a degenerate

CC nucleotide sequence of a variant of the human cytokine receptor Zcyltor14

CC designated Zcyltor14-1. The variant is a truncated form of the receptor

XX polypeptide and lacks amino acid residues 1-113 of Zcyltor14.

SO Sequence 1725 BP; 192 A; 226 C; 332 G; 216 T; 759 other;

Alignment\_scores:

Quality: 852.50 Length: 339

Ratio: 3.947 Gaps: 3

Percent Similarity: 63.717 Percent Identity: 48.968

Alignment\_block:

US-09-899-471-2\_COPY\_21\_440 x AAC85030 ..

Align seg 1/1 to: AAC85030 from: 1 to: 1735.

90 glnghSerarqshAlaserLeuglAlalagVaValleusePhegl 106  
:::||||| |||||::: ||||| ||||| |||||  
1 GARGARCCMGNAAAYCGNMNMYNCARGCNCARCCTGNTNTNMTSNTTCA 50  
106 nalaTyPrroilealeAargCysalaleuleugluValgltqVatProlaaa 123  
||||| ||||| ||| |||||: ||||| ||||| |||||  
51 RGCNRATCCMACNGCMGNTIGGTNTNTNGARGTCACAGTCNCNCNG 100  
123 splueValglInProgljglInservAlglserAlavalPlaeaspcysPhe 139  
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101 CNVTGTGTCARTTYGNCARWMSNGTGMMNSGNTGNTGNTAVGAATGTATTY 150

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201 NTAYGARAARGAYTTNAAYCAVNCARCARAYTNCNCAGTTCNCTNGY 250
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251 TNAAYGTMSNCGCAGVAGCGAGCAAYGTACNAYTNGTNTNAAGTMSN 300
181 GluGluGlnAspPheSerPheLeuLeuTyrLeuArgProValProAspAl 197
301 GARGCARCARAYTTGGGNTMTMSNTMTATGTGGAAYCARGTNCARGNCC 350
197 AlaLeuSerLeuTyrPyrItyrAsnLeuThrGlyProGlnAsnIleThr 214
351 NCCNAARCCMGNTGGCAYAAATTTNACNGGCCARCTATHTACNY 400
214 euAsnIsthrAspLeuValProCysLeuGlyIleGlnAlaIlePsrSer 230
401 TNAAYCAVACNGAYTNGTNCNCTMGTYTNGYATHTCARGTNTGGCCYTN 450
231 GluProAspSerGluArgValGluPheCysProPheArgGluAspProG 247
451 GARGCGAAYMSYCTNNGNCCNAAYATHTTGCCNTTYMGNGARGAYCCNM 500
247 yAlaHisArgAsnLeuThrPisIleAlaArgLeuArgValLeuSerPro 264
501 NGCNCAYICAAATTTNTGGCARCNGCNCMGNTMTNGYTTNTNACNTNC 550
264 yValTyrGlnLeuAspAlaProCysCysLeuProGlyIysValThrLeu 280
551 ARMSNTGGYTTNTNGAYGCCNCTGTMTSNTTNCNCGNCARGCNGCYTN 600
281 CysTyrGlnAlaProAspGlnSerProCysGlnProLeuValProProVa 297
601 TGYTGGMGNCNCCNGNGNGAYCCNTGTGCARCNCTNGTNCNCCNTY 650
297 lProGlnIysAsnAlaThrValAsnGluProGlnAspPheGlnLeuVal 314
651 NMSNTGGGAAAYGTNACNCTNAY..... 675
314 lAgIyIstProAsnLeuCysValGlnValSerThrTyrGluIysValGln 330
676 .....GTNAATYMSMSNGARAATYTCAR 699
331 LeuGlnAlaCysSerTyrPalaAspSerLeuGlyProPheIysAspAsp 347
700 YTNCAARGARTGYTNTGGCGNGAYMSYNTNGNCCNTTNAARGAYGAT 749
347 tLeuLeuValGluMetCysThrGlyLeuAsnAsnThrSerValCysAla 364
750 NTNTNTNTNGARACNMGNCCNCCARGAAYAYMGWMSYTTNGYCCNY 799
364 euGluProSerGlyCysThrProLeuProSerMetAlaSerThrArgAla 380
800 TNGARCCNMNSNGNTGTACWMSYTTNCCNMSNARGCNMSNACNMGN 849
381 AlaArgLeuGlyGluGluLeuLeuGlnAspPheArgSerHisGlnCysMe 397
850 GCNMGNNTNGNGCARFAYTYTNTNCAARGAYTTCARMSNGNCARCTY 899
397 tGlnLeuTyrPasnAspAspAsnMetIlySerLeuTyrPalaCysProMet 414
900 NCARYNTGTG...GAGAYGAYTYTNGNGCNNTYNTGGCGTGCNATYG 946
414 sPlyTyrIleHisArg 419
947 AYTAARFAYTHCAFYAR 963

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seq_documentation_block:
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NC AAH99805:

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Percent Similarity: 66.452 Percent Identity: 53.226

Alignment block:

US-09-899-471-2\_Copy\_21\_440 x AAH99805

Align seg 1/1 to: AAH99805 from: 1 to: 1210

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  |||||
17 uSerCysHisLeuTrpAspGlyAspValLeuCysLeuProGlySerLeu 34
  |||||
309 CTCTGCGCCCTGAGAGACAGACATACCTGCTGCTGGGAGACATCG 358
  |||||
34 InSerAlaProGlyProValLeuValProThrArgLeuGlnThrGluLeu 50
  |||||
359 TGCTGTCTCCGGGCCCTGCTGGGCTGAGCCTACGACCTGACAGAGAGCTG 408
  |||||
51 ValLeuArgCysProGlnLysThrAspCysAlaLeuArgValArgVala 67
  |||||
409 GTGCTGAGGTCTCCAGAGAGAGACCCACTGTGACTCTGTCTGCTGTGGC 458
  |||||
67 lValHisLeuAlaValHisGlyHisTrpAlaGluProGluGlu..... 81
  |||||
459 TGTCACCTTGCGCTGCATGGGACACTGGGAGAGAGCTGAAGATGAGAGAA 508
  |||||
82 .....AlaGlyLysSerAspSerGluLeuGlnGluSerArgAsnAlaSer 96
  |||||
509 AGTTTGGAGGAGCAGCTGCTCAGGGGTGAGAGAGCTGAGATGCTCTCT 558
  |||||
97 LeuGlnAlaGlnValValLeuSerPheGlnAlaIleArgProIleAlaArg 113
  |||||
559 CTCAGAGCCCAAGTCGTCTCTCTCTCCAGGCTACCCCTACGTGCGCGCTG 608
  |||||
113 sAlaLeuLeuGlnValValGlnValProAlaAspLeuValGlnProGlyGln 130
  |||||
609 CGTCTCTGCTGAGGTGCAAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCT 658
  |||||
130 eValGlySerAlaValPheAspCysPheGlnAlaSerLeuGlnAlaGlu 146
  |||||
659 CTGTGGGCTCTGTGTATATGACTGCTTGCAGGGCTGCGCTTACGAGAGT 708
  |||||
147 ValGlnIleTrpSerTyrThrLysProArgTyrGlnLysGlnLeuAsnLe 163
  |||||
709 GTACGATCTGTGCTTACTACTACGAGGAGTACGAGAGAGAACTCAACCA 758
  |||||
163 uThrGlnGlnLeuPro..... 168
  |||||
759 CACACAGACAGCTGCTGACTGTCAGGGGCTCGAAGCTCGAAGACATTC 808
  |||||
169 ..... 172
  |||||
809 CGAGCTGCTGGGCCCTGCTGCTCAACGTGTCAGAGATGTTGACAC 858
  |||||
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859 GTCATCTGCTTCTGAAATGCTCTGAGAGAGACGACTTCTGCTCTCTCT 908
  |||||
189 uTrpLeuArgProValProAspAlaLeuLysSerLeuTrpTyrLysAsn 206
  |||||
909 GTACTGGAATCAGTCCAGGGGCCCAAAACCCCGGTGGCAGCAAAAACC 958
  |||||
206 euThrGlyProGlnAsnIleThrLeuAsnHisThrAspLeuValPro..Cy 222
  |||||
959 TGTGTGAGGCTCCCTCCCAAGTC...CATTCCTGAGTGGCCGAG 1005
  |||||
222 sLeuCys.....IleGlnValTrpSerLeuGlnProAspS 234
  |||||
1006 CCGTGTCAAGAGACGAGTGCATATACAGAGAGATCTTCAAGAGGACT 1055
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234 eGluArgValGluPheCysProPheArgGluAspProGlyAlaHisArg 250
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```

```

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251 AsnLeuTrpHisIleAlaArgLeuArgValLeuSerProGlyValTrpG 267
1073 AATGTGTG..... 1081
267 nLeuAspAlaProCysCysLeuProGly 276
1082 .....GGGAACCTTCTGCTCTCTGCT 1102
seq_name: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:AA578822
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XX
AC AA578822;
XX
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #14626.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KM food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HXSE-) HXSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI: 2001-639362/73.
DR P-PSDB; ABG14635.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 1; SEQ ID No 14626; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, and molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging or sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AA564197/AA594564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SO Sequence 980 BP; 182 A; 313 C; 315 G; 170 T; 0 other;

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## Alignment scores:

Quality: 596.00 Length: 175  
Ratio: 4.000 Gaps: 4  
Percent Similarity: 85.143 Percent Identity: 69.714

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US-09-899-471-2\_copy\_21\_440 x AAS78822/rev ..

Align seg 1/1 to reverse of: AAS78822 from: 1 to: 980

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17 euserCysHisLeuTrpAspGlyAspValLeuCysLeuProGlySerLeu 33
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670 TCTCTGCCGCTGTGGACAGTACATCTGCTGCTGGGACATC 621
34 GlnSerAlaProGlyProValLeuVal.Pro.ThrArgLeuGlnThrGlu 49
||| ||||| ||||| ||| ||| |||.....
620 GTGCCTGCTGGGCCCCGGCTGTGGCTTAACCACTTGAGACAGAG 571
50 LeuValLeuArgCysProGlnLysThrAspCysAlaLeuArgValArgVa 66
|||||..... |||||||..... ||| ::|||
570 CTGGTGTGAGAGTCCAGAGAGACCGACTGTGACCTGTCTGCGTGT 521
66 lValValHisLeuAlaValHisGlyHisTrpAlaGluProGluGlu... 81
|:::|||||..... |||||||.....
520 GGCTGTCCACTTGGCCGTGCATGGGCACTGGGAGAGCCTGAAGATGAG 471
82 .....AlaGlyLysSerAspSerGluLeuGlnLysSerArgAsnAla 95
:::| |:::| |:::| | |||||
470 AAAAGTTGGAGAGACACTGACTTAGGGGTGGAGAGCCCTAGAAATGCC 421
96 SerLeuGlnAlaGlnValValLeuSerPheGlnAlaTyrProIleAlaIar 112
|||||..... |||||||..... |||||
420 TCTCTCCAGGCCCCAAGTGTGCTCTCCAGGCTTACCCTACTGCCCG 371
112 gCysAlaLeuLeuGlnValGlnValProAlaAspLeuValGlnProGlyG 129
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370 CTGGCTCTGCTGGAGGTGCAAGTCTGCTGCCCTTGTGCAGTTGGTC 321
129 lnservAlaGlySerAlaValPheAspCysPheGlnAlaAspSerLeuGlyAla 145
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320 AGTCTGGGGCTGTGTATATGACTGCTTGAGGCTGCCCTAGGAGAT 271
146 GluValGlnIleTrpSerTyrThrLysProArgTyrGlnLysGluLeuAs 162
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270 GAGGTAGGAATCTGTCTATATCAGCCCAAGTACGAGAGAACTCA 221
162 nLeuThrGlnLysPro 168
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220 CCACACAGAGAGCTGCT 202
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Sun Sep 29 09:32:47 2002

us-09-899-471-2\_copy\_21\_440.rni

Page 1

GM of: US-09-899-471-2\_COPY\_21\_440 to: Issued\_Patents\_NA.\* out\_format : pfs

Date: Sep 29, 2002 1:05 AM

About: Results were produced by the Gencore software, version 4.5,  
Copyright (c) 1993-2000 CompuGen Ltd.

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-GAPOP=4.000 -GAPOP=0.050 -XGAPOP=10.000 -XGAPEXT=0.000  
-GAPOP=6.000 -GAPEXT=7.000 -XGAPOP=10.000 -XGAPEXT=0.500  
-DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=blousum62  
-TRANS-human40.cdi -LIST=45 -DOCLIGN=200 -THR SCORE=pcr  
-THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL -OFFPRT=pfs  
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US09899471.ecgn1\_1132 -NCPD=6 -ICPD=3 -LONGLOG  
-DEV.TIMEOUT=120 -WARN.TIMEOUT=30 -NO\_XLPHY -WAIT -THREADS=1

Search information block:

Query: US-09-899-471-2\_COPY\_21\_440  
Query length: 420  
Database sequences: 383533  
Database length: 122816752  
Search time (sec): 183.010000

Score list:

Sequence	Strd Orig	ZScore	EScore	Len	Documentation	
cgcn2_6/prodata/2/lna/6A.COMB.seq:US-09-188-930-226		149.00	252.96	2.1e-06	1059	2165
cgcn2_6/prodata/2/lna/6B.COMB.seq:US-09-167-681-37		97.00	128.46	1.83	1842	1842
cgcn2_6/prodata/2/lna/5A.COMB.seq:US-08-342-930-1		108.50	135.68	0.5536	5455	1
cgcn2_6/prodata/2/lna/5A.COMB.seq:US-08-676-169-1		104.50	137.60	5.63	12687	1
cgcn2_6/prodata/2/lna/6A.COMB.seq:US-09-063-431A-1		104.50	137.60	5.63	12687	1
cgcn2_6/prodata/2/lna/6A.COMB.seq:US-09-017-631-23		101.50	147.55	1.57	3601	1
cgcn2_6/prodata/2/lna/5B.COMB.seq:US-09-018-883-95A-33		101.50	147.54	1.57	3602	1
cgcn2_6/prodata/2/lna/6B.COMB.seq:US-08-718-388-5		100.50	145.44	2.06	3661	1
cgcn2_6/prodata/2/lna/6B.COMB.seq:US-08-718-388-6		100.50	136.01	6.90	7824	1
cgcn2_6/prodata/2/lna/6B.COMB.seq:US-08-718-388-8		100.50	126.83	22.41	16382	1
cgcn2_6/prodata/2/lna/5A.COMB.seq:US-09-301-665-3		100.00	115.84	91.67	36741	1
cgcn2_6/prodata/2/lna/5A.COMB.seq:US-08-026-138E-7		99.50	143.35	2.69	3717	1
cgcn2_6/prodata/2/lna/6B.COMB.seq:US-09-041-886-24		99.50	140.69	3.79	4608	1
cgcn2_6/prodata/2/lna/6A.COMB.seq:US-09-062-416-13		97.50	144.38	2.36	2522	1
cgcn2_6/prodata/2/lna/6B.COMB.seq:US-09-167-681-37		97.00	128.46	1.83	1842	1
cgcn2_6/prodata/2/lna/5A.COMB.seq:US-08-444-581B-1		96.50	146.38	1.83	1842	1
cgcn2_6/prodata/2/lna/5A.COMB.seq:US-08-446-088A-1		96.50	146.38	1.83	1842	1
cgcn2_6/prodata/2/lna/6B.COMB.seq:US-08-872-757-1		96.00	141.90	3.24	2447	1
cgcn2_6/prodata/2/lna/5A.COMB.seq:US-08-050-132A-1		96.00	141.90	3.24	2447	1
cgcn2_6/prodata/2/lna/6A.COMB.seq:US-08-750-222A-1		96.00	141.90	3.24	2447	1
cgcn2_6/prodata/2/lna/6A.COMB.seq:US-08-815-652B-1		96.00	141.90	3.24	2447	1
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cgcn2_6/prodata/2/lna/6B.COMB.seq:US-08-254-353A-1		96.00	141.90	3.24	2447	1
cgcn2_6/prodata/2/lna/6B.COMB.seq:US-08-317-292-1		95.50	140.75	3.76	2487	1
cgcn2_6/prodata/2/lna/5A.COMB.seq:US-09-150-460B-5		95.50	132.19	5.22	3057	1
cgcn2_6/prodata/2/lna/6B.COMB.seq:US-09-150-460B-4		95.50	132.19	5.22	3057	1
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cgcn2_6/prodata/2/lna/6B.COMB.seq:US-09-150-460B-3		95.50	129.81	15.29	6000	1
cgcn2_6/prodata/2/lna/6B.COMB.seq:US-08-450-406-18		95.00	130.43	14.12	5288	1
cgcn2_6/prodata/2/lna/6A.COMB.seq:US-08-656-055-18		95.00	130.43	14.12	5288	1
cgcn2_6/prodata/2/lna/6A.COMB.seq:US-08-954-668-18		95.00	130.43	14.12	5288	1
cgcn2_6/prodata/2/lna/6A.COMB.seq:US-08-954-668-18		95.00	130.43	14.12	5288	1

seq\_name: /cgn2\_6/prodata/2/lna/6A.COMB.seq:US-09-188-930-226  
seq\_documentation\_block:  
Sequence 226, Application US/09188930A  
Patent No. 6150502  
GENERAL INFORMATION:  
APPLICANT: Watson, James D.  
APPLICANT: Strachan, Lorna  
APPLICANT: Steeman, Matthew  
APPLICANT: Onrust, Rene  
TITLE OF INVENTION: Compositions Isolated From Skin Cells  
FILE REFERENCE: 11000.1011c1  
CURRENT FILING DATE: 1998-11-09  
CURRENT APPLICATION NUMBER: US/09/188.930A  
NUMBER OF SEQ ID NOS: 348  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 226  
LENGTH: 2165  
TYPE: DNA  
ORGANISM: Mouse  
US-09-188-930-226

alignment\_scores:

Quality	167.50	Length: 237
Ratio	1.340	Gaps: 11
Percent Similarity	52.743	Percent Identity: 25.316

alignment\_block:

US-09-899-471-2\_COPY\_21\_440 x US-09-188-930-226

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616	AAATGTCGTGGAGCCACACGTGACCTGCTTATGATTCCTCT	665
220	lProCysLeuGlyIleGlnValTyrSerLeuGlnProAspSerGluArg	237
666	GGCCTGATGTCATAGAGCCCTCTACCTCAGAGGACACTGGAGGC	715
237	alGluThrGlyProPheArgGlnAspProGluAlaHis	252
716	GCAAAAGTGTCCCTCCAGAGCTGCGTGAAGCTTATGGCTCAGAC	765
253	TrpHisIleAlaArgLeuArgValLeuSerProGly	266
766	TGGCAGTCATAGCGTTCACGACTACAGCCAGCAATCGAGTGCAT	815
266	rgLnuLeuAspAlaProCysLeuProGlyLysThrLeuGlyTyrG	283
816	GGCTGTGACACCTCGGCGCCAGCAAGTGAAGGCGCTGCTGCTGGA	865
283	lnAlaProAspGlnSerProCysGlnProLeuValProProValProGln	299
866	GGCAGGACCCACCTACACCCCTGCAAAACCTT	897
300	lysAsnAlaThrValAsnGlnProGlnAspPheGlnLeuValAlaGly	315
898	CCCAACCCACACACAGGATGCAAGAGATGATATCTGCGAAGAT	947
316	HisProAsnLeuGlyValGlnValSerThrTyrPheValG	330
948	GGACCTTGACCCACCTGCTTATGATTCCTCA	994



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330 InLeuGlnAlaCys.....SerTIPalaasp 338
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995 GCGAGTTCGAATGTCCCCACAGAGTGGCTCTCCCATCTCGACTGTG 1044
339 SerLeuGlyProPhelLysAspAspMetLeuValGlnMetLysThrG1 355
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1045 AGCATGGATATCC...CAGGCCAGCAGCTGACGCTTCACCTTTCTTGAG 1091
355 YLeuAsnThrSerValCysAlaLeuGlnProSerGlyCys..... 369
    |||
1092 GACATATGCCACTTCATGCTGCTCTGAGTACCCAGGTTTGGGGCCG 1141
370 ..ThProLeuProSerMetAlaSerThrArgAlaAlaArgLeuGlyGlu 385
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1142 ATACCCCATGCTCTCTGTTGACAGATCAAGCCAGACCCAGGCTCAATC 1191
386 GlnLeuGlnAsp.....PheArgSerHisGlnCys 397
    |||
1192 CCAGTGAGCGCTACACTCATTCATCCCTTCCTGAGCAGAGATTCAT 1241
397 tGlnLeuThrAspAspAspAspMetLysSerLeuTP.....AlaC 411
    |||
1242 CCTGGTGTGGAGGTGAGAT...GTCCATTTCCTGAGACACGCTTTGT 1288
411 YSPrometasp 414
    |||
1289 GTCTGATGAC 1299
seq_name: /cgn2_6/ptodata/2/lna/6A_COMB.seq:US-09-188-930-6

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seq_documentation_block:
; Sequence 6, Application US/09188930A
; Patent No. 6150502

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GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murlson, James Greg
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; FILE REFERENCE: 11000.1011c1
; CURRENT APPLICATION NUMBER: US/09/188,930A
; CURRENT FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 1059
; TYPE: DNA
; ORGANISM: Mouse
US-09-188-930-6

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Alignment_scores:
Quality: 149.00      Length: 152
Ratio: 1.795         Gaps: 6
Percent Similarity: 54.605   Percent Identity: 28.289

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Alignment_block:
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Align seg 1/1 to: US-09-188-930-6 from: 1 to: 1059

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616 AAATATGTGTCTGGAGGCCACACTGTGAGACTGCTTATGAAATTCCTCT 665
220 LProCysLeuGlyGlnValThrSerLeuGlnProAspSerGlyArgVal 237
    |||
666 GCCCGCATGTGATAGAGGCTCTCCTACTGTGCAAGAGACACTGTGAGGC 715
237 aGlnPheCysProPheArgGlnAspProGlyAlaHis...ArgAsnLeu 252
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716 GCAAAAGTGTCCCTTCACAGAGTGGCTGAGACTTATGCTCAACTTC 765
253 TrpHisIleAlaArgLeuArgValLeuSerProGly.....ValTr 266
    |||
766 TGCGAGTCATATAGCTTCACTGACTGACTACAGCAGACAGACATGAGTGTCT 815
266 pGlnLeuAspAlaProCysCysLeuProGlyLysValThrLeuCysTrpG 283
    |||
816 GGCTCTGACACTCCGCTGCCACACTGAAACTGAGAGCCCTCCTCTGGA 865
283 LlnAlaProAspGlnSerProCysGlnProLeuValProProValProGln 299
    |||
866 GGCAGAGACCCACTCACACCCCTGCGAAACCTT..... 897
300 LysAsnAlaThrValAsnGlnProGlnAspPheGlnLeuValAlaGly.. 315
    |||
898 CCAGCCGACAGCAGCAGAGGTGAGAGAGATATATCTCGAATATCT 947
316 .....HisProAsnLeuGlyValGlnValSerThrTrpGlnLysValG 330
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948 GGACTTGACACCCCGACCTGCTTAACTCTCA...TTGAAAACAGCA 994
330 InLeuGlnAlaCys.....SerTIPalaasp 338
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seq_name: /cgn2_6/ptodata/2/lna/5A_COMB.seq:US-08-342-930-1

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seq_documentation_block:
; Sequence 1, Application US/08342930
; Patent No. 5821084

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GENERAL INFORMATION:
; APPLICANT: OLUSTED, ELIZABETH A.
; APPLICANT: MAURO, LAURA J.
; APPLICANT: DAVIS, ALAN R.
; APPLICANT: DIXON, JACK E.
; TITLE OF INVENTION: OSTEOBLAST-TESTICULAR PROTEIN TYROSINE
; TITLE OF INVENTION: PHOSPHATASE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESS: MORRISON & FOKSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/342,930
; FILING DATE: 21-NOV-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: KONSKI, ANTOINETTE F.
; REGISTRATION NUMBER: 34,202
; REFERENCE/DOCKET NUMBER: 20344-20975.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5455 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

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FEATURE: NAME/KEY: CDS  
LOCATION: 205..5337  
US-08-342-930-1

alignment\_scores: Quality: 108.50 Length: 548  
Ratio: 0.470 Gaps: 30  
Percent Similarity: 42.153 Percent Identity: 20.255

alignment\_block:  
US-09-899-471-2\_COPY\_21\_440 x US-08-342-930-1

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20 sleuTrpAspGlyAspValLeuCysLeu..ProGly..... 31
1106 CCGAGTGGACCTATCCCTTACCACATCTGACGTGCTGACCTCCCTTA 1155
32 .....SerLeuGlnSerAlaProGlyProValLeuValProThrArg 45
1156 CGGATGACCTCTGGGCCACGCTGGAGGACAGGCTGGAGCCCGGACGG 1205
46 LeuGlnThrGluLeu.....ValLeuArgCysPr 55
1206 CTAATGCTACGAACTTAAGTGGCCCAATGAGAGTACGTACCTCGGCC 1255
55 GlnLysThrAspCysAlaLeu.....ArgValArgValValAlaH 69
1256 CGGAGAGAGTCATGACGCTCTCCAGAGGCCCTCCGCGGACACATAC 1305
69 lsleuAlaValHisGlyHisTrpAlaGluProGluGlu..AlaGlyLysSe 85
1306 ACTTTCACCTGACGTAAGT.....TCTAGCTGACACTTA 1337
85 rAspSerGluLeuGlnGluSer.....ArgAsnAlaSerLeuG 98
1338 TGATGCTGCTGGTGGAGGCGCACTGCTGCTGCTGCTGCTGCTGCTG 1387
98 lnaAlaGlnValAla.....LeuSerPheGln 106
1388 CCAGGAGAGTCCCTGCTGCGACAGCTGTGCTAGATGACCTGGAAGCTTC 1437
107 AlaTrpProIleAlaArgCysAlaLeuLeuGluValGlnValProAlaAs 123
1438 AAGCAGCCTGGAGAGCGGCGCTACTATTCTGACGATGCCAGGCTC 1487
123 Pleu..... 124
1488 CCTAGGAGACATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1537
125 ..ValGlnProGlyGln.....SerValGlySerAlaValAlaPhe 136
1538 GCGTGGTACCTGAGCGCCACTATAGGTGAGACATTGCTCATCCACGGGG 1587
137 AspCysPheGlnAlaSerLeuGlnAlaGluValGlnIleTrpSerTrpH 153
1588 GACATCTCTCAGACATCTCAGGC.....TATAC 1616
153 llyAspAsnValLeuLeuThrLeuAspValSerGlnGluGlnAspPheSer 170
1617 AAGTCCCTGCGCCACCGCAGCTCAGTGGAGGC..... 1647
170 llyAspAsnValLeuLeuThrLeuAspValSerGlnGluGlnAspPheSer 186
1648 .....ATCAGCAGGAGACAGCCCATCTGAC 1671
187 PheLeuLeuTrpLeuArgProValProAspAlaLeu.....LysSe 200
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1722 TACCTGGCATCAGGATGGCAGACAGAGTCTCTGCGCACTTGTGACT 1771
208 ..GlyProGlnAsnIleThrLeuAsnHisThrAspLeuValPro..... 221
1772 TGGCCCTGACACTTGAAGCTGAGCTGGAATCTCTGTACCCGGCTCC 1821
222 CysLeuGlyIleGlnValTrp.....SerLeuGluProAspSe 234
1822 TGTCTACACCGGTGTGACATGGCGCTGGCGCGGAGAACCTCAGCTGAC 1871
234 rGluArgValGluPheCysPro..... 241
1872 TCAGAAATTCACAGCTCCACCCGCCCGCTCTCCACCAACCTGAGTC 1921
242 .....PheArgGluAspProGlyAlaHisArgAsnLeuTrpHis..... 254
1922 TGGGCTTTGCCACACAGCTGCGGACATGAGGCTTCTGTGATCACCA 1971
255 .....IleAlaArgLeuArgValLe 261
1972 CCGGTGGCAGAGATGCTTTCATTACGAGCTTACAGCTGAGGCTCT 2021
261 u.....SerProGlyVal.....T 266
2022 GACACTGGAAAGTGAAGAGTCTTACCTCGGAGGCCGAACTTCTCT 2071
266 rP.....GlnLeuAspAlaProCysCysLeuProGlyLysValThrLeuG 281
2072 GGGCCACAGCTACTGCAAGCTGTGAGTTCCAGATCAGCTGTCTACTTG 2121
282 TrpGlnAlaProAspGlnSerProCysGln.....Pr 292
2122 TGGGGGTCTGAGAGAGCAGAGTGCACAGCCACAGCTGGACACCC 2171
292 OLeuValProProValProGlnLysAsnAlaThrValAsnGluProGlnA 309
2172 TTGAGCTCTTACACTG.....GTAAAGCTGACAGCATGCTCTACCC 2215
309 sPheGlnLeuValAlaIleHis.....ProAsnLeuGlyValGln 322
2216 AGCTCCAAAGTCTCTGGGCGCACGTTCTGCGGGCGCGGACCGCTACCA 2265
323 ValSerThrTrpGlu..... 327
2266 GTGACCTATACACAGAGATACCCGCGACACACACAGCATATGAGGCC 2315
328 .....LysValG 330
2316 CAAGAGATGGCAGAGCTTTTGGGTTTGACTGTGGCACTAAGTACA 2365
330 lnaLeuGlnAlaCysSerTrpAlaAspSerLeu..... 340
2366 AGGTGAAGTATCTCTGCTGGCGGCCCTCTGACACAGACCAAC 2415
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2416 GTTTCCTGCGGACCTTACCCATACCAATGAGCTGCTGTCTCAAT 2465
352 tLysThrGlyLeuAsnAsnThrSerValCysAlaLeuGluProSerGlyC 369
2466 GCAAGCAGGC.....AGTGTGTGTAACTGCTGCGCCAGTGTG 2508
369 yThrProLeuProSer..... 374
2509 .....CCCTGGGGCAAGGGCCATGCCACGCCCACTCTGAGATGCTGA 2553
375 .....MetalaserThrArgAlaAlaArgLeuGlyGluLeu 387
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4708 AATGATCCTTGCAAGTCGATCGTGCCTGCTAGTCCAGACTAAT 4757  
 330 .....GlnleuGlnAla 333  
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 334 CysSerTrp..AlaAspSerLeu.....GlyProPhelAspAsp 346  
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 347 MetLeuLeuValGlnMetLysThrGlyLeuAsnAsnThrSerValCysAl 363  
 4858 TTGGTCTGCTGCTTCTTGGACCAACCAAGTAGTAGCGGTTTAGGTGCAC 4907  
 363 AlaLeu.....GluProSerGlyCysThrProLeuProSerM 375  
 4908 CATTTGTGACGTCGTTAAGAGAGACCAATGACCCCACTTAAGCCA 4957  
 375 eAlaSerThrTrpAlaAlaArg.....LeuGlyGlnGlnLeuLeu 388  
 4958 TGCCACAGCAGGAGACGCCCGCAAGGCTGCTTAAGGTCAGTTGGAG 5007  
 389 GlnAspPheArgSerHisGlnCysMetGlnLeuTrpAsnAspAsp 403  
 5008 TGGACCCCTCACCACGAGAGAGAGAGACGCCGCTGATGATGAT 5052  
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## seq.documentation\_block:

Sequence 23, Application US/09017631B  
 Patent No. 6153407  
 GENERAL INFORMATION:  
 APPLICANT: Sytkowski, Arthur J.  
 APPLICANT: Grodberg, Jennifer  
 TITLE OF INVENTION: ERYTHROPOIETIN WITH ALTERED BIOLOGICAL  
 FILE REFERENCE: NEDH92-04A22A  
 CURRENT APPLICATION NUMBER: US/09/017,631B  
 CURRENT FILING DATE: 1998-02-03  
 EARLIER APPLICATION NUMBER: US 08/808,881  
 EARLIER FILING DATE: 1997-02-28  
 EARLIER APPLICATION NUMBER: US 08/383,743  
 EARLIER FILING DATE: 1995-02-02  
 EARLIER APPLICATION NUMBER: US 08/113,080  
 EARLIER FILING DATE: 1993-08-26  
 EARLIER APPLICATION NUMBER: US 07/920,810  
 EARLIER FILING DATE: 1992-07-28  
 NUMBER OF SEQ ID NOS: 34  
 SOFTWARE: FastSeq for Windows Version 3.0  
 SEQ ID NO 23  
 LENGTH: 3601  
 TYPE: DNA  
 ORGANISM: Homo sapien  
 US-09-017-631-23

## alignment\_scores:

Quality: 101.50 Length: 504  
 Ratio: 0.495 Gaps: 34  
 Percent Similarity: 40.675 Percent Identity: 22.024

## alignment\_block:

US-09-899-471-2\_COPY\_21\_440 x US-09-017-631-23/rev ..

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 3015 TGCCTCTGAAATGCTTCTGCTTGGCCCTCAAGTGGCCCTGTGACAT 2966  
 26 lleu.....CysLeuProGlySerLeuGlnSerAlaProGlyP 39  
 |||||  
 2965 CCTTGATCTCAGAGTTGC.....TCTTGACAGTTCTCTGTGCC 2925

39 ro.....ValleuValProThrArgLeu.....GlnThrGlnLeu 50  
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 2924 CCTGAGATGTCATTTGCTGCGACTGTGAGTGTCCATGAGACAGCGTGGCGT 2875  
 51 ValleuArgCysProGlnLys.....ThrAs 59  
 2874 GAGCTGAGAGCCCTCGACGGGGTTCCAGAGAGTGGGGGAGAGGTGTGGC 2825  
 59 pCysAlaLeuArgValArgValValHisLeuAlaValHisGlyHis 75  
 2824 ACAAGCAATGTTGGTAGGAGAGGTGTGATATGCCACGTGACACACC 2775  
 76 TrpAlaLeu.....ProGlnGlnAlaGlyLysSerAspSerGlnLeuGlnI 91  
 2774 TGGTCATCTGTCCCTGCTCCGACAGC..... 2748  
 91 userArgAsnAlaSerLeuGlnAlaGlnValValLeuSerPheGlnAla 108  
 2747 .....C 2747  
 108 YrProIleAlaArgCysAlaLeuLeuGlnValGlnValProAlaAspLeu 124  
 2746 TCCCTGCTGTACACCTTCAGCTTCCCGGAGCAATTTGGACAGACTCG 2697  
 125 ValGlnProGlyGlnSerValGlySerAlaValPheAspCysPheGlu.. 140  
 2696 GAAGAGTTTGGCGAAGAGTCCAGCAGT.....GATTTTGGAGAG 2656  
 141 AlaSerLeuGlyAlaGlnValGlnIleTrp.....SerTrpThrL 154  
 2655 GAGCAGCTGAGGC.....CGCATCTGAGGGGAGATGCTCTCTTC 2615  
 154 YsPProArgTrpGlnLysGlnLeuAsnLeuThrGlnGlnLeuProAspGly 170  
 2614 TGCCAGAGAGAAACAGAGAGGCTGTCAGTCCACAG..... 2577  
 171 AspAsnValLeuLeuThrLeuAspValSerGlnGlnAspPheSerPh 187  
 2576 .....AAAGGAAGATATGCGACA 2557  
 187 eLeuLeuTrp.....LeuArgProValProAspAlaLeuLysSerLeu 202  
 2556 GTTCTCTACTCTTACGACAGACCTTCCCTCTCTTACAGAAAG.... 2511  
 202 rPTrpLysAsnLeuThrGlyProGlnAsnIleThrLeuAsnHisThrAsp 218  
 2510 .....GGCAGACGAGAG..... 2499  
 219 LeuValProCysLeuCysIleGlnValTrpSerLeuGlnProAspSerG 235  
 2498 .....TGTCCGCTCTACTACTACTGCTGCTCCACAGCCCGAAGACAG 2458  
 235 uArgValGluPhe.....CysProPheA 243  
 2457 AGTGTGAGGCTGCGAAGGCCACATGACGCTTATCATCATCATCATGACA 2408  
 243 rGlnAspProGlyAlaHis.....ArgAsnLeuTrp 253  
 2407 GG.....GGCTCCACGCGCTGGAGAGACTTACCAACAGGGCGCTGG 2367  
 254 HisIleAlaArgLeuArgValLeuSerProGlyValTrpGlnLeuAspA 270  
 2366 CCGCGAGAGACGCTTCGAGACAGAGGCCCGCTCGCAACTTCTAC 2317  
 270 lArProCysCysLeuProGlyLysValThrLeuCysTrpGlnAlaProAsp 286  
 2316 GGCCTGTGCGCCGCTACACAGAGAGTGCATC...TGGAGTACAGCTGAC 2270  
 287 GlnSerProCysGlnProLeuValProProValProGlnLysAsnAlaHis 303  
 2269 .....CCATGTACCCCTCTC...CTCTGCGCCCTCAGACAGCCCAAGC 2229

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1 REGISTRATION NUMBER: 40,261
2 REFERENCE/DOCKET NUMBER: 78441-062
3 TELECOMMUNICATION INFORMATION:
4 TELEPHONE: (416) 364-7311
5 TELEFAX: (416) 361-1398
6 INFORMATION FOR SEQ ID NO: 33:
7 SEQUENCE CHARACTERISTICS:
8 LENGTH: 3602 base pairs
9 TYPE: nucleic acid
10 STRANDEDNESS: single
11 TOPOLOGY: linear
12 MOLECULE TYPE: DNA (genomic)
13 ORIGINAL SOURCE:
14 ORGANISM: Homo sapiens
15 FEATURE:
16 NAME/KEY: CDS
17 LOCATION: join(625..637, 1201..1346, 1605..1691, 2303..2482)
18 LOCATION: join(2772)
19 FEATURE:
20 NAME/KEY: mRNA
21 LOCATION: join(625..637, 1201..1346, 1605..1691, 2303..2482)
22 LOCATION: 2617..2772)
23
24 US-08-883-795A-33

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[illegible]

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US-09-899-4/1-2\_COPY\_21\_440 x US-08-883-795A-33/rev ..  
Align seg 1/1 to reverse of: US-08-883-795A-33 from: 1 to: 3602

13	CysSerLeuGluGlyLeuSerCys.....HisLeuTrpAspGlyAspVa	26
3016	TGCTCTCTGTAATCTTCCTCTCTGTGGCCCTCAAGTTGGCCCTTGCAAT	2967
26	Ileu.....CysLeuProGlySerLeuGlnSerAlaProGly	39
2966	CCCTAATCTCAAGATTGC.....TCCTGGACAGATTCTCTCTGGCC	2926
39	ro.....ValleuValProThrArgLeu.....GlnThrGlnLeu	50
2925	CCTGAGATGATCATGCTGGCAGCATGAGATGCATGGACAGCCGTGGCGCT	2876
51	ValLeuArgCysProGlnLys.....ThrAs	59
2875	GAGCTAGAGACCCCTCGACGGGGTTACAGAGTGGCGGGGAGAGGTGTGGC	2826
59	PcysAlaLeuAlaGValArgValAlaValHisLeuAlaValHisGlyHis	75
2825	ACAAGCAAAATGGTGGAGGAGGTGTGGATATGCCAGGTGGACACACC	2776
76	TrpAlaGlu...ProGluGlnAlaGlyLysSerAspSerGlnLeuGlnG	91
2775	TGCTCATCTGTCTCCCTGTCTCTGCAGGC	2749
91	uSerArgAsnAlaSerLeuGlnAlaGlnValValLeuSerPheGlnAla	108
2748	.....C	2748
108	yrProLeuAlaArgCysAlaLeuLeuGlnValGlnValProAlaAspLeu	124
2747	TCCCTGTGTACAGCTTTCAGCTTCCCGGAGGAAATTCAGATGACCTG	2698
125	ValGlnProGlyGlnSerValGlySerAlaValPheAspCysPheGlu	140
2697	GAAAGATTGGCGGAAGTCTCAACAT.....GATGTTCGGAGTG	2657
141	AlaSerLeuGlyAlaGlnValGlnIleTrp.....SerTyrThrL	154





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108 yrProleAlaArgCysAlaLeuLeuGluValGlnValProAlaAspLeu 124
125 ValGlnProGlyGlnSerValGlySerAlaValAlaPheAspCysPheGlu 140
2697 GAGAGATTGGGAGAGAGTGTACAGAGT.....GATTGTTCGGAGTGT 2657
141 .AlaSerLeuGlyAlaGluValGlnLeuTrp.....SerTrpThrL 154
2656 GAGAGAGCTGAGGC.....CGCATCTGAGAGGAGAGATGCTTCTTC 2616
154 ysProArgTrpGlnGlyGluLeuAsnLeuThrGlnGlnLeuProAspGly 170
2615 TGCCAGAGGAGAAACAGAGAGTGTCTGACGTGACGACAG..... 2578
171 AspAsnValLeuLeuThrLeuAspAlaSerGluGluGlnAspPheSerPh 187
2577 .....MAAGGAGAGAAATACGACA 2558
187 eLeuLeuTrp.....LeuArgProValProAspAlaLeuLysSerLeu 202
2557 GTTCCTGTACTCTTACGACAGACCTTCTCCCTCTTACAGAAAG.... 2512
202 rPTrLysAsnLeuThrGlyProGlnAsnLeuThrLeuAsnHisThrAsp 218
2511 .....GGCAAGCAGAAAG..... 2500
219 LeuValProCysLeuCysIleGlnValTrpSerLeuGluProAspSerG 235
2499 .....TCTCCGCTCTACTACTACTCTGCGTCCAGAGCCCGAAACAG 2459
235 uArgValGluPhe.....CysProPheA 243
2458 AGTGTGTGCGCTGCGAAGGCCACTGACGCTTATTCACATGACAGCTGCA 2409
243 rGluAspProGlyAlaHis.....ArgAsnLeuTrp 253
2408 GG.....GGCTCCACGCGCTGGAAGAGCTGACCAACAGCGGCTGG 2368
254 .HisIleAlaArgLeuArgValLeuSerProGlyValTrpGlnLeuAsp 270
2367 CCCCAGAGACAGCTTCCGACAGAGGCGGCGCCGCGACAGCTTCTTAC 2318
270 laProCysCysLeuProGlyLysValIleLeuCysTrpGlnAlaProAsp 286
2317 GGCTGTGCTGCGGACCTACAGAGAGTGTGACTC...TGGAGTGTGAGTGC 2271
287 GlnSerProCysGlnProLeuValProProValProGlnLysAsnAlaPh 303
2270 .....CCATGTCACTCTC...CTCTGTGCGCTGACAGAGCCCAAGC 2230
303 r.....ValAsnGluProGlnAspPheGlnLeuVal..... 313
2229 ACCAAGCTGACCAACAGAGAGTATGACATTAAGACTTGTGATGATGA 2180
314 .....AlaGlyHis 316
2179 ATGATGAATGAGTGTGAGTGTGATGATGATGATGATGATGATGATGAT 2130
317 ProAsnLeuCysValGlnValSerThr..... 325
2129 ACACCCCTCATATATTTCTTTCTTTCTTTCTTTCTTTGACAGAGGCTTC 2080
326 .....TrpGluLysVal.....GlnLeuGlnAlaC 334
2079 ACTCTGTACTGTAGAGCTGTGAGTGTGTGATGATGATGATGATGATGAT 2030
334 ys.....SerTrpAlaAspSerLeuGlyProPheLysAspMetLeu 348
2029 CCTCAAAATCTGTGGGCTCAAGCGATCTCCGCTGACGCTTCAAAATAT 1980

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349 Leu..... 349
1979 CTGGAGTACACCAATTCACCACTGACCTGACTGACTAATTTTAAAGTT 1930
350 .ValGlnMet..... 352
1929 TGTAGATGTGGGATCTACTATGCTGCTAGTGTGCTGAAATCCA 1880
353 .....LysThrGlyLeuAsnAsn 358
1879 GGGCTCAACAAATTCCTCCATCTCGGCATCTGACCTGGGATTTAGAC 1830
359 ThrSerValCysAlaLeuGluProSerGlyCys.....ThrProL 372
1829 GTGAGCCTCTGGGCCAGGAGCCTCATCTGCTGCTCCATTTTACTCT 1780
372 euPro...SerMetAlaSerThrArgAlaAlaArgLeuGlyGlnGluLeu 387
1779 TCCCCGATCATCTCTCTTCTTATTCACAAATCAGGCTGCAAAATGAGATT 1730
388 LeuGln 389
1729 CTCCAA 1724

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seq\_name: /cgn2\_6/ptodata/2/ina/6B\_COMP.seq:US-08-718-388-5

seq\_documentation\_block:

Sequence 5, Application US/08718388

Patent No. 6271362

GENERAL INFORMATION:

APPLICANT: MORIKAWA, MINORU

APPLICANT: HARADA, NAOKI

TITLE OF INVENTION: GENE ENCODING Igg Fc REGION-BINDING

TITLE OF INVENTION: PROTEIN

NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:

ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH

STREET: PO BOX 747

CITY: FALLS CHURCH

STATE: VA

COUNTRY: USA

ZIP: 22040-0747

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/718,388

FILING DATE:

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: MURPHY JR, GERALD M

REGISTRATION NUMBER: 28,977

REFERENCE/DOCKET NUMBER: 0230-111

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 205-8000

TELEFAX: (703) 205-8050

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 3661 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

US-08-718-388-5

alignment\_scores:

Quality: 100.50

Ratio: 0.498

Percent Similarity: 44.690

Length: 452

Gaps: 30

Percent Identity: 22.345

Alignment block:  
US-09-899-471-2\_COPY\_21\_440 x US-08-718-388-5 ..

Align seg 1/1 to: US-08-718-388-5 from: 1 to: 3661

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13 CysSerLeuGlyLeuSerCysHisLeuTrpAspGlyAspValLeu..... 27
1832 TGTGTGGAGGGCTGCCAGTCGACGGC.....GGTTTCGTGTTAAATGTC 1875
28 .....CysLeu.ProGlySerLeuGlnSerAlaProGlyProValLeu 41
1876 TCACCGCTGTGTTCCCTCAACAAGCGCTGGCTGCTGGCCAAATGCA 1925
42 ValProThrArgLeuGlnThrGluLeuValLeuArgCysProGlnLysTh 58
1926 CCTACACAGCGCGGCGAGTGGCTTTGGCTGATGGCACCCTGCTCCAG 1975
58 rAspCysAlaLeuArgValArgVal.....ValHisLeuAlaVal 72
1976 TGTGTGCTGGCGGGCTGGGGGTGGCTGCTGCTGTCACACCTGCCAG 2025
72 aHisGlyHisTrpAlaGlu.....ProGlnGlu 81
2026 CTGTGGCG...TGGGTGAAGTGTGTGGCTCTCCATCCGCCAGCAGCAG 2072
82 AlaGlyLysSerAspSerGluLeuGlnGluSerArgAsnAlaSerLeuGly 98
2073 GCTGCCAGCCCTTCACACAGCTGAGTGCAGCGCTGGGGTGCACCCCAT 2122
98 nAlaGlnValLeuSerPheGlnAla.TyrProIleAlaArgCysAla 114
2123 TAGCTGACCTGGATGGACGACCATCAATTCCA..... 2157
115 LeuLeuGlnValGlnValProAlaAspLeuValGlnPro.GlyGlnSerV 131
2158 ..AGGCACTCGAGTACTGCTGAGTGCACCTGCCAGCGACCACTT 2204
131 aGlySerAlaValPheAspCysPheGlnAlaSerLeuGlyAlaGlnVal 147
2205 TGGGGGCTGAGAACTTCACTGCTACTGATGACCAATGAGACCGGGGAGC 2254
148 GlnIleTrpSerTyrThrLys.....ProArgTyrGlnLysGly 160
2255 CAGCGCTGACGTACACCGCGCACTGTACCCCTGCAAACTTCAACACAG 2304
160 uLeuAsnLeuThrGlnGlnLeuPro.....AspGlyAspAsnValL 174
2305 CCTGACACTGAGTGGCCGCTGGCCCGGAAGCTACAGTGGAGCGGCTGT 2354
174 euLeuThrLeuAspValSerGluGlnGlnAspPheSerPheLeuLeuYr 190
2355 TCGTCACTCTG..... 2365
191 LeuArgProValProAspAlaLeuLysSerLeuTyrTrpLysAsnLeuTh 207
2366 .....CCCTTCAGCTGAGTCTCTCTCTGACAGCAGCAGCACTGAG 2403
207 rGlyProGlnAsnIleThrLeuAsnHisThrAspLeuValProCysLeuC 224
2404 CGGCGCGCGCGGCTGGTGACCAACACTAGGGCTC..... 2440
224 yAlaGlnValTrpSerLeuGluProAspSerGlu..... 235
2441 .....TCGCTGGCTTTGAGCGGGGACACTTCTGCGGCTG 2476
236 ArgVal.....GlyPheCys.....ProPh 242
2477 CGCGTGGCGCGCGGTACCGGGCTCTCTCTGCTTATGCGGGAATA 2526
242 eArgGlnAspProGlyAlaHisArgAsnLeuTrpHisIleAlaArgLeuA 259
2527 CAACAAGGACCGCGGAGCAGC.....CTGA 2552

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259 rValLeu.....SerProGlyValTrpGln..... 267
2553 AGGCGGTGGCGGGAGAGCCCGCGGATGCGAGTGGCGCGCCAGAGCG 2602
268 .....LeuAspAlaProCys.....CysLeuProGlyLys 277
2603 TGGCGGAAATGTGTCTCAAGCCATGCCCGCTGCGCGCTGACCCCAAGCA 2652
277 sValThrLeuCysTrpGlnAlaProAspGln..... 287
2653 GCAGAG...TCCTTGGCGGGCGGAGCCGCGGCGGTGATCTCCGCA 2699
288 .....SerProCysGlnProLeuValProProValProGln 299
2700 CCGAGCGCCCTGCGCGCGCTGCGCACGCGCTGTGCTCCGCGCGG 2743
300 LysAsnAlaTrpValAsnGluProGlnAspPheGln..... 311
2744 .....CAGTACTTCCAGGCGCTGCTGCTGA 2769
312 .....LeuValAlaGlyHisPro...AsnLeuCysValGlnValSerT 325
2770 CGCTGCCAATTCAGGGCATCTCGAGAGCGCTCTGCTGCAATGCGCA 2819
325 hTrpGluLysValGlnLeuGlnAlaCysSerTrpAlaAspSerLeuGly 341
2820 CCTAC.....GTGGCAGCCTGTACAGCGCGCTGGGGCC..... 2851
342 ProPheLysAspAspMetLeuLeuValGlnMetLys.ThrGlyLeuAsnA 358
2852 .....CAGCTCCGCGAGTGGAGGGCGGC 2874
358 snTrpSerValCysAlaLeuGluProSerGlyCysThrPro..... 371
2875 GGACTTCTGTC.....CCTTCAGTGGCTTGCACAGCACT 2912
372 .....LeuProSerMetAlaSerThrArgAlaAlaArg 382
2913 ACGAGCTGCGGGTACCTGCTGCTGGAGGCTGCCGAGCGCTGGG 2960

seq_name: /cgn2_6/prodata/2/lna/bb_COMB.seq:US-08-718-388-6

seq_documentation_block:
: Sequence 6, Application US/08718388
: Patent No. 6271362
: GENERAL INFORMATION:
: APPLICANT: MORIKAWA, MINORU
: TITLE OF INVENTION: GENE ENCODING Igg Fc REGION-BINDING
: TITLE OF INVENTION: PROTEIN
: NUMBER OF SEQUENCES: 29
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
: STREET: PO BOX 747
: CITY: FALLS CHURCH
: STATE: VA
: COUNTRY: USA
: ZIP: 22040-0747
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/718,388
: FILING DATE:
: CLASSIFICATION: 536
: ATTORNEY/AGENT INFORMATION:
: NAME: MURPHY JR, GERALD M
: REGISTRATION NUMBER: 28,977
: REFERENCE/DOCKET NUMBER: 0230-111
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (703) 205-8000

```

TELEFAX: (703) 205-8050  
 INFORMATION FOR SEQ ID NO: 6:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 7824 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 21..7802  
 US-08-718-388-6

alignment\_scores:  
 Quality: 100.50 Length: 452  
 Ratio: 0.498 Gaps: 30  
 Percent Similarity: 44.690 Percent Identity: 22.345

alignment\_block:  
 US-09-899-471-2\_COPY\_21\_440 x US-08-718-388-6 ..

Align seg 1/1 to: US-08-718-388-6 from: 1 to: 7824

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13 CysSerLeuGlyLeuSerCysHisLeuTrpAspGlyAspValLeu..... 27
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28 .....CysLeu.ProGlySerLeuGlnSerAlaProGlyProValLeu 41
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6011 TGACCGCTGTGTTCCCTCAACACGAGCGTGGCTGCTGGGCCAATGCCA 6060
42 ValProThrArgLeuGlnThrGluLeuValLeuArgCysProGlnIstb 58
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6061 CCTACACAGCGCGGCGAGTGTGAGTTGGCTGATGCGACCTGCTCCAG 6110
58 rAspCysAlaLeuArgValArgValVal.....ValHisLeuAla 72
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6111 TGGTGTGCTGGCGGCGCTGGGGGTGGCTGCTGTCACACCTGCCAG 6160
72 aHisGlyHisTrpAlaGlu.....ProGlnIstb 81
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6161 CTGTGGGC...TGGGTGAAGTGTGTGGCTCTGCCATCCGGCCAGCAGC 6207
82 AlaGlyLysSerAspSerGluLeuGlnIstbArgAsnAlaSerLeuGlu 98
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
6208 GTGCGACGCGCGCTGACGACAGTGTGCGAGCGTGGGGTGGACCCCAT 6257
98 nAlaGlnValValLeuSerPheGlnAla.TyrProIleAlaArgCysAla 114
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6258 TACGTACACTGTGATGGCGACCGCATTCATTTCCA..... 6292
115 LeuLeuGlnValGlnValProAlaAspLeuValGlnPro.GlyGlnSer 131
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6293 ...AGGCACCTGCGAGTACTGCTGTGAGTGCACCCCTGCCAGGACCACT 6339
131 aGlySerAlaValPheAspCysPheGlnAlaSerLeuGlnAlaGlnVal 147
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6340 TGGGGCTGAGAACTTCACTGTCACTGTAGCCCAATGACACCGGGGAGC 6389
148 GlnIleTrpSerTyrThrLys.....ProArgTyrGlnLysGlu 160
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
6390 CAGGCTGTACGTACACCGCGAGTGTACACCTCAATTCACACACGAG 6439
160 uLeuAsnLeuThrGlnGlnLeuPro.....AspGlyAspAsnVal 174
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
6440 CCTGACACTGAGTGCCTGGCGCCGCGAAGTACAGGTGAGGCGGCTGT 6489
174 euleuThrLeuAspValSerGluGlnAspPheSerPheLeuLeuTyr 190
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
6490 TCGTACTCTG..... 6500
191 LeuArgProValProAspAlaLeuLysSerLeuTrpTyrLysAsnLeuTh 207

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6501 .....CCCTTCAGTGGAGCTGTCTGTCCAGCAGACCTGTAG 6538
207 rGlyProGlnAsnIleThrLeuAsnHisThrAspLeuValProCysLeu 224
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6539 CGCGCGAGCTGTGGTGTACACCAACCTCAGGCTC..... 6575
224 ystIleGlnValTrpSerLeuGluProAspSerGlu..... 235
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6576 .....TCCTGGCTTTCAGAGGGGAGACGTTGTCGCGCTG 6611
236 ArgVal.....GluPheCys.....Proh 242
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6612 CGCGTGGCGCGCGGTACGCGGCTGTCTGTGGCTTATGGCGGAAGA 6661
242 eArgGlnAspProGlyAlaHisArgAsnLeuThrHisIleAlaArgLeu 259
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
6662 CAACAGAGACCCCGAGACGAC.....CTGA 6687
259 rValLeu.....SerProGlyValTrpGln..... 267
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6688 AGCGGTGTGGCGGAGAACCCCGCGATGCGACGTGGCGCGCCAGGCG 6737
268 .....LeuAspAlaProCys.....CysLeuProGlyLys 277
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6738 TCGCGGAAATGTGTCCAGCCATGCCCGTGTGCGCGTGCACCCAGAGA 6787
277 sValThrLeuCysTrpGlnAlaProAspGln..... 287
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312 .....LeuValAlaGlyHisPro...AsnLeuCysValGlnValSer 325
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358 snThrSerValCysAlaLeuGluProSerGlyCysThrPro..... 371
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7010 GGACTTGTCTC.....CCTTCAGTGCCTGCGCCACAGCAGCACT 7047
372 .....LeuProSerMetAlaSerThrArgAlaAlaArg 382
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7048 ACCAGCTGTGCGGTGACTCTCTGTGGAGACTGCGCAGCTGTGCG 7095
seq_name: /cgn2_6/plodata/2/ina/5B_comb.seq.us-08-718-388-8
seq_documentation_block:
: Sequence 8, Application us/08718388
: Patent No. 6271362
: GENERAL INFORMATION:
: APPLICANT: MORIKAWA, MINORU
: TITLE OF INVENTION: GENE ENCODING I9G FC REGION-BINDING
: NUMBER OF SEQUENCES: 29
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
: STREET: PO BOX 747

```

CITY: FALLS CHURCH  
 STATE: VA  
 COUNTRY: USA  
 ZIP: 22040-0747  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0.  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/718,388  
 FILING DATE:  
 CLASSIFICATION: 536  
 ATTORNEY/AGENT INFORMATION:  
 NAME: MURPHY JR, GERALD M  
 REGISTRATION NUMBER: 28,977  
 REFERENCE/DOCKET NUMBER: 0230-111  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (703) 205-8000  
 TELEFAX: (703) 205-8050  
 INFORMATION FOR SEQ ID NO: 8:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 16382 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 9..16223  
 US-08-718-388-8

[illegible]

alignment\_block:  
US-09-899-471-2\_COPY\_21\_440 x US-08-718-388-8

Align seg 1/1 to: US-08-718-388-8 from: 1 to: 16382

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13 CysSerLeuGluGlyLeuSerCysHisLeuTrpAspValysPvalleu..... 27
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5955 TGCTGTGGAGGGCGTCCACATGCCAGCC...GGTTTCGTGTAAAGTC 5998B
28 .....CysLeu.ProGlySerLeuGlnSerAlaProGlyProValleu 41
||||| :||| :||| |||||:
5999 TGACCSCGTGTGTTCCCTCAACAAGCGCTCGCGCTGTGGCCAAATGCA 6048B
42 ValProThrArgLeuGlnInThrGluLeuValIleuArgCysProGlnLysrTh 58
||||| :||| :|||
6049 CCTACACACAGAGGGCGGCAGTAGACTTTTGCGCTATGCACACTGCTCCAG 6098B
58 rAspCysAlaLeuArgValArgValVal.....ValHisLeuAlav 72
:||| ||| :|||: :||| |||
6099 TCGTGTGCGTGGCGGGCTGGGGGTGGCTCGCTGCTGTGCACACACTGCGCAG 6148B
72 alHisGlyHisTrpAlaGlu.....ProGluGlu 81
:||| |||||: :|||
6149 CTGTGGCC...TGGTGGAAGTGTGTGGCGCTCTCGCCCATCCGGCCAGACG 6195B
82 AlaGlyLysSerAspSerGluLeuGlnGluSerArgAsnAlaSerLeuGl 98
||||| :||| :||| |||:
6196 GCTGCACAGCCCGCACACACAGCTGAGTGCACGGCGTGGGGGTAGACCCCAT 6245B
98 nAlaGlnValIleuSerPheGlnAla.TyrProIlealaArgCysAla 114
:||| :||| :||| |||
6246 TAGCGTACACTGTGAATGGGACCGCATTCAAATTCCA..... 6280B
115 LeuLeuGluValGlnValProAlaAspLeuValGlnPro.GlycInServ 131
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6281	..	AGGACACCTGGCGAGTACCTCTGTGAGTGACACCTGGACCGACACCT	6327
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Sun Sep 29 09:32:47 2002

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Date: Sep 28, 2002 9:43 PM

About: Results were produced by the Gencore software, version 4.5,  
Copyright (c) 1993-2000 Compugen Ltd.

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-LIST=45 -DOCALLIGN=200 -THR.SCORE=pct -THR.MAX=100 -THR.MIN=0  
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Query length: 420

Database sequences: 13736207

Database length: 1841457050

Search time (sec): 7183.320000

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VERSION BB609618.1 GI:16451334  
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SOURCE house mouse.  
ORGANISM Mus musculus.  
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 1006)

## REFERENCE

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Unpublished (2001)  
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Fax: 81-45-503-9216  
Email: genome-resgsc.riken.go.jp,  
URL: http://genome.resgsc.riken.go.jp/  
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Computational Analysis of Full-length Mouse cDNAs Compared with  
Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)  
Please visit our web site (<http://genome.resgsc.riken.go.jp>) for  
further details.  
e mouse tissues.

## FEATURES

### source

Location/Qualifiers  
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380 aalaargleuglucyluvalleuasnleutrphtislealarg 396
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503 tgcctgcctggagagagatgctgtccacacacctgttccctgt 552
|||||
397 metglnleutrpasnaspasmetlserleutrpalaacysp 413
|||||
553 atgcagctgtggaacgacacacacctgttccctgtgctgtgct 602
|||||
413 taspylstryllehlargarg 420
|||||
603 ggacaaagtacatccacacacctgttccctgtgctgtgctgct 624
|||||
seq_name: gb_est2:BI332055
seq_documentation_block:

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LOCUS BI332055 697 bp mRNA linear EST 30-JUL-2001  
DEFINITION 602982878P1 NCI\_CGAP\_L19 Mus musculus CDNA clone IMAGE:5135755 5',  
RNA sequence.  
ACCESSION BI332055  
VERSION BI332055.1 GI:15016712  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 697)  
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: Jeffrey E. Green, M.D.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LIML at:  
<http://image.llnl.gov>  
Plate: L1M11333 row: k column: 20  
High quality sequence stop: 697.  
Location/Qualifiers  
1..697  
/organism="Mus musculus"  
/strain="FVB/N"  
/db\_xref="taxon:10090"  
/clone="IMAGE:5135755"  
/clone\_id="NCI\_CGAP\_L19"  
/lab\_host="DH10B (T1 phage-resistant)"  
/note="Organ: liver; Vector: pCMV-SPORT6; Site\_1: NotI;  
Site\_2: SalI; Cloned unidirectionally. Primer: Oligo dt.  
Average insert size 1.9 kb. Constructed by Life  
Technologies. Note: this is a NCI\_CGAP Library."

## FEATURES

location/Qualifiers  
1..697  
/organism="Mus musculus"  
/strain="FVB/N"  
/db\_xref="taxon:10090"  
/clone="IMAGE:5135755"  
/clone\_id="NCI\_CGAP\_L19"  
/lab\_host="DH10B (T1 phage-resistant)"  
/note="Organ: liver; Vector: pCMV-SPORT6; Site\_1: NotI;  
Site\_2: SalI; Cloned unidirectionally. Primer: Oligo dt.  
Average insert size 1.9 kb. Constructed by Life  
Technologies. Note: this is a NCI\_CGAP Library."

## BASE COUNT

141 a 212 c 205 g 139 t

## alignment\_scores:

Quality: 930.00 Length: 172  
Ratio: 5.471 Gaps: 1  
Percent Similarity: 98.837 Percent Identity: 98.256

## alignment\_block:

US-09-899-471-2\_COPY\_21\_440 x BI332055 ..

Align seg 1/1 to: BI332055 from: 1 to: 697

```

250 argasnleutrphtislealargleuargvalleuysertprogl 266
|||||
2 argasnleutrphtislealargleuargvalleuysertprogl 266
|||||
266 pglneuaspaalaprocyseuysileglnvaltrpserle 283
|||||
52 gcagctagatggcctgtgctgtgctgtgctgtgctgtgctgtg 101
|||||
283 lnalaproaspinsrprocyseuysileglnvaltrpserle 299
|||||
102 aggcacacacacacacctgttccctgtgctgtgctgtgctgtg 151
|||||
300 lysasnleutrphtislealargleuargvalleuysertpro 316
|||||
152 aagaacacacacacacctgttccctgtgctgtgctgtgctgtg 201
|||||
316 lsrpasphevalgluvaltrpgrlnleuasnleutrphtisle 332
|||||
202 acccaccctgtgtgtccaggtgacacctgtggaaggttccactc 251
|||||
333 alacysertrpalaaspsrleugluprophelysaspmetleu 349
|||||

```

252 GCGTCTGTGGCTGACTCCTGGGGCCCTTCACAGATGATGCTGT 301  
 349 VAlGluMetLysThrGlyLeuAsnAspThrSerValCysAlaLeuGluP 366  
 302 AGTGGAGTGAACCGGCTTCACACACATCAGCTGTGCTTGGAC 351  
 366 roSerGlyCysThrProLeuProSerMetAlaSerThrArgAlaAlaArg 382  
 352 CCACTGGCTGTACACACTGCCACATGCGCTCCACGAGAGCTGCTGC 401  
 383 LeuGlyGluGluLeuLeuGlnAspPheArgSerHisGlnCysMetGln 399  
 402 CTGGAGAGGGGTGCTGCAAGACTTCGATCACAACAGTATGACAGCT 451  
 399 UTTPAspAspAspAspMetGlySerLeuTrpAlaCysPrometAspLysT 416  
 452 GTGACAGCATACACATGAGGATGCTATGGCGCTGCCCATGAGACAGT 501  
 416 YrLEHsArgArg 420  
 502 ACATCCACAGCGCC 515

seq\_name: gb\_est2:BI251117

seq\_documentation\_block:

LOCUS BI251117 839 bp mRNA linear EST 17-JUL-2001  
 DEFINITION 602994315F1 NCL\_CGAP\_Mam5 Mus musculus cDNA clone IMAGE:5150378 5',  
 mRNA sequence.  
 ACCESSION BI251117  
 VERSION BI251117.1 GI:14800198  
 KEYWORDS EST.  
 SOURCE house mouse.  
 ORGANISM Mus musculus.  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 839)  
 NIH-MGC http://mgi.nci.nih.gov/  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgabps-remail.nih.gov  
 Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
 http://image.llnl.gov  
 Plate: L1AM11371 row: m column: 03  
 High quality sequence stop: 836.

## FEATURES

SOURCE

Location/Qualifiers  
 1..839  
 /organism="Mus musculus"  
 /strain="C57/B6"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:5150378"  
 /clone\_lib="NCL\_CGAP\_Mam5"  
 /tissue\_type="tumor, gross tissue"  
 /dev\_stage="7 months"  
 /lab\_host="DH10B"  
 /note="Organ: mammary; Vector: pCMV-SPORT6; Site:1: Salt;  
 Site:2: Not; Cloned unidirectionally. Primer: Oligo dT.  
 Library constructed by Life Technologies. Investigators  
 providing samples: Lothar Hennighausen/Robin Humphreys,  
 NIH."

BASE COUNT 146 a 248 c 268 g 177 t  
 ORIGIN

Alignment\_scores:  
 Quality: 866.50 Length: 191  
 Ratio: 5.009 Gaps: 2  
 Percent Similarity: 90.576 Percent Identity: 90.576

alignment\_block:

US-09-899-471-2\_COPY\_21\_440 x BI251117

Align seg 1/1 to: BI251117 from: 1 to: 839

1 LeuGluArgLeuMetLupProGlnAspThrAlaArgCysSerLeuGlyLe 17  
 259 CTGGAGAGACTATGAGGCTTCAGACACTGACAGCGCTGCTCTAGAGCCT 308  
 17 uSerCysHisLeuTrpAspGlyAspValLeuGlySerLeuGlySerLeu 34  
 309 CTCCTGACCACTCTGGAGATGATGATGCTGCTGCTGCTGGAAGCCTCC 358  
 34 InSerAlaProGlyProValLeuValProThrArgLeuGlnThrGluLeu 50  
 359 AGTCGACCCACAGGCCCTGTGCTAGTGCCTACCCGCTGACAGAGCCTG 408  
 51 ValLeuArgCysProGlnLysThrAspCysAlaLeuArgValA 67  
 409 GTGCTGAGGTGTCACAGAGAGATGCGCCCTGTGCTGCTGCTGCTGCT 458  
 67 lValHisLeuAlaValHisGlyHisTrpAlaGluProGluGluAlaGlyL 84  
 459 GGTCCACTGGCCGTGCTATGAGGCTGAGGCTGAGAGCTGGAAGAGCTGGA 508  
 84 ySerAspSerGluLeuGlnGluSerArgAsnAlaSerLeuGlnAlaGln 100  
 509 AGTCGATTCACACATCCACAGAGCTAGAGACCCCTCTCCAGGCCAG 558  
 101 ValValLeuSerPheGlnAlaTrpProIleAlaArgCysAlaLeuLeuG 117  
 559 GTGCTGCTCTCTCTCCAGGCTACCCATGCGCCGCTGCTGCTGCTGGA 608  
 117 VAlaGluValProAlaAspLeuValGlnProGlyGlnSerValGlySerA 134  
 609 GGTCCAGGTGCGGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 658  
 134 lValPheAspCysPheGlnAlaSerLeuGlyValaGluValGlnIleTrp 150  
 659 CGGTATTTGACTGTTCCAGGCTAGCTTGGGGCTAGAGTACAGATCTGG 708  
 151 Ser TyrThrLysProArgTyrGlnLysGluLeuAsnLeuThrGlnGlnL 167  
 709 TCCCTAACACAGAGCCAGGTACAGAAAGAGCTCAACTCACACAGAGC 758  
 167 eupProAsp..... 169  
 759 TGCCGTGACTGCAGGCTCTGAAGTCCGGAGACAGATCCAGAGCTGCTGG 808  
 170 ...GlyAspAsnValLeuLeu 175  
 809 AATGCTGACATGCTCTCTCTG 829

seq\_name: gb\_est2:BI765330

seq\_documentation\_block:

LOCUS BI765330 922 bp mRNA linear EST 25-SEP-2001  
 DEFINITION 603050641F1 NIH\_MGC\_116 Homo sapiens cDNA clone IMAGE:5150442 5',  
 mRNA sequence.  
 ACCESSION BI765330  
 VERSION BI765330.1 GI:15756908  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens.  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 922)  
 NIH-MGC http://mgi.nci.nih.gov/  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgabps-remail.nih.gov

Tissue Procurement: Life Technologies, Inc.  
 CDNA Library Preparation: Life Technologies, Inc.  
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.lnl.gov>  
 Plate: L14M11476 Row: b Column: 11  
 High quality sequence stop: 794.

## FEATURES

## source

Location/Qualifiers

1. 922  
 /organism="Homo sapiens"  
 /db\_xref="taxon:3606"  
 /clone="IMAGE:5190442"  
 /clone\_id="NIH\_MGC\_116"  
 /lab\_host="DH10B"  
 /note="Organ: pooled colon, kidney, stomach; Vector:  
 pCMV-SPORT6; Site:1: NOTI; Site:2: EcoRV (destroyed); RNA  
 source anonymous pool of 3 colons, age 26 yo male, 49 yo  
 female, 71 yo male colon; 46 yo male kidney, and pool of 2  
 stomachs, 62 yo male and 70 yo female. Library is  
 oligo-dT primed and directionally cloned (EcoRV site is  
 destroyed upon cloning). Average insert size 1.4 kb.  
 Insert size range 1-3 kb. Library is normalized and  
 enriched for full-length clones and was constructed by C.  
 Gruber (Invitrogen). Research Genetics tracking code  
 023. Note: this is a NIH\_MGC library."

BASE COUNT 147 a 297 c 272 g 206 t  
 ORIGIN

alignment\_scores:  
 Quality: 866.50 Length: 329  
 Ratio: 3.610 Gaps: 8  
 Percent Similarity: 72.948 Percent Identity: 57.751

## alignment\_block:

US-09-899-471-2\_COPY\_21\_440 x B1765330

Align seg 1/1 to: B1765330 from: 1 to: 922

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7 ProGlnAspThrAlaArgCysSerLeuGlyLeuSerCysHisLeuTrpAs 23
|||||.....:|||||.....:|||||.....:|||||.....:
6 CcTtAGGCGcCTACcCAGcCTcTcCGGcGcCTcTcCGcGcCTcTcGGA 55
23 pGlyAspValLeuCysLeuProGlySerLeuGlnSerAlaProGlyPro 40
|||||.....:|||||.....:|||||.....:|||||.....:
56 CAGTGAcATAcTtGcCCTGcGcGcGAGAcTtGcCTGcTcGcGcGcGc 105
40 AlLeuValProThrArgLeuGlnThrGluLeuValLeuArgCysProGln 56
|||||.....:|||||.....:|||||.....:|||||.....:
106 TGcTGcGcGcCTAcCAGcCAGcAGAcGAGcGcTGTGAGGcGcGcAG 155
57 LysThrAspCysAlaLeuArgValArgValAlaHisLeuAlaValHis 73
:::|||||.....:|||||.....:|||||.....:|||||.....:
156 GAGAcCAGcCTGAcCTcTGTGcTGTGcGcTGTGcCTGcCAGcCTGcGA 205
73 sGlyHisTrpAlaGluProGluGluAlaGlyLysSerAspSerGluLeu 90
|.....:.....:.....:.....:.....:.....:.....:
206 T.....:.....:.....:.....:.....:.....:.....: 206
90 InGluSerArgAsnAlaSerLeuGlnAlaGlnValValLeuSerPheGln 106
|||||.....:|||||.....:|||||.....:|||||.....:
207 .....:.....:.....:.....:.....:.....:.....: 242
107 AlaTyProIleAlaArgCysAlaLeuLeuGluValGlnValProAlaAs 123
|||||.....:|||||.....:|||||.....:|||||.....:
243 GcCTAcCCTAcTcGcGcCTGcGcTGTGAGGcGcCAGAcTcCTGcTcG 292
123 pLeuValAlaProGlyLysLeuValGlySerAlaHisValPheAspCysPheG 140
|||||.....:|||||.....:|||||.....:|||||.....:
293 CcTtTGcCAcTtTGcTGTGcGcCTGcTGTGcTGTATATAcTcCTGcG 342

```

```

140 LuAlaSerLeuGlyAlaGluValGlnIleTrpSerTyThrLysProArg 156
|||||.....:|||||.....:|||||.....:|||||.....:
343 AGcCTGcCCTAcAGGAGcAGcAGcTAcGATcTGTcCTAcTAcAGcCAG 392
157 TyTrGlnLysGluLeuAsnLeuThrGlnGlnLeuPro.....: 168
393 TAcGAGAcAGAcACTcAcACAcACAcAGAcGcTGTcGcCTGcGcCTGc 442
169 .....:.....:.....:.....:.....:.....:.....: 181
443 AcGcTGTAcCAGAcAGcAGcTGTAcAcAcGcTGTcGcTGTcGATGTcTGA 492
181 uGluGlnAspPheSerPheLeuLeuTyThrLeuArgProValProAspAla 198
493 GAGAcAGAcACTTGTGcGcCTGTcCTGTAc.....:.....: 520
198 euLysSerLeuTrpTyThrLysAsnLeuThrGlyProGlnAsnIleThrLeu 214
521 .....:.....:.....:.....:.....:.....:.....: 553
215 AspHisThrAspLeuValProCysLeuCysIleGlnValTrpSerLeuG 231
|||||.....:|||||.....:|||||.....:|||||.....:
554 AcCAGAcACAcAGcCTGTcCTGcCTGTcCTGTATAcAGcTGTGcCTGTG 603
231 LuProAspSerGluArgValGluPheCysProPheArgGluAspProGly 247
604 AcCTAcTcCTGTGTAcAGAcACAcAcTGTcCTGTcAGGAGAcACcCCTG 653
248 AlaHisArgAsnLeuTrpHisIleAlaArgLeuArgValLeuSerProG 264
|||||.....:|||||.....:|||||.....:|||||.....:
654 GcAGAcACAcAGAcCTGTGcGcAGcAcGcGcAGcTGTGcAGcCTGTGcA 702
264 yValTrpGlnLeuAspAlaProCysCysLeuProGlyLysValThrLeu 281
703 GAGcTGTGTGTGcAGcAGcCTGTGTGTGTGcGcGcAGAcAGcGcAGcT 752
281 ySTrPAlaProAspGlnSerProCysGlnProLeuValProProVal 297
753 GcTGTGcGcGcCTGcGcGcGcGcAGcCTGTGcGcGcCTGc.....: 796
298 ProGlnLysAsnAlaThrValAsnGluProGlnAsp...PheGlnLeuVal 313
797 GTTAcCTGTGAcAGAcAGcCTGTGTGTGcGcAGcCTGTGTGAGcTGTGT 846
313 lAlaGlyHisProAsnLeuCysValGlnValSer 324
847 TGAAGGcAGAcCTAcAcCTGTGTGTGTGcGTGAc 880

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seq\_name: gb\_est1:A1463827

## seq\_documentation\_block:

LOCUS A1463827 422 bp mRNA linear EST 09-MAR-1999  
 DEFINITION V332a03.y1 Gaywoodford Beiler mouse kidney day 7 Mus musculus cDNA  
 clone IMAGE:733036 5', mRNA sequence.

ACCESSION A1463827  
 VERSION A1463827.1 GI:4317857

KEYWORDS EST.  
 SOURCE house mouse.  
 ORGANISM Mus musculus

REFERENCE  
 1 (bases 1 to 422)  
 Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## AUTHORS

Marrin, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,  
 Underwood, K., Stepien, M., Theising, B., Allen, M., Bowers, Y., Person  
 B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter  
 E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,  
 Waterson, R. and Wilson, R.

The WashU-NCI Mouse EST Project 1999

## JOURNAL

Unpublished (1999)  
 Contact: Marra M/WashU-NCI Mouse EST Project 1999  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800

## COMMENT

Fax: 314 286 1810  
Email: mousest@watson.wustl.edu  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium (infoimage.lnl.gov) for further information.  
MGI:450084

This read is a RESEQUENCE of a previously sequenced mouse clone  
This read has been verified (found to hit its original self in the  
correct orientation)

Seq primer: Primer name ambiguous  
High quality sequence stop: 402.

## FEATURES

source

Location/Qualifiers

1. 422

/organism="Mus musculus"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone\_image="733036"

/clone\_lib="GuayWoodford Beler mouse kidney day 7"

/tissue\_type="kidney"

/dev\_stage="juvenile (7 days old)"

/lab\_host="SOLR (kanamycin resistant)"

/note="Organ: kidney; Vector: pBluescript SK-; Site\_1:  
EcoRI; Site\_2: XhoI; Cloned unidirectionally. Primer:  
Oligo dt. Average insert size: 1.0 kb; Uni-ZAP XR Vector;  
-5' adaptor sequence: 5' GAATTCGGCAGCAG 3' -3' adaptor  
sequence: 5' CTCGAGTTTCTTTTCTTTTCTTTT 3' Library provided  
by Lisa Guay-Woodford."

BASE COUNT 92 a 127 c 123 g 79 t 1 others

## ORIGIN

## alignment\_scores:

Quality: 748.00 Length: 140  
Ratio: 5.500 Gaps: 0  
Percent Similarity: 97.143 Percent Identity: 97.143

## alignment\_block:

US-09-899-471-2\_COPY\_21\_440 x A1463827

Align seg 1/1 to: A1463827 from: 1 to: 422

```

244 GluaspProglialaHlaArgAsnLeuTrpHisIleAlaArgLeuArgVa 260
3 GAAGATCCCGGTGCACACAGAGACCTGCGCACAAGCCAGCGTGGGG 52
260 lLeuSerProglialaTrpGlnLeuAspAlaProCysCysLeuProglial 277
53 ACCTGTCCCAAGGGGTATGCGAGTATGCGCTGTCTGCGCGGCA 102
277 yValThrLeuCysTrpGlnAlaProAspGlnSerProCysGlnProleu 293
103 AGGTAACTGTGCTGGCAGCAGCAGACAGAGTCCCTGCGACGACATT 152
294 ValProValProGlnAlaCysSerTrpAlaAspSerLeuGlnProleu 310
153 GTGCGACAGTGGCCAGAGAGAGAGCCAGTGTGATGAGCCACAGATT 202
310 eGlnLeuValAlaCysHisProAsnLeuCysValGlnValSerThrTrp 327
203 CCAGTTGGTGGCAGGCCACCCCAACTCTGTCTCCAGGTGAGACACTGGG 252
327 lutyValGlnLeuGlnAlaCysSerTrpAlaAspSerLeuGlnProleu 343
253 AGAAGGTTCAGCTCAAGCGCTGTGTGGCTGACCTCTTGGGCGCTTC 302
344 LysAspAspMetLeuLeuValGlnMetLysThrGlnLeuAsnAsnThse 360
303 AAGGATGATATGCTGNTAGTGAAGTGAAGAACCGGCTCAACACACATC 352
360 rValCysAlaLeuGlnProSerGlyCysThrProleuProSerMetAlas 377
353 AGTGTGCGCTTGGACACAGTGTGATACCACTGCCACAGCAGGCT 402
377 eThrArgAlaAlaArgLeu 383

```

403 CCAGGAGACTGCTGCTGCTG 422

seq\_name: gb\_test2:BG761977

seq\_documentation\_block:

LOCUS BG761977 935 bp mRNA linear EST 15-MAY-2001

DEFINITION 602718928F1 NIH\_MGC\_49 Homo sapiens cDNA clone IMAGE:4858806 5',

ACCESSION BG761977

VERSION BG761977.1 GI:14072630

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

TITLE Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

JOURNAL NIH-MGC http://mgi.nci.nih.gov/

COMMENT Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cga@bts-femail.nih.gov

Tissue Procurement: ATCC/DCTD/DFP

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:

http://image.lnl.gov

Plate: L10CM1713 row: h column: 07

High quality sequence stop: 813.

Location/Qualifiers

1. 935

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone\_image="4858806"

/clone\_lib="NIH\_MGC\_49"

/tissue\_type="melanotic melanoma, high MDR (cell line)"

/lab\_host="DH10B (phage-resistant)"

/note="Organ: skin; Vector: pORF7; Site\_1: XhoI; Site\_2:  
EcoRI; cDNA made by oligo-dt priming. Directionally cloned  
into EcoRI/XhoI sites using the following 5' adaptor:  
GGCAGAGAG(g). Size-selected >500bp for average insert size  
1.8kb. Library constructed by Ling Hong in the laboratory  
of Gerald M. Rubin (University of California, Berkeley)  
using ZAP-cDNA synthesis kit (Stratagene) and Superscript  
II RT (Life Technologies). Note: this is a NIH\_MGC  
Library."

BASE COUNT 154 a 301 c 291 g 189 t

## alignment\_scores:

Quality: 745.00 Length: 205  
Ratio: 4.306 Gaps: 3  
Percent Similarity: 84.390 Percent Identity: 67.317

## alignment\_block:

US-09-899-471-2\_COPY\_21\_440 x BG761977

Align seg 1/1 to: BG761977 from: 1 to: 935

```

217 ThrAspLeuValProCysLeuGlnIleGlnValTrpSerLeuProAs 233
2 ACAGACCTGGTCCCTGCTGCTGATACAGTGTGCTGCGACCTGA 51
233 pSerGlnArgValGlnProCysProPheArg. GluAspProglialaHis 249
52 CTCCCTTAGGAGCAGACATCTGCCCTTCAGGGGAGAGAGACCCCGACAC 101
250 ArgAsnLeuTrpHisIleAlaArgLeuArgValLeuSerProglialaTr 266
102 CAGAACTCTGGCAGAGCCGCCGACTGCGAGTGTGACCTGCGAGAGCTG 151

```



198 eulysSerleutrP 202  
 :::::|||||  
 766 TCCAGAGCTGCTGG 779

seq\_name: gb\_estl:BI689749

seq\_documentation\_block:

LOCUS BI689749 829 bp mRNA linear EST 18-SEP-2001  
 DEFINITION 603316255F1 NCI\_CGAP\_Mam6 Mus musculus cDNA clone IMAGE:5356237 5',  
 mRNA sequence.

ACCESSION BI689749  
 VERSION BI689749  
 KEYWORDS EST.

SOURCE house mouse.

ORGANISM

Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 829)  
 NIH-MGC http://mgi.nci.nih.gov/

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgaaps-remail.nih.gov  
 Tissue Procurement: Jeffrey Green M.D.  
 CDNA Library Preparation: Life Technologies, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLML1905 row: n column: 14  
 High quality sequence start: 4  
 High quality sequence stop: 671.  
 Location/Qualifiers

FEATURES

source

1..829

/organism="Mus musculus"

/strain="FVB/N"

/db\_xref="taxon:10090"

/clone="IMAGE:5356237"

/clone\_lib="NCI\_CGAP\_Mam6"

/sex="female, virgin"

/tissue\_type="infiltrating ductal carcinoma"

/dev\_stage="5 months"

/lab\_host="DH10B"

/note="Organ: mammary; Vector: pCMV-SPORT6; Site: 1: SalI;  
 Site: 2: NotI; Cloned unidirectionally. Primer: Oligo dT.  
 Library constructed by Life Technologies. Investigator  
 providing samples: Jeffrey Green, M.D., NIH"

BASE COUNT 145 a 237 c 272 g 175 t

alignment\_scores:

Quality: 720.50 Length: 179  
 Ratio: 4.420 Gaps: 7  
 Percent Similarity: 91.061 Percent Identity: 87.709

alignment\_block:

US-09-899-471-2\_COPY\_21\_440 x BI689749 ..

Align seg 1/1 to: BI689749 from: 1 to: 829

1 LeuGluArgLeuMetGluProGlnAspThrAlaArgCysSerLeuGlyLe 17  
 |||||  
 246 CTGGAGAGACTGATGAGCCTCAGACACTGCACGCTCTCTAGGCTT 295  
 |||||  
 17 uSerCysHisLeuTrpAspGlyAspValLeuGlnCysLeuProGlySerLeu 34  
 |||||  
 296 CTCTGACACCTCTGGGATGCTGAGCTGCTCTGCTGGAAGGCTTC 345  
 |||||  
 34 InSerAlaProGlyProValLeuValProThrArgLeuGlnThrGluLeu 50  
 |||||  
 346 AGCTGCCCCAGGCCCTGTGTAGTGTCTACCCGCTGAGAGGAGCTG 395

51 ValLeuArgCysProGlnLysThrAspCysAlaLeuArgValArgVala 67  
 |||||  
 396 GTGCTGAGGTGTCCACAGACAGATTGCCCTCTGTCTCTGCTGTGT 445

67 ValHisLeuAlaValHisGlyHisTrpAlaGluProGlnGluAlaGlyL 84  
 |||||  
 446 GTTCCACTGTGGCCGTGCATGGCAGCTGGGAGAGCTGTGAAGAGCTG 495

84 ySerAspSerGluLeuGlnGlnSerArgAsnAlaSerLeuGlnAlaGln 100  
 |||||  
 496 AGTCTGATTCAGAACTCCAGAGCTAGAGAACGCTCTCTCCAGGCCAG 545

101 ValValLeuSerPheGlnAlaTrpProIleAlaArg CysAlaLeuLeuG 117  
 |||||  
 546 GTGTGCTCTCTCTCCAGGCTTACCCATCCGCGCTGTGCTGCTGCTG 595

117 ValValGlnValProAlaAspLeuValGlnProGlyGlnSerValGlySer 133  
 |||||  
 596 AGCTCAGAGTGGCCCGCTGACCTGTGCAGCTGTCAGCTGCTGCTGCT 645

134 AlaValPheAspCysPheGluAlaSerLeuGlyAlaGlnValGlnI 149  
 |||||  
 646 GCGGATTTTGACTGTTTCAGAGCTAGTTCGTGGGCTGAGAGGCTACAAA 695

149 LeuPheSerTyrThrLys.....ProArgTyrGlnLysGlnLeuAs 162  
 |||||  
 696 TCTGGTCTTACACAGAGGCCAGGGAACCAAGAAAGAGTACACCTCA 745

162 nLeuThrGlnGlnLeuProAspGly 170  
 |||||  
 746 AAACAGAGATGCTGCTGACAGAGG 770

seq\_name: gb\_estl:AA403935

seq\_documentation\_block:

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

house mouse.

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 397)

AUTHORS

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,

Geisler,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,

Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,

Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and

Waterston,R.

The WashU-HMI Mouse EST Project

Unpublished (1996)

CONTACT: Marra M/Mouse EST Project

WashU-HMI Mouse EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8581, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@wustl.edu

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:450084

High quality sequence stop: 359.

FEATURES

source

1..397

Location/Qualifiers

/organism="Mus musculus"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="IMAGE:733036"

/clone\_lib="Guaywoodford Beier mouse kidney day 7"

/tissue\_type="kidney"



/dev stage="juvenile (7 days old)"  
/lab\_host="SOLR (kanamycin resistant)"  
/note="Organ: Kidney; Vector: pBluescript SK-; Site\_1:  
EcoRI; Site\_2: XhoI; Cloned unidirectionally. Primer:  
0.190 dt. Average insert size: 1.0 kb; Uni-ZAP XR Vector;  
-5' adaptor sequence: 5' GAATTCGGCAGCAG 3' -3' adaptor  
sequence: 5' CTCGAGTCTTTTCTTTTCTTTT 3' Library provided  
by Lisa Guay-Woodford."

BASE COUNT 88 a 117 c 116 g 76 t  
ORIGIN

Alignment\_scores:  
Quality: 706.00 Length: 132  
Ratio: 5.431 Gaps: 0  
Percent Similarity: 98.485 Percent Identity: 98.485

Alignment\_block:  
US-09-899-471-2\_COPY\_21\_440 x AA403935 ..

Align seg 1/1 to: AA403935 from: 1 to: 397

244 GUAAPPROGLYALAHISARGASNLTPHISILALAHARGLEUARGVA 260  
|||||  
3 GAAGATCCCGGTGCACACAGAACTCTGGCACATACCCAGGCTGGGGGT 52  
260 LLEUSERPROGLYVALTPGLNLEUASPALAPROCYSCYLEUPROGLYL 277  
53 ACTGCCCCAGGGGTATAGCAGCTAGATGCGCTGCTGCTGCGGGGCA 102  
277 YSVALTHLEUCYSTIRPGINALAPROASPLINSEPRCYSGINPROLEU 293  
|||||  
103 AGGTACACTGTGCTGGCAGCACACAGACAGATCCCTCCACCACTT 152  
294 VALPROVALPROGLINLYSASNALATHVALASGLUPROGLNAPPH 310  
153 GTGCCACAGTCCCCAGAGAAAGCGCACGTGAATGAGCCACAAAGATT 202  
310 EGLNLEUVALAGLYHISPROASNLEUCYSVALGINVALSERTHTRPG 327  
203 CCAGTTGGGAGGAGGACCCCACTCTGTGTCCAGTACAGCACTGGG 252  
327 LULYSVALGINLEUCLINALCYSSERTPALASPSEULEUGLYPROPH 343  
253 AGAAGCTTCAGCTGCACAGC.TGCTTGTGGGCTGACCTCTGGGGCCCTTC 301  
344 LYSASPAPMETLEULEUVALGIMETLYSTHGLYLEUASNSNTHRSE 360  
302 AAGGATGATATGCTGTAGTGAGAGAAACCGGCTCAACACACATC 351  
360 VALCYSLALEUGLUPROSERGLYCYSTHRPROLEUPROSERMET 375  
352 AGTGTGCTCTTGGAACCCAGTGGCTGTACACCACTGCCAGCATG 397

Seq name: gb\_esc2:BI770219

Seq\_documentation\_block:

Locus BI770219 855 bp mRNA linear EST 25-SEP-2001  
DEFINITION 603053287F1 NIH\_MGC\_122 Homo sapiens cDNA clone IMAGE:5203005 5',  
MRNA sequence.

Accession BI770219 GI:15761797

Keywords EST.  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 855)  
AUTHORS NIH-MGC http://mgc.ncl.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
CONTACT: Robert Strausberg, Ph.D.  
Email: c9apbs-remail.nih.gov

Tissue Procurement: Life Technologies, Inc.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLM1508 row: m column: 22  
High quality sequence stop: 827.

FEATURES  
source  
Location/Qualifiers  
1. 855  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5203005"  
/clone\_lib="NIH\_MGC\_122"  
/lab\_host="DH10B"

/note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;  
Site\_1: NotI; Site\_2: EcoRV (destroyed); RNA source  
anonymous pool of 24 week female lung, 16 week female  
spleen, and 20-22 week male spleens. Library is oligo-dT  
primed and directionally cloned (EcoRV site is destroyed  
upon cloning). Average insert size 1.4 kb, insert size  
range 1-3 kb. Library is normalized and enriched for  
full-length clones and was constructed by C. Gruber  
(Invitrogen). Research Genetics tracking code 026. Note:  
this is a NIH MGC Library."

BASE COUNT 147 a 268 c 265 g 175 t  
ORIGIN

alignment\_scores:  
Quality: 697.00 Length: 225  
Ratio: 3.916 Gaps: 4  
Percent Similarity: 79.111 Percent Identity: 63.111

Alignment\_block:  
US-09-899-471-2\_COPY\_21\_440 x BI770219 ..

Align seg 1/1 to: BI770219 from: 1 to: 855

1 LEUGLNUARGLEUMETGLUPROGLNAPSPHRLAARGCYSSERLEUGLYE 17  
|||||  
214 CTGGAGAGGCTTGTGGGGCTCAGAGACGCTACCCACTGCTCCGGGCT 263  
17 USERGHSILEUTRPAAPGLYASPVALLLEUCYSLEUPROGLYSERLEUG 34  
|||||  
264 CTCTTGGCGGCTCTGGGACAGTCAATCTCTGCTGCTGGGACATG 313  
34 INSERLAPROGLYPROVALLEUVALPROTHARGLEUINLTHRGLEU 50  
|||||  
314 TGCTGTCTCCGGGGCCCTGCTGCGCCCTACGACCTCAGACACAGCTG 363  
51 VALLEUARGCYSPROGLINLYSTHRASPCYSALALEUARGVALARGVA 67  
|||||  
364 GTGCTGAGGTGTCAGAGAGACCGACTGTGACCTGTGCTGCTGCTG 413  
67 IVALHISLEUALVALHISGLYHISTPRALGLUPROGLYGLU..... 81  
|||||  
414 TGTCACCTTGCGCTGATGGGACGTGGAGAGAGCCTGAGCTGAGGAAA 463  
82 .....ALAGLYSSERASPSERGLUENGLUENGLUENGLUENGLUENGL 96  
464 AGTTTGGAGAGACGCTGACTCAGGGGTGGAGAGACCTAGGATGCTCT 513  
97 LEUGLNUAGLNUVALLEUSERPHEGLNALATYRPROILEALARGCY 113  
|||||  
514 CTCAGAGCCCAAGTCGTCTCTTCCAGGCTACCTACTAGCCGGTG 563  
113 SALALEUENGLUVALGINVALPROALASPLEUVALGINPROGLYGLNS 130  
564 CGTCCTGCTGAGGTGCAAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCT 613  
130 EVALGLYSERLALVALPHNASPCYSPHEGLNUALASERLEUGLYALAGLU 146

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|||||.....|||||.....|||||.....
614 CTGGGGCTCTGTGTATATGACTGCTTGAGGCTCCCTAGGGAGTGAG 663
147 ValGlnIleTyrSerTyrThrLysProArgTyrGlnLysGlnLeuAsnLeu 163
|||||.....|||||.....|||||.....
664 GTACGAATCTGTCTCTATACAGCCAGGAGTACAGAGAGAACTCAACCA 713
163 uThGlnGlnLeu.....ProAspGly 171
|||||.....
714 CACACAGACGCTGCTGCCCTGCTCAACGTCTGACAGAGATGCTG 763
171 sPanValLeuLeuThrLeuAspValSerGlnGlnAspPheSerP 187
|||||.....
764 ACAACGTCACTGTGGTCTGATGTCTGTGAGAGACAGACACTTGGGCT 813
187 eLeuLeuTyrLeuArgProValProAspAlaLeuLysSerLeuTyrP 204
|||||.....
814 CTCCCTGTAC.....TGGCAAT 830
204 yAsnLeuThGlyProGlnAsn 211
|||||.....
831 CAGGCTCCAGGGCCCCCAAAAC 853

```

seq\_name: gb\_est1:AA238911

seq\_documentation\_block:

LOCUS AA238911 459 bp mRNA linear EST 03-MAR-1997  
DEFINITION mx92404.r1 Soares mouse NML Mus musculus cDNA clone IMAGE:693774  
5', mRNA sequence.

ACCESSION AA238911

VERSION AA238911.1 GI:1862936

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 459)

REFERENCE  
Matta, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,  
Geisler, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,  
Schellenberg, K., Stepien, M., Tan, F., Underwood, K., Moore, B.,  
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and  
Waterston, R.

TITLE The WashU-HMI Mouse EST Project  
JOURNAL Unpublished (1996)  
COMMENT Contact: Matta M/Mouse EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810

Email: mouseest@wustl.edu  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium (info@image.lnl.gov) for further information.  
MGI:427334  
Seq primer: -28ml3 rev2 EF from Amersham  
High quality sequence stop: 432.

#### FEATURES

source

1. 459  
/organism="Mus musculus"  
/db\_xref="taxon:10090"  
/clone="IMAGE:693774"  
/clone\_id="Soares mouse NML"  
/tissue\_type="Liver"  
/lab\_host="DH10B"  
/note="Vector: pT73D-Pac (Pharmacia) with a modified  
polylinker. Site 1: Not I; Site 2: Eco RI; 1st strand cDNA  
was primed with a Not I - oligo (dT) primer [5'  
TGTACCAATCTGAAGTGAAGCGCGCGATCTTTTCTTTTCTTTT 3'];  
double-stranded cDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Not I and cloned into the Not I  
and Eco RI sites of the modified pT73 vector. Library  
constructed and normalized by Bento Soares and M. Fatima  
Bonaldo."

BASE COUNT 99 a 135 c 122 g 103 t  
ORIGIN

#### alignment\_scores:

Quality: 694.00 Length: 153  
Ratio: 5.380 Gaps: 1  
Percent Similarity: 84.314 Percent Identity: 84.314

#### alignment\_block:

US-09-899-471-2\_COPY\_21\_440 x AA238911  
Align seg 1/1 to: AA238911 from: 1 to: 459

```

148 GlnIleTyrSerTyrThrLysProArgTyrGlnLysGlnLeuAsnLeu 164
|||||.....
1 CAGATCTGCTCTTACAGAGAGCCAGGTACAGAAAGAGCTCAACTCAC 50
164 rGlnGlnLeuPro.....
51 ACAGCAGCTGCTGCTGACTGACAGGGGCTTGAGTCCGGAGACATCCAGA 100
169 .....AspGlyAspAsnVal 173
101 GCTGTGGTCTGCTGCCCTGCTCAATGTCTTACAGAGTGTGACAAATGTC 150
174 LeuLeuThrLeuAspValSerGlnGlnAspPheSerPheLeuLeu 190
|||||.....
151 CTCTGTACACTGTGATGTCTGTGAGAGACAGACCTTACTTACTGTA 200
190 rLeuArgProValProAspAlaLeuLysSerLeuTyrPtyrLysAsnLeu 207
|||||.....
201 CCTGCTCCAGCTCCCGGATGCTCTCAATCTTGTGTACAAACCAACCTGCA 250
207 hGlyProGlnAsnIleThrLeuAsnHisThrAspLeuValProCysLeu 223
|||||.....
251 CTGGACCTCAGAACATTACTTTAAACACACAGACCTGGTCCCTGCTGC 300
224 CysAlaGlnAlaTyrPserLeuGluProAspSerGluArgValGluPheC 240
|||||.....
301 TGCATTACAGTGTGTGTGTGTGACAGCCAGACACTGTGAGAGGTCGATT 350
240 sProPheArgGluAspProGlyAlaHisArgAsnLeuThrHisIleAla 257
|||||.....
351 CCCCTTCCGGGAGATCCCGGTGCACACAGAACCTGTGCACATAGCCA 400
257 rGluLeuArgValLeuSerProGlyValTyrGlnLeuAspAlaProCys 273
|||||.....
401 GGCTGGGGTACTGTCCCAAGGGGTATGCACTAGATGCCCTTGTCTGT 450
274 LeuProGly 276
|||||.....
451 CTGCCGGGC 459

```

seq\_name: gb\_est1:AV752013

seq\_documentation\_block:

LOCUS AV752013 843 bp mRNA linear EST 19-OCT-2000  
DEFINITION AV752013 NPD Homo sapiens cDNA clone NPDHC06 5', mRNA sequence.

ACCESSION AV752013

VERSION AV752013.1 GI:10909861

KEYWORDS EST.

SOURCE human.

ORGANISM human.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 843)

AUTHORS Song, H., Peng, Y., Gu, Y., Yang, Y., Gao, G., Xiao, H., Xu, X., Li, N.,  
Qian, B., Liu, F., Ou, J., Gao, X., Cheng, Z., Xu, Z., Zeng, L., Xu, S., Gu  
W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Ye, M., Zhang, Q.,  
Han, Z., Chen, Z., Hu, R. and Chen, J.  
Homo sapiens NPD library cDNA clones  
Unpublished (2000)

## COMMENT

Contact: Qinghua Zhang  
Shanghai Institute of Endocrinology, Rui-Jin Hospital  
197 Rui-Jin II Road, Shanghai 200025, P. R. China  
Tel: 86-21-64370045(ex.663332)  
Fax: 86-21-64743206  
Email: mbs@ems.stn.sh.cn  
This clone is available at Shanghai Hematology Institute in Shanghai.  
Chinese National Human Genome Center at Shanghai  
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong.  
Location/Qualifiers

## FEATURES

source

1. 843  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_1lb="NPD"  
/tissue\_type="pituitary"  
/dev\_stage="adult"  
/lab\_host="SOLR"  
/note="Vector: pBluescript sk(-); Site\_1: EcoRI; Site\_2: XhoI"

ASE COUNT 150 a 243 c 268 g 181 t 1 others

## Alignment\_scores:

Quality: 693.50 Length: 298  
Ratio: 3.485 Gaps: 10  
Percent Similarity: 66.779 Percent Identity: 52.685

## Alignment\_block:

US-09-899-471-2\_COPY\_21\_440 x AV752013 ..

Align seg 1/1 to: AV752013 from: 1 to: 843

```

1  LeuGluArgLeuMetGluProGlnAspThrAlaArgCysSerLeuGlyLe 17
   |||||
16 CTGAGAGAGCTTGTGGGCTCAGACGCTACCCACTGCTCCGGGCT 65
   |||||
17 userCysHisLeuTrpAspGlyAspValLeuGlySerLeuG 34
   |||||
66 CTCTGGCGGCTGTGGACAGTACATCTGCTCCCTGGGGACATCG 115
   |||||
34 InsertAlaProGlyProValLeuValProThrArgLeuGlnThrGluLeu 50
   |||||
116 TGCCCTGCTCCGGGCCCGCTGCGCGCTACGACCTGCAGACAGAGCTG 165
   |||||
51 ValLeuArgCysProGlnLysThrAspCysAlaLeuArgVala 67
   |||||
166 GTGCTGAGGTCCAGAGAGACCGACTGTGACTGTGCTGCTGGCTGGC 215
   |||||
67 ValHisLeuAlaValHisGlyHisTrpAlaGluProGlnGlu..... 81
   |||||
216 TGTCACACTGGCCGTCATGGGCACCTGGAGACGCTGAAGAGAGAGAA 265
   |||||
82 ....AlaGlyLysSerAspSerGluLeuGlnGluSerArgAsnAlaSer 96
   |||||
266 AGTTTGAGAGGACGACTGACTCAGGGGTGAGAGAGCCTAGGAATGCTCT 315
   |||||
97 LeuGlnAlaGlnValValLeuSerPheGlnAlaTrpProIleAlaArgCys 113
   |||||
316 CTCACAGGCCCAAGTCGTGCTCTCTCCAGGCTTACCCCTACTGCCCCGCTG 365
   |||||
113 SalLeuLeuGlnValValGlnValProAlaAspLeuValGlnProGlyGlns 130
   |||||
366 CGTCTGCTGAGAGTGCAGAGTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 415
   |||||
130 erValGlySerAlaValPheAspCysPheGlnAlaSerLeuGlyAlaGlu 146
   |||||
416 CTGAGGCTGCTGCTGATATGACTGCTGAGGCTGCTGAGGAGGAGTGAAG 465
   |||||
147 ValGlnIleTrpSerTrpThrLysProArgTrpGlnLysGluLeuAsnIle 163
   |||||

```

seq\_name: gb\_est2:B1820026

seq\_documentation\_block:

LOCUS B1820026

DEFINITION 603037207P1 NIH\_MGC\_115 Homo sapiens cDNA clone IMAGE:5178409 5', mRNA sequence.

ACCESSION B1820026

VERSION B1820026.1 GI:15931576

KEYWORDS EST

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

NIH-MGC http://mhc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cga@bbs.remall.nih.gov

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:

http://image.llnl.gov

plate: L1444 row: m column: 02

High quality sequence stop: 884.

## FEATURES

source

1. 886  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5178409"  
/clone\_1lb="NIH\_MGC\_115"  
/lab\_host="DH10B"  
/note="Organ: pooled brain, lung, testis; Vector: pCMV-Sport6; Site\_1: NotI; Site\_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is

oligo-dr primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH-MGC Library."

BASE COUNT 154 a 275 c 272 g 185 t  
ORIGIN

alignment\_scores: Quality: 683.50 Length: 226  
Ratio: 3.797 Gaps: 6  
Percent Similarity: 79.646 Percent Identity: 63.274

alignment block:

US-09-899-471-2\_COPY\_21\_440 x B1820026 ..

Align seg 1/1 to: B1820026 from: 1 to: 886

```

1  LeuGluArgLeuMetGluProGlnAspThrAlaArgCysSerLeuGlyLe 17
  |||||||..... |||||||..... |||||
247 CTGAGAGAGGCTGTGGGCGCTCAGGACGCTACCCAGCTCTCCGGGCT 296
17  userCysHisLeuTrpAspGlyAspValLeuCysLeuProGlySerLeu 34
  |||||||..... |||||||..... |||||||
297 CTCTCGCCGCTCTGGGACAGTACATCTCTGCTGCTGGGGACATCG 346
34  InsertAlaProGlyProValLeuValProThrArgLeuGlnThrGluLeu 50
  |||||||..... |||||||..... |||||||
347 TGCCCTGCTCCGGGCCCCGCGTGGGGCCCTACGACCTCGACAGACAGCTG 396
51  ValLeuArgCysProGlnLysThrAspCysAlaLeuArgValArgVala 67
  |||||||..... |||||||..... |||
397 GTGCTGAGGTGCGACAGAGAGACCGACTGTGACTGTCTGCGTGTGGC 446
67  lValHisLeuAlaValHisGlyHisTrpAlaGluProGluGlu..... 81
  |||||||..... |||||||..... |||||||
447 TGTCACACTGGCGCTGACATGGGACACTGGAGAGACCTGAGAGAGAGAAA 496
82  ....AlaGlyLysSerAspSerGluLeuGlnLysSerAlaAsnAlaSer 96
  |||||..... |||||..... |||||
497 AGTTGGAGGAGACAGCTGACTAGGGGTGGAGAGAGCTAGAGATGCCCTCT 546
97  LeuGlnAlaGlnValValLeuSerPheGlnAlaTyrProIleAlaArgCys 113
  |||||||..... |||||||..... |||||||
547 CTCCAGGCCCAAGTGTCTCTCTCCCTCCAGGCCCTACCTACTGCCGCTG 596
113  sAlaLeuLeuGluValGlnValProAlaAspLeuValGlnProGlyGlns 130
  |||||..... |||||..... |||||
597 CGTCTGCTGGAGGTGAGAGTGCCTGCTGCCCTTGTGCACTTGGTCTAGT 646
130  erValGlySerAlaValPheAspCysPheGlnAlaSerLeuGlyAlaGlu 146
  |||||||..... |||||||..... |||||||
647 CTGAGGGCTGTGTGATATGACTGCTTGAGGCTGCCCTAGAGGAGAGAG 696
147  ValGlnIleTyrPseTyrThrLysProArgTyrGlnLysGluLeuAsnLe 163
  |||||||..... |||||||..... |||||||
697 GTAGAACTGTGCTCTATATCAAGCCAGGTACGAGAGAACTCAACCA 746
163  uThrGlnGln..... Leu.Pro..... AsnGly 170
  |||||||..... |||||
747 CACACAGCAGTGCCTTGCCTGCTGCTCAACGTGTTCAGCAGATGTT 796
171  AspAsnValLeuLeuThrLeuAspValSerGluGlnAspPheSerPh 187
  |||||||..... |||||||..... |||||||
797 GACAACGTGCATCTGTCTGATGTCTCTGAGGAGACAGACATCTGGGGCT 846
187  eleu.LeuTyrLeuArgProValProAspAlaLeuLysSerLeuTyrP 203
  |||||..... |||||
847 CTTCCTCTGTAC..... TGG 860
204  LysAsnLeuThrGlyProGlnAsn 211

```

861 AATCAGGTCCAGGCGCCCAAAAC 884

seq.name: gb\_test2:BF791762

seq.documentation\_block:

LOCUS BF791762 946 bp mRNA linear EST 12-JAN-2001

DEFINITION 602251953f1 NIH\_MGC\_84 Homo sapiens cDNA clone IMAGE:4344301.5,

ACCESSION BF791762 GI:12096816

VERSION BF791762.1

KEYWORDS EST.

SOURCE human.

ORANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

TITLE NIH-MGC http://imgc.ncl.nih.gov/.

JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cga@bbs-remail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: L1M962 row: j column: 14

High quality sequence stop: 680.

Location/Qualifiers

1..946

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:4344301"

/clone\_lib="NIH\_MGC\_84"

/tissue\_type="adrenal cortex carcinoma, cell line"

/lab\_host="pH10B (phage-resistant)"

/note="Organ: adrenal gland; Vector: pCMV-SPORT6; Site:1;

NotI; Site:2: SalI; Cloned unidirectionally: oligo-dr

primed. Average insert size 1.229 kb. Library enriched for

full-length clones and constructed by Life Technologies.

Note: this is a NIH\_MGC Library."

BASE COUNT 209 a 278 c 265 g 194 t

alignment\_scores:

Quality: 679.50 Length: 256

Ratio: 3.432 Gaps: 7

Percent Similarity: 77.344 Percent Identity: 62.891

alignment block:

US-09-899-471-2\_COPY\_21\_440 x BF791762 ..

Align seg 1/1 to: BF791762 from: 1 to: 946

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102  ValLeuSerPheGlnAlaTyrProIleAlaArgCysAlaLeuLeuGluY 118
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3  GTTCCTCTCTCCAGGCTTACCTACTGCCCCGCTGCGCTGCTGGAGG 52
118  aGlnValProAlaAspLeuValGlnProGlyGlnSerValGlySerAla 134
  |||||||..... |||||||..... |||||||
53  TGCACACTGCTGCTGCTGCTGTGTCAGTTGTGTCAGTGTGAGGCTCTGTG 102
135  ValPheAspCysPheGlnAlaSerLeuGlyAlaGluValGlnIleTyrPse 151
  |||||||..... |||||||..... |||||||
103  GTATATGACTGCTTCGAGGCTGCCCTTAGGAGTGTAGTACCAATCTGTGTC 152
151  TTYrThrLysProArgTyrGlnLysGluLeuAsnLeuThrGlnGlnLeuP 168
  |||||||..... |||||||..... |||||||
153  CTATATCAGCCAGGTACAGAGAACTACACACACACAGCAGCTGC 202

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168 ro.....AspGlyaspasnValLeu 175
203 CPGCCCTGGCCCTGGCTCAACGTGTAGCAGAGATGGTGCACAACGTGACTCG 252
176 ThrLeuAspValSerIugIugInaSPheSerPheLeuLeuTyrrLeuAr 192
:::|||||:::|||||:::
253 GTTCGAAATGTTCTTGAGAGACGACACTTCGGCTCTCCCTGTACTGGAA 302
192 gProValProAspAlaLeuIlysSerLeuTyrrLytylAsnLeuThrGlyP 209
: ||| ||| ::|||:::
303 TCAGGT .CGAGGCCCCCCAAAACCOCGGGTGGCCACAAAACCTACTGAC 351
209 roGlnAsnLleThrLeuAsnHlsThrAspLeuValProCysLeuCysIle 225
352 CGCAATCATCTTACCTGTGAACCAACACAGACTCGTCCCTGCTCGTGTATT 401
226 GlnValTPSerLeuGlnuProAspSerGluArgValGluPhcysProph 242
||||||| ||||||||| |||:::
402 CAGGTGTGCTCTGTGGAACCTGACTCCGTTAGGACGAAACATCTGCCCTT 451
242 eArgGluAspProGlyAlaHisArgAsnLeuTrpHisIleAlaArgLeu 259
452 CAGGAGAGACCCCCCGCACACAGAACTCTTGCGAAGCCGCCGACTGC 501
259 rGValLeuSerProGlyValTyrrGlnLeuAspAlaProCysCysLeuPro 275
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276 GlyIysValThrLeuCysTyrrGlnAlaProAspGlnSerProCysGlnPr 292
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552 CAGAAGCG .GCACGTGTGTGGGGGCTCGGTGGGAGACCCCTGCGAG .CC 599
292 OleuValProProValProGlnIlysAsnAlaThrVal AsnGluProGln 308
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600 ACTGTGTCCACCGCTTCTCTGGAGAG...ACGTACCTGGGGGACAGAAGTTCT 646
309 AspPheGlnLeuValAlaGlyHisProAsnLeuCysValGlnValSerTh 325
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647 CGAGTTCATGTGCTGAAGGC...ACATracCTGTGTTCAGGTG...AC 690
325 rTPeGluIysValGlnLeuGlnAlaCysSerTPalaAspSerLeuGlyLP 342
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342 ropHelYasDasp 346
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740 CT...CAGACGAT 750

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301	ArgLeuAlaGValLeuSerProGlyValITrpGlnLeuAspAlaProCysGly	317
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317	slaeProGlyLysValIrhLeuCysTrpGlnAlaProAspGlnSerProC	334
1149	TCTGCGGGGCAAGGTAAACGTCGTGGCGAGGACACGACGACAGTGCCT	1198
334	ysGlnProLeuValIProProValIProGlnLysAsnAlaThrValAsnGlu	350
1199	GCCAGCCACTGTGTGCACCAAGTGGCCCAAGAAAGACGCACTGTGAAATGAG	1248
351	ProGlnAspPheGlnLeuValAlaGlyYHISProAsnLeuCysValGln	367
1249	CCACAAAGCTTTTCCACTGTGTGGCAGACGCCACCCAACTCTGTGTCCAGGT	1298
367	lSerThrTrpLulysValGlnLeuGlnAlaCysSerTrpAlaAspSerL	384
1299	GAGCAACCTGGGAGAGAGTTCACCTGCACGTCGACTCTGTGGCGTACCTCT	1348
384	eugLysProPheLysAspAspMetLeuValGlnMetLysThrGlyLeu	400
1349	TGGGGCCCTTAAGGATATATGCTGTGTGTGGAGATGAAAAACCGGCTC	1398
401	AsnAsnThrSerValCysAlaLeuGlnLupProSerGlyCysThrProLeuP	417
1399	AACAAACATGACTGTGTGTGCCCTGGAAACCCAGTGGCTGTACACCACTGCC	1448
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434	spPheArgSerHisGlnGlyMetGlnLeuThrAsnAspAspAspMetGly	450
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451	SerLeuThrPalacyProMetAspLysTyrIleHisArgArgTyrValLe	467
1549	TCCGTATGGGCTGCTGCCCATGTGACAAATGATCCACAGGGCTGGGTCT	1598
467	uValITrpLeuAlaCysLeuLeuLeuAlaAlaAlaLeuPhePheLeuL	484
1599	AGATGGCTGGCTGTGCTACTCTTGTGGCTGGCGCTTCTTCTTCTCTCC	1648
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1699	CTCCTCCACTCCCGCAGAGGAGCGGGCTTACGAGCGCTGGTGGAGCACT	1748
517	uAlaSerAlaLeuSerGlnMetProLeuArgValAlaValAlaAspLeuTrpS	534
1749	GGGTCGGCGTTGAGCGAGATGCCACTGTGGCGGTGGCGGAGCACTGTGGA	1798
534	eArgArgGluLeuSerAlaHisGlyAlaLeuAlaSerPheHisHisGln	550
1799	GCGCGCCCGAGCTAGCGCGCAGCGAGGCGCTTACCGCTGTCCACCAACAG	1848
551	ArgArgArgIleLeuGlnGlnGlyValValIleLeuLeuPheSerP	567
1849	CGAGCGCGTATCCTCGACGAGAGGTGGCTGGTAACTCTTCTTCTTCGCC	1898
567	oAlaAlaValAlaGlnCysGlnGlnITrpLeuGlnLeuGlnIThrValGluP	584
1899	CGCGCGCGTGGCGCAGTGTCAAGCACTGGCTGCAGCTCCACAGCACTGGAGC	1948
584	roGlyProHisLysAlaLeuAlaAlaITrpLeuSerCysValLeuProAsp	600
1949	CGGGGCGCATGACGCCCTGCGCGCTGTGCTAGCTGGCGGTCTACCCGAT	1998

CC translation generic cDNA.

701 AYYTNMGNCCNGTNCNGAYGCNYTNARWSNYTNTGGTAYARAAYTN 75







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1556 CCCATCTCTCTTCCAAAAGATCACCGAAGCGCCGACGAGGCG 1605
497 ArgThrAlaLeuLeuLeuHisSerAlaAspGlyAlaGlyTyrGluArgLe 513
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1606 CGCGGGGGCTGTCTCTACTACGCGATGACTGGGTTTCGAGCGCT 1655
513 uValGlyAlaLeuAlaSerAlaLeuSerGlnMetProLeuArgValAlaVal 530
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530 aAlaSerLeuPserArgArgGluLeuSerLahHisGlyAlaLeuAlaTrp 546
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547 PheHisLahGlnArgArgArgLileuGlnGlyGlyValValIleLe 563
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563 uLeuPserProAlaAlaValAlaGlnCysGlnGlnTrpLeuLeuG 580
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1806 GCTCTTCTCTCCCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTG 1855
580 LnfThrValGluPro.....GlyProHisAspAlaLeuAlaAlaTrp 593
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1856 GGGTCTCCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTCG 1905
594 LeuSerCysValLeuProAspPheLeuGlnGlyArgAlaThrGlyArgTy 610
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1906 CTCACCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1955
610 rValGlyValTyrPheAspGlyLeuLeuHisProAspSerValProSerP 627
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1956 CGTGGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2005
627 ropPheArgValAlaProLeuPheSerLeuProThrGlnLeuProAlaPhe 643
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seq_documentation_block:
ID AAS46223 standard; cDNA: 2380 BP.
AC AAS46223:
XX
XX
XX 18-DEC-2001 (first entry)
XX
XX Human DNA encoding PRO polypeptide sequence #299.
XX
XX PRO polypeptide; mammal; tumor; cancer; human; cattle; horse; sheep; ss;
XX dog; cat; pig; goat; rabbit; tumor necrosis factor alpha; TNF-alpha;
XX blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
XX adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder;
XX PCR primer.
XX Homo sapiens.
XX
XX MO200168848-A2.

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XX 20-SEP-2001.
PD
XX
XX 28-FEB-2001; 2001WO-US06520.
PF
XX
XX 01-MAR-2000; 2000WO-US05601.
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XX 02-MAR-2000; 2000WO-US05841.
PR
XX 03-MAR-2000; 2000US-187202P.
PR
XX 06-MAR-2000; 2000US-186968P.
PR
XX 14-MAR-2000; 2000US-189320P.
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XX 14-MAR-2000; 2000US-189328P.
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XX 15-MAR-2000; 2000WO-US06884.
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XX 21-MAR-2000; 2000US-190828P.
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XX 21-MAR-2000; 2000US-191007P.
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XX 21-MAR-2000; 2000US-191048P.
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XX 21-MAR-2000; 2000US-191314P.
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XX 28-MAR-2000; 2000US-192655P.
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XX 29-MAR-2000; 2000US-193032P.
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XX 29-MAR-2000; 2000US-193033P.
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XX 30-MAR-2000; 2000WO-US08439.
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XX 04-APR-2000; 2000US-194449P.
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XX 04-APR-2000; 2000US-194647P.
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XX 11-APR-2000; 2000US-195975P.
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XX 11-APR-2000; 2000US-196000P.
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XX 11-APR-2000; 2000US-196187P.
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XX 11-APR-2000; 2000US-196690P.
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XX 11-APR-2000; 2000US-196820P.
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XX 18-APR-2000; 2000US-198121P.
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XX 18-APR-2000; 2000US-198585P.
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XX 25-APR-2000; 2000US-199387P.
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XX 25-APR-2000; 2000US-199350P.
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XX 25-APR-2000; 2000US-199654P.
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XX 03-MAY-2000; 2000US-201516P.
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XX 17-MAY-2000; 2000WO-US13705.
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XX 22-MAY-2000; 2000WO-US14042.
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XX 30-MAY-2000; 2000WO-US14941.
PR
XX 02-JUN-2000; 2000WO-US15264.
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XX 05-JUN-2000; 2000US-209832P.
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XX 28-JUL-2000; 2000WO-US20710.
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XX 22-AUG-2000; 2000US-0644848.
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XX 24-AUG-2000; 2000WO-US23328.
PR
XX 08-NOV-2000; 2000WO-US30952.
PR
XX 01-DEC-2000; 2000WO-US32678.
PR
XX 20-DEC-2000; 2000WO-US34956.
XX
XX (GETH ) GENENTECH INC.
XX
XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
XX Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
XX WPI; 2001-602746/68.
XX P-PSDB; AAU29322.
XX
XX Novel nucleic acids encoding PRO polypeptides, used to diagnose the
XX presence of tumours, such as prostate and breast tumours, in mammals and
XX to screen for modulators of the compounds.
XX
XX Claim 2, Fig 597, 774pp, English.
XX
XX Sequences AAS45925-AAS46231 represent DNA molecules encoding and PCR
XX primers for PRO polypeptides of the invention. The sequences of the
XX invention can be used to detect the presence of a tumour in a mammal by
XX comparing the level of expression of a PRO polypeptide in a test sample
XX of cells from the animal and a control sample of normal cells, whereby a
XX higher level of expression in the test sample indicates the presence of a
XX tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep,
XX pigs, goats and rabbits but are preferably human. The polypeptides can
XX be used to stimulate tumour necrosis factor (TNF) alpha release from human
XX blood, when contacted with it. A specific polypeptide can be used to
XX stimulate the proliferation or differentiation of chondrocyte cells. The
XX PRO proteins can be used to determine the presence of tumours and also
XX susceptibility to tumour development, particularly adrenal, lung, colon,
XX breast, prostate, rectal, cervical, or liver tumours, in mammalian

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1782 CCCTGCGGCTGCGCTGTGTCAGACTGCGCGCTGCGCGCTGAGACTG 1831
533 TRPSERARGARGGILEUENSERALAHISGLYALALEUALATRPHEHSHI 549
1832 TGGACCCCTGCTGAACTGAGCGCGACGAGGCGCGCTGCTGTTCACGC 1881
549 SGLNARGARGARGGILEUENGLNGLNGLYGLYVALVALILEUENPHESES 566
1882 GCAGCGGCGCGACCTGTCAGAGAGGCGCGCTGCTGTTCCTCTCTCT 1931
566 ERPROVALALVALALAGLNCYSGLNGLNTRPLEUGLNLEUGLNTHVAL 582
1932 CTCCCGGCGCGCTGCGCTGTCAGAGAGGCTACAGAGTGGGGTGTCC 1981
583 GLUPRO.....GLYPROHISAPALALEUALATRPHEUSERCY 596
1982 GGGCGCGGCGCGACGCGCGACGAGCGCTTCCGCGCTGCTGCTGACTG 2031
596 SVALLEUPROASPHLEUGLNGLNGLYARGALATRPGLYARGTYVALGLY 613
2032 CGTGTGCGCGCTGCTGTCAGAGGCGCGCGCTGCTGCTGCTGCTGCTG 2081
613 ALTYRPHASPGILEUENHISPROASPSERVALPROSERPROPHARG 629
2082 CCGCTTGCAGAGGCTGCTGTCACCGCGAGCGCGCTGCTGCTGCTGCTG 2131
630 VALALAPROLEUPHESERLEUPROTHRGINLEUPROALAPHELEUSAPAL 646
2132 ACCGTGCGCGCTGCTGTCACACTGCGCTCCCACTGCCAGACTTCCGGGG 2181
646 ALEUGLNGLYGLYCYSSERTHSERALAGLYARGPROALASPARGLYALG 663
2182 CCGTGTGCGCGCTGCTGTCAGAGGCGCGCGCTGCTGCTGCTGCTGCTG 2231
663 LUARGVALTHRGINALEUARGSERALALEUSPERSERCY.....THR 677
2232 AGCAGAGTGTCCGCGCGCTGTCAGCGCGCTGCTGCTGCTGCTGCTGCTG 2281
678 SERSERGLUALAPROGLY 684
2282 CCGGGGACTCCCGCGCGCGGGA 2302
Seq_name: /SIDS1/gcgdate/geneseq/geneseqn-emb1/NA2001A.DAT.AAS09515
Seq_documentation_block:
ID AAS09515 standard; cDNA; 2380 BP.
AC AAS09515;
XX
XX
XX 24-OCT-2001 (first entry)
DE Human cDNA encoding Interleukin 17 receptor, IL-17RH2.
XX
XX Human: Interleukin-17 receptor; IL-17RH2; agonist; antagonist; ss;
XX PRO20040: DNA 164625-2890; systemic lupus erythematosus;
XX rheumatoid arthritis; osteoarthritis; diabetes mellitus;
XX allergic disease; asthma; demyelinating disease;
XX degenerative cartilaginous disorder; transplantation associated disease.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
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XX /product- "IL-17RH2"
XX sig_peptide 233..292
XX /tag- b
XX mat_peptide 293..2344
XX /tag- c
XX /label- Mature_IL_17RH2
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XX WO200146420-A2.
XX
XX
XX

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PD 28-JUN-2001.
XX
XX 20-DEC-2000; 2000WO-US34956.
PF
XX 23-DEC-1999; 99US-0172096.
PR
XX 30-DEC-1999; 99MO-US31274.
PR 11-JAN-2000; 2000US-0175481.
PR 18-FEB-2000; 2000MO-US04341.
PR 02-MAR-2000; 2000MO-US05841.
PR 21-MAR-2000; 2000US-0191007.
PR 21-MAR-2000; 2000MO-US07532.
PR 02-JUN-2000; 2000MO-US15264.
PR 22-JUN-2000; 2000US-0213087.
PR 22-AUG-2000; 2000US-0644848.
PR 24-AUG-2000; 2000MO-US23328.
PR 24-OCT-2000; 2000US-0242837.
PR 10-NOV-2000; 2000MO-US30873.
PR 28-NOV-2000; 2000US-0253646.
PR 01-DEC-2000; 2000MO-US32678.
XX
XX (GENE ) GENENTECH INC.
XX
XX Chen J, Filvaroff E, Fong S, Goddard A, Godowski PJ, Grimaldi CJ,
PI Gunney AL, Li H, Hillan KJ, Tumas D, Van Lookeren M, Vandlen RL,
PI Watanabe CK, Williams PM, Wood WI, Yansura DG;
XX
XX WPI: 2001-451708/48.
XX
XX P-FSDB: AA004956.
XX
XX Novel PRO polypeptides homologous to interleukin-17, useful for the
PT diagnosis and treatment of immune related disease e.g. rheumatoid
PT arthritis and diabetes -
PT
XX
XX Claim 1; Fig 13; 18pp; English.
PS
XX
XX The sequence (DNA 164625-2890) encodes a PRO polypeptide (PRO20040)
XX which is the human interleukin 17 receptor, IL-17RH2. A composition
XX containing ant/agonists to the PRO polypeptides or individual components
XX are useful for treating a mammal with an immune related disease, e.g.
XX systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
XX juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an
XX idiopathic inflammatory myopathy, Sjogren's syndrome, systemic
XX vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
XX thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal
XX disease, a demyelinating disease, an autoimmune or immune-mediated skin
XX disease, contact dermatitis, an allergic disease e.g. food
XX hypersensitivity, asthma, a transplantation associated disease, or a
XX chronic inflammatory demyelinating polyneuropathy. Treating a
XX degenerative cartilaginous disorder comprises administering a PRO1031 or
XX PRO1122 polypeptide agonist, or antagonist to the mammal. Numerous
XX examples of the diseases and disorders are given in the specification.
XX
XX Sequence 2380 BP; 411 A; 776 C; 743 G; 450 T; 0 other;
SQ

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alignment\_scores:

Quality:	2376.00	Length:	707
Ratio:	4.118	bits:	7
Percent Similarity:	81.612	Percent Identity:	65.912

alignment\_block:

US-09-899-471-5 x AAS09515

Align seg 1/1 to: AAS09515 from: 1 to: 2380

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17 ValValSerLeuGlnArgLeuMetGlnProGlnAspThrAlaArgCys 34
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283 GGTCTTCTCTGAGAGGCTGTGCGCGCTGCTGAGAGGCTACCGACAGCT 332

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[illegible]

protein may also be employed as molecular weight markers for protein

213 p01yaspaValLeuLeuInrLeuaspValserGIUGIUGInaspPhes 23

838 TGGTGACCAACGTGCATCTGGTCTCTGAATGTCTCTGAGGAGCAGCACTTCG 88

230 erpHeLeuLeuTyrLeuArgProValPProAspAlaLeuLysSerLeuTrp 246  
 888 GCGCTCCCTGACTGAGATGAGTCCAGGGGCCCCCAAAAACCCGGGTGG 937  
 247 TyrLysAsnLeuThrGlyProGlnAsnIleThrLeuAsnHisThrAspLe 263  
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 988 GGTTCCTCCGCTCTGATTCAGGWTGGGCTGGAACCTGACCTCCGCTTA 1037  
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 380 rPalaSerSerLeuGlyProPheLysAspAspMetLeuLeuValGluMet 396  
 1338 GGGCTGACTCCCTGGGGCCTCTCAAGACGATGTGCTACTGTGGAACA 1387  
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 1388 CGAGCCCCCAGACAAAGATCCCTCTGTGCTTGGACCCAGTGGCTG 1437  
 413 sThrProLeuProSerMetAlaSerThrArgAlaAlaArgLeuGlyGlu 430  
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 430 LuLeuLeuGlnAspPheArgSerHisGlnCysMetGlnLeuTrpAsnAsp 446  
 1488 ACTTACTACAAGACCTGACGACGACGACGCTGTGACGACATGG...GAC 1534  
 447 AspAsnMetGlySerLeuTrpAlaCysPrometAspLysTyrIleHisArg 463  
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 463 gArTrpValLeuValTrpLeuAlaCysLeuLeuAlaAlaLeuPhe 480  
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 1932 CTCGCGGTGGGTGGCGCTGTGACGAGTGTGTACAGATGGGGTGTCC 1981  
 583 GluPro.....GlyProHisAspAlaLeuAlaAlaTrpLeuSerCys 596  
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 AC AAS18130;  
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 DT 26-MAR-2002 (first entry)  
 XX  
 DE Human DNAX cytokine receptor subunit 7 (DCRS7) cDNA.  
 KW Human; DNAX cytokine receptor subunit 7; DCRS7; phosphate labelling; ss;  
 KW gene therapy; protein therapy; immunological disorder.  
 OS Homo sapiens.  
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 FT CDS 181..2292  
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 FT /product="Human DCRS7"  
 FT  
 PN WO200190358-A2.  
 XX  
 PD 29-NOV-2001.  
 XX  
 XX 23-MAY-2001; 2001WO-US16767.  
 PF  
 XX 24-MAY-2000; 2000US-206862P.  
 PR  
 XX  
 PA (SCHE ) SCHERING CORP.



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931	CACAAAACCTGACGTGAGCCGCGAGATCATTAACCTTGAAACCAACAGACT	980
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DE Human cDNA encoding a membrane or secretory protein clone PSEC0233.  
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XX  
XX Human; secretory protein; membrane protein; vaccine; gene therapy;  
KW Rheumatoid arthritis; diabetes; ss.  
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OS Homo sapiens.  
PN EPI067182-A2.  
PD 10-JAN-2001.  
PE  
PF 07-JUL-2000; 2000EP-0114090.  
PR 08-JUL-1999; 99JP-0194179.  
PR 11-JAN-2000; 2000JP-0118775.  
PR 02-MAY-2000; 2000JP-0183766.  
XX  
XX (HELI-) HELIX RES INST.  
PA  
XX  
PI Ota T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;  
PI WPI; 2001-093989/11.  
DR P-PSDB; AAB86448.  
XX  
XX Nucleic acids encoding secretory proteins/membrane proteins, useful in  
PT gene therapy or as candidate target molecules in drug development -  
XX  
PS Claim 1; SEQ ID 263; 609pp + CD ROM; English.  
XX  
XX This invention relates to nucleic acid sequences AAF93744 - AAF93916  
CC which encode human secretory or membrane proteins represented by  
CC AAB88317 - AAB88419. Included in the invention are primers  
CC AAF93917 - AAF94295 and AAF62232 - AAF62235 which are used to isolate the  
CC cDNA sequences of the invention. The invention also includes methods for  
CC the production of antibodies directed against the proteins, and cDNA  
CC sequences, which can be used in vaccines. The polynucleotide sequences  
CC can be used in gene therapy. The polynucleotide sequences and the  
CC proteins they encode may be used in the prevention, treatment and  
CC diagnosis of diseases associated with inappropriate secretory  
CC protein/membrane protein expression. The nucleic acids and complementary  
CC sequences may also be used as DNA probes in diagnostic assays  
CC (e.g. polymerase chain reactions (PCR)) to detect and quantify the  
CC presence of similar nucleic acid sequences in samples. They may also be  
CC used to study the expression and function of secretory proteins/membrane  
CC polypeptides and their role in metabolism. The polypeptides may be used  
CC as antigens in the production of antibodies against them and in assays to  
CC identify modulators (agonists and antagonists) of expression and  
CC activity. The antibodies (agonists and antagonists may also be used as therapeutic  
CC agents to down regulate expression and activity. The antibodies may also  
CC be used as diagnostic agents for detecting the presence of the  
CC polypeptides in samples (e.g. by enzyme linked immunosorbent assay  
CC (ELISA)). Examples of diseases which may be treated include rheumatoid  
CC arthritis and diabetes.  
XX  
XX Sequence 2499 BP; 418 A; 821 C; 764 G; 496 T; 0 other;

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AC	AAF93875:
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DT	23-MAY-2001 (first entry)

  

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1 MetProValSerTrpPheLeuLeuSerLeuAlaLeuGlyArgAsnProVal 17
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17 ValValSerLeuCluArgLeuMetGluProGlnAspThrAlaArgCys 34

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17 IValValSerLeuGluArgLeuMetGluProGlnAspThrAlaArgCys 34

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1013 GAGGACTACCCCAAGCAAGGAAATGTGTGGGGAACCTGCTGCTTCC 1062
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579 eugInthValaIuPro.....GlyProH1aAspAlaLeuAlaAa.592
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XX AAC85029;
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XX 08-MAY-2001 (first entry)
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XX Human variant Zcytor14 protein Zcytor14-1 encoding cDNA.
XX
XX CytoKine receptor; Zcytor14; human; inflammation; rheumatoid arthritis;
XX antiInflammatory; gene therapy; vaccine; variant; Zcytor14-1, ss.
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XX WO200104304-A1.
XX
XX 18-JAN-2001.
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XX 30-JUN-2000; 2000WO-US18383.
XX
XX 07-JUL-1999; 99US-0348854.
XX
XX (ZYMO ) ZYMOGENETICS INC.
XX
XX Presnell SR, Burkhead SK, Powder SL;
XX
XX WPI: 2001-112618/12.
XX
XX P-PSDB: AAB61881.
XX

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PT New polypeptide encoding a human cytokine receptor Zcytoril4, for  
treating inflammation e.g. rheumatoid arthritis -

PS XX Disclosure: Page 95-98; 112pp; English.

XX The invention provides a new human cytokine receptor designated Zcytoril4.  
CC Zcytoril4 can be expressed by standard recombinant methodology. The  
CC encoding nucleic acid is useful for detecting the expression of a  
CC Zcytoril4 gene in a biological sample. Anti-Zcytoril4 antibodies can be  
CC used to screen biological samples in vitro for the presence of Zcytoril4.  
CC proteins, polypeptides and peptides having Zcytoril4 activity can be  
CC administered to a subject who lacks an adequate amount of this  
CC polypeptide, for treating inflammation and conditions such as Rheumatoid  
CC arthritis. In contrast, Zcytoril4 antagonists (e.g. anti-Zcytoril4  
CC antibodies) can be used to treat a subject who produces an excess of  
CC Zcytoril4. Zcytoril4 nucleotide sequences can also be used to provide  
CC Zcytoril4 to a subject. The present sequence represents a cDNA encoding  
CC a variant of the human cytokine receptor Zcytoril4, designated Zcytoril4-1  
CC The variant is a truncated form of the receptor polypeptide and lacks  
CC amino acid residues 1-113 of Zcytoril4.  
XX  
XX Sequence 1753 BP; 287 A; 584 C; 548 G; 334 T; 0 other;

alignment\_scores:  
Quality: 1888.50 Length: 594  
Ratio: 4.053 Gaps: 7  
Percent Similarity: 78.451 Percent Identity: 63.805

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52 GGCTTACCCTACTGCCTCCGCTCGTCTCTGAGGTGCAAGTGCCGTCG 101  
  
143 spleuValGlnProGlyGlnSerValGlySerAlaValPheaSpCySph 159  
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202 GTAGAGAGAAGAACTCAACACACACAGAGAGCTGCT ..... 238  
  
193 euGluValAlaArgspSerIleGlnSerCysTrpValIleuProTrpleuasn 209  
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239 ..... GCCCTGCCCTGGCTCAAC 256  
  
210 ValSerThrAspGlyAspAsnValLeuLeuThrSerAlaValSerGlnI 226  
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257 GTGTACAGAGATGGTGACAACGTGATCGGTGTCATATCATCTCTGANGA 306  
  
226 uGlAspPheSerPheLeuLeuTyrLeuArgProValProAspAlaLeuL 243  
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243 ysSerLeuTrpTyrLysAsnLeuThrGlyProGlnAsnIleThrLeuasn 259  
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 856 CCTTGGAGACTTACTTACAAAGACCTGACAGCCAGGCTGCTGCTGCTG 905  
 443 euTrpAsnAspAspAspMetGlySerLeuTrpAlaCysProMetAspLys 459  
 906 TATGG.....GACGATGACTGTGGAGCGCTATGCGCTGCCATGACAAA 952  
 460 TyrIleHisArgTrpValLeuValAlaValAlaCysLeuLeuLeuAl 476  
 953 TACATCCACAAGCGCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1002  
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 1003 CCGTGGCTTTCCTCATCTCTCTCAAAAAGATCAGCGAAAGGCT 1052  
 492 .....AlaAlaArgGly 495  
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 496 SerArgThrAlaLeuLeuLeuHisSerAlaAspGlyAlaGlyTyrGlu 512  
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 512 gLeuValGlyAlaLeuAlaSerAlaLeuSerGlnMetProLeuAlaVal 529  
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 529 LysAlaLeuTrpSerArgArgGluLeuSerAlaHisGlyAlaLeuAla 545  
 1200 CCGTAGACCTTGGAGCGCTCTGAACCTAGCGCGAGGCGCGCGTGGCT 1249  
 546 TrpPheHisHisGlnArgArgArgGlnGlnGlnGlnGlnGlnGlnGln 562  
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562 eLeuLeuPheSerProAlaAlaValAlaGlnCysGlnGlnTrpLeu 579  
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 XX  
 AC AAZ65269;  
 XX  
 DT 23-MAR-2000 (first entry)  
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 DE Human secreted protein gene 20.  
 XX  
 KW Human; secreted protein; cancer; tumour; developmental abnormality;  
 KW foetal deficiency; blood disorder; immune system disorder; inflammation;  
 KW autoimmune disease; allergy; Alzheimer's disease; cognitive disorder;  
 KW schizophrenia; arthritis; asthma; psoriasis; sepsis; skin disorder;  
 KW atherosclerosis; diabetes; cardiovascular disorder; kidney disorder;  
 KW digestive disorder; endocrine disorder; infection; AIDS; leukaemia;  
 KW therapy; chromosome 3; ds.  
 KW  
 OS Homo sapiens.  
 XX  
 PN WO9958660-A1.  
 XX  
 PD 18-NOV-1999.  
 XX  
 PE 06-MAY-1999; 99WO-US09847.  
 XX  
 PR 12-MAY-1998; 98US-0085093.  
 PR 12-MAY-1998; 98US-0085094.  
 PR 12-MAY-1998; 98US-0085105.  
 PR 12-MAY-1998; 98US-0085180.  
 PR 18-MAY-1998; 98US-0085906.  
 PR 18-MAY-1998; 98US-0085920.  
 PR 18-MAY-1998; 98US-0085921.  
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 PR 18-MAY-1998; 98US-0085923.  
 PR 18-MAY-1998; 98US-0085924.  
 PR 18-MAY-1998; 98US-0085928.  
 PR 18-MAY-1998; 98US-0085925.  
 PR 18-MAY-1998; 98US-0085927.  
 PR 18-MAY-1998; 98US-0085927.  
 XX



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1476 TACTTACTACTCCAGCAAGCCCTCCAGAGGACAGCTGCTTGAGAGACT 1525  
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1526 ACTTACTACAGACCTGACAGCCAGCTGTCTGACACTATGG...GAC 1572  
447 AspAsnMetGlySerLeuTrpAlaCysProMetAspLysTyrIleHisArg 463  
1573 GATGACTTGGAGAGCGATATGGCGCTGCCCATGACAAATACATCCACAA 1622  
463 gATGTPVAlleuValTrpLeuAlaCysLeuLeuLeuAlaAlaLeuP 480  
1623 GCGCTGGGCGCTGCTGTGGCGCTGCTTCTTCTGCTGCT...T 1669  
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1670 TCCCTCATCTCTCTCAAAAAGATCAGCGGAAA 1705  
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seq\_documentation\_block:  
D AAC85028 standard; cDNA; 2076 BP.  
ACAC85028;  
08-MAY-2001 (first entry)  
Human cytokine receptor zcytor14 degenerate nucleotide sequence.  
Cytokine receptor; zcytor14; human; inflammation; rheumatoid arthritis;  
antiinflammatory; gene therapy; vaccine; ss.  
Homo sapiens.  
WO200104304-A1.  
18-JAN-2001.  
30-JUN-2000; 2000MO-US18383.  
07-JUL-1999; 99US-0348854.  
(ZYMO ) ZYMOGENETICS INC.  
Presnell SR, Burkhead SK, Powderer SH;  
WPI: 2001-112618/12.  
P-PSDB: AAB61880.  
New polypeptide encoding a human cytokine receptor zcytor14, for  
treating inflammation e.g. rheumatoid arthritis -  
Claim 8; Page 94-95; 112pp; English.  
The invention provides a new human cytokine receptor designated zcytor14.  
zcytor14 can be expressed by standard recombinant methodology. The  
encoding nucleic acid is useful for detecting the expression of a  
zcytor14 gene in a biological sample. Anti-zcytor14 antibodies can be  
used to screen biological samples in vitro for the presence of zcytor14.  
Proteins, polypeptides and peptides having zcytor14 activity can be  
administered to a subject who lacks an adequate amount of this  
polypeptide, for treating inflammation and conditions such as rheumatoid  
arthritis. In contrast, zcytor14 antagonists (e.g. anti-zcytor14  
antibodies) can be used to treat a subject who produces an excess of  
zcytor14. zcytor14 nucleotide sequences can also be used to provide  
zcytor14 to a subject. The present sequence represents the human  
cytokine receptor zcytor14 degenerate nucleotide sequence.

Sequence 2076 BP: 232 A: 273 C: 399 G: 265 T: 907 other:

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Ratio: 3.757 Gaps: 5  
Percent Similarity: 64.358 Percent Identity: 47.186  
alignment\_block:  
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1 ATGCCGNTGNCCTGTTTNTNTNMSNTGNCNTYNGNNGNMSNCCNGT 50  
17 lValAlaSerLeuGlnArgLeuMetGluProGlnAspThrAlaArgCys 34  
51 NGTNTNMSNTNGAMNYTNGTNGNCCNCARGAYGCACNCAYTYGW 100  
34 erLeuGlyLeuSerCysHisLeuTrpAspGlyAspValLeuCysLeuPro 50  
101 SNCCGNYTNTNMSNTGNTGNTGGAATWSNCAATHTNTGTTCN 150  
51 GlySerLeuGlnSerAlaProGlyProValLeuValProThrArgLeuG 67  
151 GGNGAYATHTGTCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCC 200  
67 nThrGluLeuValLeuArgCysProGlnLysThrAspCysAlaLeuArg 84  
201 RACNGARNTGNTNTMGTCARARARACNGAYTGAYTYTNTGY 250  
84 AlArgValAlaValHisLeuAlaValHisGlyHisTrpAlaGluProGlu 100  
251 TTMGNTGNCNTNCAATYTGNCNTGATGNCATYGGARGARCCNGAR 300  
101 Glu.....AlaGlySerAspSerGluLeuGlnGlnSerArg 113  
301 GAYGARARAAATTYGGNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCC 350  
113 gAsnAlaSerLeuGlnAlaGlnValLeuSerPheGlnAlaTyrPro 130  
351 NAAVCNMSNTNTNCARGCNCARGTNTNTNMSNTTYCARGCATCCNA 400  
130 leAlaArgCysAlaLeuLeuGlnValGlnValProAlaAspLeuValGln 146  
401 CNGCMGNTGYTNTNTNGARGTNCARGTNCNCCNCCNCCNCCNCCNCCNCC 450  
147 ProGlyGlnSerValGlySerAlaValPheAspCysPheGlnAlaSer 163  
451 TTYGNCARWSNCTNGNMSNCTNTAYGAYTGTYTGARGCNCNT 500  
163 uGlyAlaGlnValGlnIleTrpSerTyrThrLysProArgTyrGlnLys 180  
501 NGNMSNARGTNGNATHTGWSMTAAVANCARCCNMNTAAGAAARG 550  
180 IuLeuAsnLeuThrGlnGlnLeuProAspCysArgGlyLeuGlnValArg 196  
551 ARYNAACATACNARCARTNCCN..... 576  
197 AspSerIleGlnSerCysTrpValLeuProTrpLeuAsnValSerThrAs 213  
577 .....GCNTNCCNTGTYTAAAGTWSNCCNGA 605  
213 pGlyAspAsnValLeuLeuThrLeuAspAlaSerGlnGlnAspPhe 230  
606 YGGGATATATGTCNCAYYTNGTNTNAAAGTWSNCCNARGARCAVATYTG 655  
230 erPheLeuLeuTyrLeuArgProValProAspAlaLeuLysSerLeuTrp 246  
656 GNTYNTMSNTNTATYGAAYCARGTNCARGNCCNCCNCCNCCNCCNCCNCC 705  
247 TyrLysAsnLeuThrGlyProGlnAsnIleThrLeuAsnHisThrAspLe 263

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706 CATAAARATYTNACNGCCNCARATHTACNTYNAATCAATCAATCAAT 755
706 uvalProCysLeuGlyIleGlnValTrpSerLeuGluProAspSerGlu 280
756 NGTNCNTGTYTNTGATHCARAGTGTGGCCTNTGACCCNGAATWSGTNA 805
280 ryalGluPheCysProPheArgGluAspProGlyAlaHisArgAsnLeu 296
806 GNAACNAATGATGTCNTTGMNGARAGATCCNMGCNCATCAARAATYTN 855
297 TrpHisIleAlaArgLeuArgValLeuSerProGlyValTrpGlnLeu 313
856 TGGCARGCCNCNMGTNTMGNTTNTNACNTTNCARMSNTGTNTNTNCA 905
313 palAProCysCysLeuProGlyLysValTrpLeuCysTrpGlnAlaPro 330
906 YGCNCNTGTYTNTGATHCARAGTGTGGCCTNTGACCCNGAATWSGTNA 955
330 spGlnSerProCysGlnProLeuValProProValProGlnLysAsnAla 346
956 GNGCNGATCCNTGTCARCCNTGTCNCNCNTGTCNCNTGTCNCNTGTCNC 1005
347 ThrValAsnGluProGlnAspPheGlnLeuValAlaGlyHisProAsnLe 363
1006 ACAGTNCATATAGTNTGATGATTCCTTNTNTNAAAGCCATCCNAATYT 1055
363 uCysValGlnValSerThrTrpGluLysValGlnLeuGlnAlaCysSer 380
1056 NTGTCNCATGATNAATYATWSNMGARAAATYTCARATTCARATGTYTNT 1105
380 rPalAspSerLeuGlyProPheLysAspAspMetLeuValGluMet 396
1106 GGGCNGATWSNMGTCNCNTTNAARAGATGTYTNTYNTNTGACACAC 1155
397 LysThrGlyLeuAsnAsnThrSerValCysAlaLeuGluProSerGlyCys 413
1156 MGNGCCNCARAGATATATMGMSNTTNTGTCNTTNGACCCWSMGNTG 1205
413 sThrProLeuProSerMetAlaSerThrArgAlaAlaArgLeuGluG 430
1206 YACNMSNTTNCMSNNAARCCNMSNACNMGNCNMGNTTNGGAGAT 1255
430 LuLeuLeuGlnAspPheArgSerHisGlnCysMetGlnLeuTrpAsnAsp 446
1256 AYTNTNTNCARAGATYTCARMSNCGNCARATGTYTNCARATYNTG...GAT 1302
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1403 SNTNTATHTNTNTTNAARARAGATCAAGCNAARCGCNCNMGNTNGN 1452
497 ArgThrAlaLeuLeuHisSerAlaAspGlyAlaGlyTrpGluArgLe 513
1453 MGNGCNCNTTNTTNTTATWSNMGATGATYATGATYATGATGAT 1502
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530 alaAspLeuTrpSerArgArgGluLeuSerAlaHisGlyAlaLeuAlaTrp 546
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610 rValGlyValTrpPheAspGlyLeuLeuHisProAspSerValProSer 627
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seq.document_block:
ID AAS18131 standard; cDNA; 2109 BP.
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AC AAS18131:
XX
DT 26-MAR-2002 (first entry)
XX
DE Human DCRS7 reverse translation generic cDNA.
XX
KW Human; DNA cytokine receptor subunit 7; DCRS7; phosphate labelling; ss;
XX gene therapy; protein therapy; immunological disorder.
XX
OS Homo sapiens.
XX
PN W0200190358-A2.
XX
PD 29-NOV-2001.
XX
PF 23-MAY-2001; 2001WO-US16767.
XX
PR 24-MAY-2000; 2000US-206862P.
XX
PA (SCHE ) SCHERING CORP.
XX Gorman DM;
XX
DR WPI; 2002-106198/14.
XX
PT Isolated antigenic human or mouse DNA receptor subunit-like
PT polypeptide useful for detecting antibodies generated in response to
PT presence of increased protein levels or immunological disorders -
XX
PS Disclosure; Page 15-16; 148pp; English.
XX
CC The invention relates to primate and rodent DNA cytokine receptor
CC subunit (DCRS) polypeptides and the polynucleotides encoding them. The
CC receptors, or their portions may be useful as phosphate labelling enzymes

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\$Q Sequence 2109 BP; 234 A; 267 C; 415 G; 269 T; 924 other;

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1797 NTNCNCNGATTTTTCARGCARGCNGCNCNGCNCMSNTATGTCNGCNCNT 1846
614 yrPheAspGlyLeuLeuHisProAspSerValProSerProPheArgVal 630
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1897 GTNCNGTNTTTCACNTTNCNCNCARNTCCNGAYTTTTCGNCNCNT 1946
647 uGlnGlyGlyCysSerThrSerAlaGlyArgProAlaAspArgValGlu 664
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2047 GGNACMNSMNCNCNCNCN 2064

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eq_documentation_block:
D AAC85030 standard; cDNA: 1725 BP.
X AAC85030:
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X AAC85030:
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X 08-MAY-2001 (first entry)
X
X Human Zcytor14 variant Zcytor14-1 degenerate nucleotide sequence.
W Cytokine receptor; Zcytor14; human; inflammation; rheumatoid arthritis;
W antiinflammatory; gene therapy; vaccine; variant; Zcytor14-1; ss.
X Homo sapiens.
X
X NC0200104304-A1.
X
X 18-JAN-2001.
X
X 30-JUN-2000; 2000MO-US18383.
X
X 07-JUL-1999; 99US-0348854.
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XX
PA (ZYMO ) ZYMOGENETICS INC.
XX
PI Presnell SR, Burkhead SK, Powder SL;
XX
DR WPI: 2001-112618/12.
DR P-PSDB: AAB61881.
PT New polypeptide encoding a human cytokine receptor Zcytor14, for
PT treating inflammation e.g. rheumatoid arthritis
PS Disclosure: Page 101; 112pp; English.
XX
XX The invention provides a new human cytokine receptor designated Zcytor14.
XX Zcytor14 can be expressed by standard recombinant methodology. The
XX encoding nucleic acid is useful for detecting the expression of a
XX Zcytor14 gene in a biological sample. Anti-Zcytor14 antibodies can be
XX used to screen biological samples in vitro for the presence of Zcytor14.
XX proteins, polypeptides and peptides having Zcytor14 activity can be
XX administered to a subject who lacks an adequate amount of this
XX polypeptide, for treating inflammation and conditions such as rheumatoid
XX arthritis. In contrast, Zcytor14 antagonists (e.g. anti-Zcytor14
XX antibodies) can be used to treat a subject who produces an excess of
XX Zcytor14. Zcytor14 nucleotide sequences can also be used to provide
XX Zcytor14 to a subject. The present sequence represents a degenerate
XX nucleotide sequence of a variant of the human cytokine receptor Zcytor14,
XX designated Zcytor14-1. The variant is a truncated form of the receptor
XX polypeptide and lacks amino acid residues 1-113 of Zcytor14.
XX
SQ Sequence 1725 BP; 192 A; 226 C; 332 G; 216 T; 759 other;

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Percent Similarity: 61.214 Percent Identity: 45.025

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||||| ||| |||::: ||||| ||||| |||||
51 RGCNTAYCCNACNCNCNCNCNCNCNCNCNTGTCARNTTCARNTCNCNC 100
143 spldeuValGlnProGlyGlnSerValGlySerAlaValPheAspCysPhe 159
||||| ||||| |||||::: ||||| ||||| |||||
101 CNTNTGTCARNTTTCGNCARMSNGTNGCNCNCNTTTCAYGATYTTY 150
160 GluAlaSerLeuGlnGlnValGlnIleTrpSerTrpThrIysProAr 176
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151 GARGCNCNCNTTNGCNCNCNCNCNCNCNCNCNCNCNCNCNCNCNCNC 200
176 gTyGlnLysGlnLeuAsnLeuThrGlnGlnLeuProAspCysArgGlyL 193
||||| ||||| ||| ||||| |||
201 NTAYCARAARARNTAAAYCAVACNCARCARNTCCN..... 237
193 euGlnValArgAspSerIleGlnSerCysTrpValLeuProTrpLeuAsn 209
::: ||||| |||
238 .....GCTTNCCTGCTTNAAY 255
210 ValSerThrAspGlyAspAsnValLeuLeuThrLeuAspValSerGlu 226
|||||::: ||||| ||||| ||||| |||||
256 CTNMSNCNCAGCGAGTAAAYTCNTCAYYTNGTNTTAAAGTMSNCARCA 305
226 uGlnAspPheSerPheLeuLeuTyrLeuArgProValProAspAlaLeu 243
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[illegible]

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ID AAH9805 standard; cDNA; 1210 BP.  
XX  
AC AAH9805;  
XX  
DT 16-OCT-2001 (first entry)  
XX  
DE Human protein encoding cDNA sequence SEQ ID NO:640.  
XX  
KW Human; cancer; ulcer; HIV infection; human immunodeficiency virus;  
KW antileukemia; antirheumatic; antiarthritic; immunosuppressive;  
KW antibacterial; endocrine; cardiac; central nervous system; viricide;  
KW anti-HIV; fungicide; antimutagen; cardiovascular; antianemic; anaemia;  
KW antiagregant; haemostatic; vulnerary; antitumor; osteopathic; eczema;  
KW dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic;  
KW neuroprotective; antidepressant; nootropic; antiparkinsonian; infection;  
KW immunostimulant; gene therapy; antisense therapy; vaccine; inflammation;  
KW antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;  
KW cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;  
KW thrombocytopaenia; osteoporosis; severe combined immunodeficiency;  
KW allergic rhinitis; diabetes; multiple sclerosis; depression;  
KW Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;  
KW neurological disorder; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200153455-A2.  
XX  
PD 26-JUL-2001.  
XX

PF 22-DEC-2000; 2000MO-US35017.  
PR 23-DEC-1999; 99US-0471275.  
PR 21-JAN-2000; 2000US-0488725.  
PR 25-APR-2000; 2000US-0552317.  
XX  
PA (HXSE-) HXSEQ INC.  
XX  
PI Tang YT, Liu C, Drmanac RT;  
XX  
DR WPI: 2001-457603/49.  
DR P-PSDB: AAM25864.  
XX  
XX  
PT Isolated human polynucleotides encoding polypeptides, useful for the  
PT treatment and diagnosis of e.g. cancer, ulcers and HIV infection -  
XX  
XX  
Claim 1: Page 659-660; 1217pp; English.

AAG99166 to AAH99904 encode the human proteins given in AAM25225 to  
AAM25963. The proteins can have activities based on the tissues and  
cells they are expressed in, such as: antineoplastic; antifungal;  
antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant;  
central nervous system; virucide; anti-HIV; fungicide; antimutagen;  
cardiovascular; antianaemic; antiaggregant; haemostatic; vulnerary;  
CC antiulcer; osteoporotic; dermatological; antiallergic; antisthmatic;  
CC antidiabetic; cytosolic; neuroprotective; antidepressant; nootropic;  
CC antiparkinsonian; and immunostimulant. The proteins and polynucleotides  
encoding them can be used in gene therapy, antisense therapy and vaccine  
production. The proteins and polynucleotides are useful for screening for  
agonists or antagonists of a protein and for the treatment and diagnosis  
of disorders associated with the activity of a protein e.g. inflammation,  
rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,  
neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal  
infections, autoimmunity, genetic diseases, haematopoietic disorders,  
anemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers,  
osteoporosis, severe combined immunodeficiency, eczema, allergic  
rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression,  
Alzheimer's disease, Parkinson's disease, neurodegenerative and  
neurological disorders.

SO Sequence 1210 BP; 227 A; 377 C; 352 G; 254 T; 0 other;

Alignment\_scores:  
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Ratio: 3.941 Gaps: 6  
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alignment\_block:  
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17 ValValSerLeuGluArgLeuMetGluProGlnAspThrAlaArgCys 34  
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34 erLeuGlyLeuSerCysHisLeuTrpAspIleValLeuCysLeuPro 50  
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51 GlySerLeuGlnSerAlaProGlyProValLeuValProThraArgLeuG 67  
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67 nThrlauValLeuArgCysProGlnInsThraAspCysAlaLeuArgV 84  
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399 GACAGAGCTGTGCTGAGGTGGCAGAAGAGACCGAGCTGACCTCTGCTG 448

[illegible]

XX Homo sapiens.  
XX PN MO200155320-A2.  
XX PD 02-AUG-2001.  
XX PF 17-JAN-2001; 2001MO-US01339.  
XX PR 31-JAN-2000; 2000US-0179065.  
PR 04-FEB-2000; 2000US-0180628.  
PR 24-FEB-2000; 2000US-0184664.  
PR 02-MAR-2000; 2000US-0186350.  
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PR 08-DEC-2000; 2000US-0251989.  
PR 11-DEC-2000; 2000US-0254097.  
PR 05-JAN-2001; 2001US-0259678.  
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DM of: US-09-899-471-5 to: GenEmbl: \* out-format : pfs

Date: Sep 29, 2002 1:05 AM

About: Results were produced by the Gencore software, version 4.5,  
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## Search information block:

Query: US-09-899-471-5  
Query Length: 698  
Database: GenEmbl: \*  
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b.pat:AX350976	3723.00	4398.30	1.3e-236	2314	AX350976 Sequence 10 from Pat
b.pat:BC004759	3153.50	3725.17	3.9e-199	2015	BC004759 Mus musculus, clone M
b.pat:AX350978	2756.00	3254.14	6.8e-173	2094	AX350978 Sequence 12 from Pat
b.pat:AX073993	2389.50	2819.50	1.1e-148	2255	AX073993 Sequence 1 from Pat
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ACCESSION AX350976  
VERSION AX350976.1 GI:18616352  
KEYWORDS  
SOURCE unidentified.  
ORGANISM unidentified.  
REFERENCE 1 (sites)  
AUTHORS Gorman, D.M.  
TITLE Mammalian receptor proteins: related reagents and methods  
JOURNAL Patent: WO 0190358-A 10-29-NOV-2001;  
SCHERING CORPORATION (US)  
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299 CTCTAGGCT 348



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Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
USA  
NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
Contact: MGC help desk  
Email: [cgaps-remail.nih.gov](mailto:cgaps-remail.nih.gov)  
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.  
cDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: Baylor College of Medicine Human Genome  
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Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>  
Contact: [villalobdc@bcm.tmc.edu](mailto:villalobdc@bcm.tmc.edu)  
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REFERENCE  
1 (bases 1 to 2380)  
Chen,J., Filvaroff,E., Fong,S., Goddard,A., Godowski,P.J.,  
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Lookeren,M., Vandlen,K.L., Malanabe,C.K., Williams,P.M., Wood,W.I.  
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ORGANISM unidentified.
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JOURNAL Patent: WO 0190358-A 7 29-NOV-2001;
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 JOURNAL Helix Research Institute (JP)

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LOCUS AX073996 1753 bp DNA linear PAT 06-FEB-2001
DEFINITION Sequence 4 from Patent WO0104304.
ACCESSION AX073996
VERSION AX073996.1 GI:12710228
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1753)
AUTHORS Presnell,S.R., Burkhead,S.K. and Powder,S.L.
TITLE Human cytokine receptor
JOURNAL Patent: WO 0104304-A 4 18-JAN-2001;
ZymoGenetics, Inc. (US)
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LOCUS AX073995 2076 bp DNA linear PAT 06-FEB-2001
DEFINITION Sequence 3 from Patent WO0104304.
ACCESSION AX073995
VERSION AX073995.1 GI:12710227
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
artificial sequence.
REFERENCE
1 (bases 1 to 2076)
AUTHORS Plesnell,S.R., Burkhead,S.K. and Powder,S.L.
TITLE Human cytokine receptor
PATENT: WO 0104304-A 3 18-JAN-2001
JOURNAL ZymoGenetics, Inc. (US)
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LOCUS AX073998 1725 bp DNA linear PAT 06-FEB-2001
DEFINITION Sequence 6 from Patent WO0104304.
ACCESSION AX073998
VERSION AX073998.1 GI:12710230
KEYWORDS
SOURCE
ORGANISM synthetic construct.
artificial sequence.
REFERENCE
1 (bases 1 to 1725)
Presnell,S.R., Burkhead,S.K. and Powder,S.L.
Human cytokine receptor
Patent: WO 0104304-A 6 18-JAN-2001;
JOURNAL
ZymoGenetics, Inc. (US)
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 1152 NGTNGGNCNTNGCNCMNSGNCNTNTGTCARATNCNTTNGTNGCNG 1201  
 530 aIaSpLeuTyrPserArgArgGluLeuSerAlaHisGlyAlaLeuAla 546  
 1202 TNGAYTNTGMSMNGMNGARGATYTMNSGNCARGCNGCNGTNGCNG 1251  
 547 PheHisGlnArgArgArgGlyLeuGlnGlnGlyValValIleLe 563  
 1252 TYTCATGCNCARBNMNGNCACACATYTNCAARGANGNGTNGTNGTNT 1301  
 563 uLeuPheSerProAlaAlaValAlaGlnCysGlnGlnTyrPheLeuG 580  
 1302 NTNTYTMNSGNCNGCNGCNGCNGCNGTNTNTGYMNSGARGTNGTNCARG 1351  
 580 InThrValAlaPro..... GlyProHisAspAlaLeuAlaAlaTyr 593  
 1352 GNGTNGMNSGNCNGCNGCNCAYGNCNCAYGAYGNTTYMNGCNCMNS 1401  
 594 LeuSerCysValLeuProAspPheLeuGlnGlyArgAlaThrGlyArg 610  
 1402 YTMNSNTGTYTNTTNCNCNGATYTYTNCAARGMNGCNCNGMNSMTA 1451  
 610 rValGlyAlaTyrPheAspLysLeuLeuHisProAspSerValProSer 627  
 1452 YGTNGGNCNTGYTYGAYMNTYTNCAAYCCNGAYGNCGNTNCNGNT 1501  
 627 ropPheArgValAlaProLeuPheSerLeuProThrGlnLeuProAlaPhe 643  
 1502 TNYTNGMNCNTNCNGTNTYTAACNTYTNCCMNSNCARNTYTNCCNGAY 1551  
 644 LeuAspAlaLeuGlnGlyGlyCysSerThrSerAlaGlyArgProAlaAs 660  
 1552 YTNNGGNCNTYTNCAARCCMNGCNCMNGMNSGNGMNGTNCARGA 1601  
 660 pArgValGluArgValThrGlnAlaLeuArgSerAlaLeuAspSerCys 676  
 1602 RMGNCNGARCARGTMNSMNGCNCNTNCARCCNGCYTNGAYMNSATY 1651  
 677 ..... ThrSerSerGluAlaProGly 684  
 1652 TYCACCCNCNCNGMNCNCNGCNCNGN 1680

seq\_name: gb\_hlg:AC024612

seq\_documentation\_block:

LOCUS AC024612 166620 bp DNA linear HTG 06-MAY-2001

DEFINITION Homo sapiens chromosome 3 clone RP11-481H17 map 3, WORKING DRAFT

SEQUENCE, 22 unordered pieces.

AC024612

AC024612.2 GI:9929740

KEYWORDS HTG: HTGS\_PHASE1, HTGS\_DRAFT.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;



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misc_feature      124917..142057
                  /note="assembly_fragment"
misc_feature      142158..157943
                  /note="assembly_fragment"
misc_feature      158044..166620
                  /note="assembly_fragment"
misc_feature      /note="assembly_fragment"
                  vector_end:17
BASE COUNT      42182 a 40159 c 39756 g 42421 t 2102 others
ORIGIN

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Alignment_scores:
  Quality: 692.50      Length: 470
  Ratio: 2.663         Gaps: 14
  Percent Similarity: 55.319   Percent Identity: 39.574

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Alignment block:  
us-09-899-471-5 x AC024612 ..

Align seg 1/1 to: AC024612 from: 1 to: 166620

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322 ValThrLeuGlySerGlnAlaProAspGlnSerProGlnProLeuVal 338
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72050 GTTGTGTTGTTGTTGTTGTTGAGAGAGAGCTCACCCCTGCGCCAGGCTG 72099
    338 lProProValProGlnLysAsnAlaThrValAsnGlnProGlnAspPheG 355
    ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
72100 GAGTGCATGCGCGATCGCGCTCAGTCAACCTCGCTCCAGATTC 72149
    355 lIleuValAlaGlyHisProAsnLeuGlyValGlnValSerThrTrpGlu 371
    || ::::: |||
72150 AAGCGATT.....CTCTGCTCAGCTCC.....GAG 72178
    372 LysValGlnLeuGlnAlaGlySerTrpAlaAspSerLeuGlyProPheGly 388
    ::::: |||||::|||::|||::|||::|||::|||::|||::|||
72179 TAGCTGGGATTACAGCGGTG.....GCCACACAGCCCGGCTAAATT.. 72220
    388 sAspAspMetLeuLeuValGlnMetLysThrGlyLeuAsnAsnThrSerV 405
    ::::: |||||::|||::|||::|||::|||::|||::|||::|||
72221 ....TTGTATTATTAGTAGAG.....ACGGGGTTTCACCGTGTAGGCC 72260
    405 aICysAlaLeuGlnProSerGlyCysThrProLeuProSerMetLaser 421
    ::::: |||||
72261 AGGATGGCTTGAT.....GTCTGTGACC 72283
    422 ThrArgAlaAlaIleArgLeuGlyGlnGlnLeuLeuGlnAspPheArgSer.. 437
    ::::: |||||::|||::|||::|||::|||::|||::|||::|||
72284 TGTGATTCGCCCGCGCTCGGCTCCCAAGAGCTGGGATTATATAAGGC 72333
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    ::::: |||||
72334 ATGAGCACCACGACCGCGCCCAATTCATTTCTGTTAAGTCTCAGTTTTC 72383
    445 .....AsnAspAspAsnMetGlySerLeuTrp 453
    ::::: |||||
72384 TTCTCTGTGAGAGGTAGATTCTTAACCTTCTCTGCGGTCTC..... 72427
    454 AlaCysProMetAspLysTrpIleHisArgArgTrpValLeuValTrpLe 470
    ::::: |||||
72428 .....CCAGCATCCACAGAGCGCTGGGCGCTGCTGTGGCT 72462
    470 uAlaCysLeuLeuLeuAlaAlaIleuPhePhePheLeuLeuLeuLysL 487
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72463 GCGCTGCTCACTCTTGGCGGCTTCCCTCCATCTCTCTCAAAA 72512

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487 yAspArgArgLys..... 491
    |||||::|||
72513 AGCATCACCGCAAGAGTGAGCGCTTCCGGCTCCCAATTCCTGGGGGA 72562
    491 ..... 491
72563 GGACAGAGTGGCTGTGGAGTTCCTCCAGAGAAACCGCGCGGAGCTC 72612
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72613 ACTGCTGCTCCGCCCTCTCCCTACAGAGGTGCTGAGGCTTTGAA 72662
    491 ..... 491
72663 ACAGAGCTCCGCTGGGGGGGTAGTGGAGCAAGCGCTGGCGGAGGCC 72712
    491 ..... 491
72713 CGCCCGCGGGAGCCAGGCTGTGCCAGTCACTCTTCCCTCCCATCT 72762
    492 .....AlaAlaArgGlySerArgThrAlaLeuLeuH 503
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    ::|||::|||::|||::|||::|||::|||::|||
72960 AGACCTGTCAGAGAGGGCGCGGTGTGTGTCTCTCTCTCCCGGTGCG 73009
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    |||||::|||::|||::|||::|||::|||::|||::|||
73010 GTGGGCTGTGCGAGAGTGGCTACAGATGGGTGTCCCGCGCGGGCG 73059
    585 ....GlyProHisAspAlaLeuAlaAlaTrpLeuSerCysValLeuPro 600
    |||||::|||::|||::|||::|||::|||::|||::|||
73060 GCACGCGCGCGCAGACGCTTCCGCGCTCGCTCAGCTGCTGCTGCGCG 73109
    600 sPheLeuGlnGlyArgAlaThrGlyArgTyrglyValGlyValTyrglyPheAsp 616
    |||||::|||::|||::|||::|||::|||::|||::|||
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Seq\_name: gb\_pr:AC007783

seq\_documentation\_block: 168665 bp DNA linear PRI 03-NOV-2001

LOCUS AC007783 Homo sapiens 3 BAC CTFB-140019 (Cal Tech Human BAC Library B)

DEFINITION complete sequence.

ACCESSION AC007783

VERSION AC007783.26 GI:16572920

KEYWORDS HTG.

SOURCE human

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 168665)

AUTHORS Mammalia: Eutheria: Primates: Catarrhini: Hominoidea: Homo.

Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-ouman,F.R., Allen,C., Alsbrooks,S.L., Amaralunga,H.C., Are,J.R., Banks,T., Barbarta,J., Benton,J., Bimaga,K., Blankenburg,K., Bonnin,D., Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Z., Chowdhury,I., Christopoulos,C., Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O., Den,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J., Earhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T., Gara,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K., Harris,C., Harris,K., Hart,M., Haylak,P., Hayes,A., He,X., Hernandez,J., Hernandez,O., Hodgson,A., Hoggins,M., Hollway,C., Hollins,B., Homsi,F., Howard,S., Huber,J., Huliy,S., Hume,J., Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korval,J., Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L., Li,J., Li,Z., Licharge,O., Lieu,C., Liu,J., Liu,W., Louisedge,H., Lozano,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J., Maheshwari,M., Mapa,P., Martin,R., Martindale,A., Martinez,E., Massey,E., Mawhinney,E., McLeod,M.P., Meador,M., Mel,G., Metzger,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Moore,S., Morgan,M., Moorish,T., Morris,S., Moser,M., Neal,D., Nelson,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokwenkwo,S., Ogun,M., Okunolu,G., Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y., Rives,L., Rojals,A., Rojupokan,I., Rolfe,M., Ruiz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shoshitari,N., Sisson,I., Sodergren,E., Sonleit,T., Sparks,A., Stanley,H., Stone,H., Sutton,A., Sutek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H., Tansey,J., Taylor,C., Taylor,T., Tellod,B., Thomas,N., Thomas,S., Usmali,K., Vasquez,L., Vera,V., Villalob,D., Vinson,R., Wall,R., Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S., Williams,G., Williamson,A., Wlecczyk,R., Woodson,S., Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Naylor,S.L., Weinstein,G. and Gibbs,R.

TITLE Direct Submission

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 168665)

AUTHORS Worley,K.C.

TITLE Direct Submission

JOURNAL Submitted (11-JUN-1999) Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

REFERENCE 3 (bases 1 to 168665)

AUTHORS Worley,K.C.

TITLE Direct Submission

JOURNAL Submitted (01-NOV-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

REFERENCE 4 (bases 1 to 168665)

AUTHORS Worley,K.C.

TITLE Direct Submission

JOURNAL Submitted (03-NOV-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

## COMMENT

On Nov 1, 2001 this sequence version replaced gi:16519453.  
 INFORMATION: <http://www.hgsc.bcm.tmc.edu/> or email  
[gc-help@bcm.tmc.edu](mailto:gc-help@bcm.tmc.edu)

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the features listing.

## ANNOTATION OF FEATURES:

STSs are identified using EPCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as low coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: <http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html>.

## QUALSTAT-REPORT

Summary Statistics		
Contig length:	168665	
Phrap values in estimate:	166919	
Average error rate (BCM-Phrap estimate):	9.71965e-05	
Fraction of Phrap values less than 40 :	0.0295473	
Number of N's in consensus :	0	
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744	cgctccgcg(n)ttcatgcct	cgctccgcg(n)ttcatgcct
756	tcagccat(n)tcgtgcctc	tcagccat(n)tcgtgcctc
759	tgccat(n)tgccgcgac	tgccat(n)tgccgcgac
780	tcacagtag(n)ggactacag	tcacagtag(n)ggactacag
784	agtagcag(n)ctacagtgac	agtagcag(n)ctacagtgac
802	tcagccac(n)accccgctc	tcagccac(n)accccgctc
811	ccagcccg(n)taattttg	ccagcccg(n)taattttg
841	tagagaggg(n)ttcannan	tagagaggg(n)ttcannan
847	cgagtttca(n)annnnan	cgagtttca(n)annnnan
849	gggtttca(n)nnnnan	gggtttca(n)nnnnan
850	ggtttca(n)nnnnan	ggtttca(n)nnnnan
851	ttcannan(n)nnnnan	ttcannan(n)nnnnan
853	ttcannan(n)nnnnan	ttcannan(n)nnnnan
855	caannntna(n)nnnnan	caannntna(n)nnnnan
857	naannntna(n)nnnnan	naannntna(n)nnnnan
859	nnnnan(n)nnnnan	nnnnan(n)nnnnan
860	nnnnan(n)nnnnan	nnnnan(n)nnnnan
861	nnnnan(n)nnnnan	nnnnan(n)nnnnan

99898	GAGTGCATGCGCGGATCTCGCTCACTGCACCACTCTGCCTCCGAGTTC	99849
355	IntLeuValAlaGlyHisProAsnLeuCysValGlnValSerThrProIu	371
99848	AACGGATT.....CTCTGCCCTAGCCCTCC.....GAG	99820
372	lysValGlnLeuGlnAlaCysSerThrProAlaSerLeuGlyProPheIy	388
99819	TAGCTGGGATTACAGGGCTGT.....GCCACACAGCGCCGGCTAATT..	99778
388	saSPasPmeIleuValGlnMetIlyThrGlyLeuAsnAsnThrSerV	405
99777	.....TTTGTATTATTATAGTAGAG.....ACGGGGTTTCACCGTCTTAGCC	99738
405	alCysAlaLeuGlnProSerGlyCysThrProLeuProSerMetAlaSer	421
99737	AGCATGGCTTGAT.....GTCTCAGCC	99715
422	ThrArgAlaalaArgLeuGlyGlnGlnLeuGlnAspPheArgSer.	437
99714	TCGTGATCTGCCCGCTCGGCTCCCGAAGTCGTGGATTATATAAAGGC	99655
438	.....HisGlnCys..MetGlnLeuTrp.	444
99664	ATGAGCCACCGCACCCGCCCAATTCTATTCTTTAAGTCTCACTTTTTC	99615
445	.....AsnAspAspAsnMetGlySerLeuTrp	453
99614	TTTCTCTGAGAGGTAAGTTTCTAAGTCTCTCTCTGCGGCTC.....	99571
454	AlaCysProMetAspPlyStrIleHisArgArgTrpValLeuValTrpLe	470
99570	.....CCAGACATCTCCACAAAGCGGTGGCGCCCTCGTGGTCT	99536
470	uAlaCysLeuLeuLeuAlaAlaLeuPhePhePheLeuLeuLeuLysL	487
99535	GGCTTGGCTACTCTTTGGCGCTGCGCTTCCCTCATCTCTCTTCAAAA	99486
487	ysaSPasPArgLys.....	491
99485	AGGATCAACGCGAAGAAGTAGAGCTTCCCGGCTCCCACTTCCCTGGGGGA	99436
491	.....	491
99435	GGACACAGATGCGCTGTGGAGATTCTCCAGAGGAAGCGGCGCGCACTC	99386
491	.....	491
99385	ACTGGCTGCTCCGCGCCCTCTCCCTTAACAGAGGTGGGTGAGGCTTTGAA	99336
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99285 CGCCCCCGGGAGCAGCCGCTGTGCAGCTCACCCGTTCCCTCCCAATCT 992336
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99235 GTTTTCGCCGACGCGCGCCAGGAGGC...CGCGGGCTCTGTGCTCTCT 99189
503 ISeSerAlaAGLyAlaGlyTyrGlyArgLeuValGlyAlaLeuAlaSer 519
99188 ACACAGCGCAGTACTGGGTTCAGAGCCCTGATGGCGCCCTGCGCTCG 99139

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520 AIdEusergImctProLeunrGyAlAValAspLeunrpsrrAgar 536  
||||| ||::||| ||::||| ||::||| ||::|||  
99138 GCCCTGGCCAGTCGCCCTGGCGCTGGCGGTAGACCTTGAGACCCTGC 99089

536 gGIuLeuSerAlaIscgIyAlaLeuAlatrrPheNtSHISglNaqrGa 553  
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GM of: US-09-899-471-5 to: Issued\_Patents\_NA: \* out\_format : pfs

Date: Sep 29, 2002 1:06 AM

About: Results were produced by the Gencore software, version 4.5,  
Copyright (c) 1993-2000 Compugen Ltd.

#### Command line parameters:

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-Q=/cgn2\_1/uspro.spool/US09899471/runat\_27092002.142439.17925/app-query.fasta\_1.2519  
-DB=Issued\_Patents\_NA -OFMT=fastap -SUFFIX=rni -GAPOP=12.000  
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000 -XGAPEXT=0.000  
-OGAPOP=4.500 -OGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500  
-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500  
-DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=blonsum62  
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR\_SCORE=pct  
-THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs  
-NORM-ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US09899471.ecgnl.1132 -NCPU=6 -ICPG=3 -LONGLOC  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -NO\_XLPHY -WAIT -THREADS=1

#### Search information block:

Query: US-09-899-471-5  
Query length: 698  
Database: Issued\_Patents\_NA: \*  
Database sequences: 383533  
Database length: 122816752  
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#### Score list:

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cg2_6/pdata/2/1na/6B.COMB.seq	US-09-022-253-1	184.50	274.13	1.4e-07	3288	1		
cg2_6/pdata/2/1na/6A.COMB.seq	US-08-978-773-1	184.50	274.13	1.4e-07	3288	1		
cg2_6/pdata/2/1na/6A.COMB.seq	US-09-022-253-1	184.50	274.13	1.4e-07	3288	1		
cg2_6/pdata/2/1na/6A.COMB.seq	US-09-022-253-1	184.50	274.13	1.4e-07	3288	1		
cg2_6/pdata/2/1na/6B.COMB.seq	US-09-022-259-1	184.50	274.13	1.4e-07	3288	1		
cg2_6/pdata/2/1na/6B.COMB.seq	US-09-022-257-1	184.50	274.13	1.4e-07	3288	1		
cg2_6/pdata/2/1na/6A.COMB.seq	US-09-188-930-6	152.00	232.45	1.4e-05	1059	1		
cg2_6/pdata/2/1na/5B.COMB.seq	US-08-620-694A-9	151.50	217.74	0.0002	3223	1		
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cg2_6/pdata/2/1na/6A.COMB.seq	US-09-022-253-9	151.50	217.74	0.0002	3223	1		
cg2_6/pdata/2/1na/6A.COMB.seq	US-09-022-259-9	151.50	217.74	0.0002	3223	1		
cg2_6/pdata/2/1na/6B.COMB.seq	US-09-022-257-9	151.50	217.74	0.0002	3223	1		
cg2_6/pdata/2/1na/6A.COMB.seq	US-09-022-257-9	135.00	181.76	0.0195	5962	1		
cg2_6/pdata/2/1na/5A.COMB.seq	US-08-981-459-1	135.00	172.36	0.0652	12687	1		
cg2_6/pdata/2/1na/6B.COMB.seq	US-09-063-431A-1	135.00	172.36	0.0652	12687	1		
cg2_6/pdata/2/1na/5B.COMB.seq	US-08-583-562B-7	128.00	165.53	0.1565	8367	1		
cg2_6/pdata/2/1na/5B.COMB.seq	US-08-779-113-7	128.00	165.53	0.1565	8367	1		
cg2_6/pdata/2/1na/5B.COMB.seq	US-09-060-836-2	126.50	163.69	0.1981	7886	1		
cg2_6/pdata/2/1na/6B.COMB.seq	US-09-184-445-2	126.50	163.69	0.1981	7886	1		
cg2_6/pdata/2/1na/5B.COMB.seq	US-08-841-483-3	125.00	171.27	0.0750	3490	1		
cg2_6/pdata/2/1na/6B.COMB.seq	US-09-382-911-3	125.00	171.27	0.0750	3490	1		
cg2_6/pdata/2/1na/5B.COMB.seq	US-08-841-483-5	125.00	169.28	0.0968	4094	1		
cg2_6/pdata/2/1na/6B.COMB.seq	US-09-382-911-5	125.00	169.28	0.0968	4094	1		
cg2_6/pdata/2/1na/5A.COMB.seq	US-08-404-354B-1	124.00	162.86	0.2206	5975	1		
cg2_6/pdata/2/1na/5A.COMB.seq	US-08-314-083B-1	124.00	162.86	0.2206	5975	1		
cg2_6/pdata/2/1na/5A.COMB.seq	US-08-435-675B-1	124.00	162.86	0.2206	5975	1		
cg2_6/pdata/2/1na/6A.COMB.seq	US-08-884-599-1	124.00	162.86	0.2206	5975	1		
cg2_6/pdata/2/1na/5A.COMB.seq	US-08-336-257A-3	121.00	157.71	0.4569	5975	1		
cg2_6/pdata/2/1na/5A.COMB.seq	US-08-342-930-1	120.50	157.98	0.4211	5455	1		
cg2_6/pdata/2/1na/5B.COMB.seq	US-09-276-531-7	119.00	162.48	0.2314	3090	1		
cg2_6/pdata/2/1na/5B.COMB.seq	US-08-460-751-1	119.00	144.68	2.27	12912	1		
cg2_6/pdata/2/1na/6A.COMB.seq	US-08-658-136-4	119.00	143.62	2.60	14060	1		

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cg2\_6/pdata/2/1na/5A.COMB.seq:US-07-960-389-1 + 114.50 153.30 0.7515 3475

#### Seq documentation block:

Sequence 226, Application US/09188930A  
Patent No. 6150502  
GENERAL INFORMATION:  
APPLICANT: Watson, James D.  
APPLICANT: Strachan, Lorna  
APPLICANT: Sleeman, Matthew  
APPLICANT: Onrust, Rene  
TITLE OF INVENTION: Compositions Isolated From Skin Cells  
FILE REFERENCE: 11000.1011c1  
CURRENT APPLICATION NUMBER: US/09/188,930A  
NUMBER OF SEQ ID NOS: 348  
SOFTWARE: FASTSEQ for Windows Version 3.0  
SEQ ID NO 226  
LENGTH: 2165  
TYPE: DNA  
ORGANISM: Mouse  
US-09-188-930-226

#### alignment\_scores:

Quality: 313.50 Length: 632  
Ratio: 1.059 Gaps: 24  
Percent Similarity: 46.835 Percent Identity: 24.051

#### alignment\_block:

US-09-899-471-5 x US-09-188-930-226 ..  
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312 CCAAGAGAGAGCTGCTAGGAGCCCTCCCTGCTAGGAGAGCCATCGAA 361  
115 LaserLeuGlnAlaGlnValValLeuSerPheGlnAlaTyProIleAla 131  
|||||.....  
362 TTTCATCTCCCTCCCTCAGCCATC...TCCACAGAGCCCAACGCCA 408  
132 ArgGlyAlaLeuLeuGlnValGlnValProIleAspLeuValGlnProG 148  
|||||.....  
409 AGGCCCGAGCTTACGCTGACAGAGAGAGAACATCTCCCTGAGCAGG 458  
148 Y...GlnSerValGlySerAlaValPheAspCysPheGlnAlaSerLeu 164  
|||||.....  
459 GTCCACAAAGGTGGAGAGACCTGAA.....TTCTCTTTGATTGTC 499  
164 LysAlaGlnValGlnIleTyrPheSerTyThrLysPheGlyGlnLysGln 180  
|||||.....  
500 TGCCCGAGTCCAGGCTGTCGGGTGATTCCTGACGCCCAAGGCC 549  
181 LeuAsnLeuThrGlnGlnLeuProAspCysArgGlyLeuGlnValArgAs 197  
549 .....  
197 PserIleGlnSerCys.....TyrValLeuProTyrLeuAsnValSer 212  
|||||.....  
550 AGGTGCGCCCTTTGATTTCAGTGGGACATGGAATGGAAGCTTACGTA 598  
212 hrAspGlyAspAsnValLeuLeuThrLeuAspValSerGluGlnAsp 228  
|||||.....  
599 GCCCTTTTGATAC..... 612

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229 PheSerPheLeuLeuTyrlLeuArgProValProAspAlaLeuLysSerLe 245
612 ..... 612
245 uTrpTyrlLysAsnLeuThrGlyProGlnAsnIleThrLeuAsnHisThrA 262
613 ....CAGAAATTTGTCTGAGAGCCACACTGTAGACTGCTTATGAT 658
262 splLeuValProCysLeuLysIleGlnValTrpSerLeuGluProAspSer 278
659 TCCTTCCTGCTGATGCTAGAGAGCCCTCTTACCTGCAAGAGAGACACT 708
279 GluArgValGluPheCysProPheArgGluAspProGlyAlaHis..Ar 294
709 GTAGGCGCAAAAGTGTCTCCAGAGCTGAGCTTGAAGCTTATGCTC 758
294 GAsnLeuTrpHisIleAlaArgLeuArgValLeuSerProGly..... 308
759 AGACTTCGGGAGCTCAATACGCTTCACTACTGACAGCAGCAATCA 808
309 ..ValTrpGlnLeuAspAlaProCysCysLeuProGlyLysValThrLeu 324
809 TGCTATGAGCTCTGACACTCCGCTGCCACTGAATGAGAGCCCTCCCTC 858
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341 lProGlnLysAsnAlaThrValAsnGluProGlnAspPheGlnLeuVala 358
898 .....CCCAAGCCACAGCAGAGAGTGAAGATGATATCTCTGG 940
358 laGly.....HisProAsnLeuCysValGlnValSerThrTrpGlu 371
941 AGAATGTGACTTGCACCCAGCTGCTTAAAGTCTCA...TTTGA 987
372 LysValGlnLeuGlnAlaCys.....SerTr 380
988 AACAGAGCCAGCTTGAATGTCTCCACAGAGTGGCTCTCCCATCTG 1037
380 palAspSerLeuGlyProPheLysAspMetLeuLeuValGlnMetL 397
1038 GACTGTGAGCATGATAC...CAGGCCAGCAGCTACCTTACTT 1084
397 ysthGlyLeuAsnAsnThrSerValCysAlaLeuGluProSerGlyCys 413
1085 CTTGAGAGACATATGCCACTTCACTGCTGAGTGCAGCCAGCTTGG 1134
414 .....ThrProLeuProSerMetAlaSerThrArgAlaAlaArgLe 427
1135 GGGCCGGATACCCCATGCTCTCTGTACAGCATCAGCCAGAGCCAGG 1184
427 uGlyGluLeuLeuGlnAsp.....PheArgSerHisG 439
1185 CTCAGTCCACAGTACGCTGACCTCATCCCTTCTGAGGAGGAGA 1234
439 lncYMetGlnLeuTrpAsnAspAspAsnMetGlySerLeuTrpAlaCys 455
1235 ATTGCATCTGCTGAGAGTCAAT..... 1260
456 PrometAspLysTyrIleHisArgArgTrpValLeuVal..... 468
1261 .....GTCCATTTTGGCTGAGAGCAGCTTGTGTCTGTA 1295
469 .....TrpLeuAlaCysLeuLeuLeuAlaAlaAlaLeuPhePheP 482
1296 TGAGCCCTTACCTACTGACCTGTGCTC..... 1326
482 heLeuLeuLeuLysAspArgGlyAlaAlaArgLysArgThr 498
1327 .....CGTCCCTAGGCTCCGCTGAGCAAGAGCCA 1356
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515 YAlaLeuAlaSerAlaLeuSerGlnMet.....ProLeuArgVala 529
1407 AGCTTTGGCCCAACTGCTGCGAGCGCGCTGGAGGTGAGACCGAGCTGA 1556
529 lAlaAspLeuTrpSerArgArgGluLeuSerAlaHisGlyAlaLeuAla 545
1457 TCGTGATCTCTGGGAGAGGAGGACGATAGCAGGCTTGGACACTGGCG 1506
546 TrpPheHisHisGlnArgArgArgIleLeuGlnGlyValValI 562
1507 TGCTTTGGGAGCGCGGAGCGCTGGCGGAGCAGGAGCAGACTGCT 1556
562 eLeuLeuPheSerProAlaAlaValAlaGlnCysGlnGlnTrpLeuGln 579
1557 GCTCTGTGACACTGTGCGGTCCAGC..... 1584
579 euGlnTrpValGluProGlyProHisAspAlaLeuAlaAlaTrpLeuSer 595
1585 ..ACCGCTGACGAGGCTGACCGGAGGCTGCTCCCTTGGCACTTGTG 1632
596 CysValLeuProAspPheLeuGlnGlyArgAlaThrGlyArgValGl 612
1633 TGCGCTGCTCCACGCTCCGCTG.....CTGCT 1658
612 YValTrpPheAspGlyLeuLeuHisProAspSerValProSerProPhe 629
1659 CGCTTACTTCACTGCTGCTGCGCCAAAGTGAACATCCCGCGCTGCT 1708
629 rGValAlaProLeuPheSerLeuProThrGlnLeuProAlaPheLeuAsp 645
1709 GCGCTTGCACAGCTACCGCTGCTGCTGAGACTGCGGCGCTGAGAGA 1758
646 AlaLeuGlnGlyGlyCysSerThrSerAla.....Gl 656
1759 GCATGTGATGCTCAGCCTGACCCCTGAGCTGCTGAGTCACTGCTGG 1808
656 YArgProAlaAspArgValGluArgValThrGlnAla.....L 669
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669 euArgSerAlaLeuAspSerCysThrSerSerGlnAlaPro 683
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seq_name: /cgn2_6/ptodata/2/ina/5b_COMB.seq:US-08-620-694A-1
seq_documentation_block:
; Sequence 1, Application us/08620694A
; Patent No. 5869286
; GENERAL INFORMATION:
; APPLICANT: Tao, Zhengbin
; APPLICANT: Springs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 5869286el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; APPLICATION NUMBER: US/08/620,694A
; FILING DATE: 21 MARCH 1996

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CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/538,765  
FILING DATE: 7 AUGUST 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/410,535  
FILING DATE: 23 MARCH 1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia Anne  
REGISTRATION NUMBER: 34,695  
REFERENCE/DOCKET NUMBER: 2617-B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3288 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
HYPOTHEICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Mouse  
STRAIN: HVS13 receptor  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 121..2715  
US-08-620-694A-1

Alignment scores:  
Quality: 184.50 Length: 655  
Ratio: 0.666 Gaps: 32  
Percent Similarity: 42.290 Percent Identity: 20.763

Alignment block:  
US-09-899-471-5 x US-08-620-694A-1  
Align seg 1/1 to: US-08-620-694A-1 from: 1 to: 3288

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124 GCGATTCGCGCGCTGCTGCGCAGCGCTGCCGCGCGCGCTGGATG 173  
207 PLeuAsnValSerThrAspGlyAspAsnValLeuLeuThrLeuAspVal 224  
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174 GCTG.....CTTCTGCTGCTGAACGTTTC 196  
224 erGluGlnAspPheSerPheLeuLeuTyrlLeuArgProValPro... 239  
197 TGGCCCCGCGCGCGCTCCCGCGCTCTCGACTTCGCGCTCCGCTC 246  
240 .....AspAlaLeu 243  
247 TGGCGGAGAGAGGGGTGAGTGCAGAGTCAGAGATAGTACTTCTCGA 296  
243 sSerLeuTrpTyr.....LysAsnLeuThr.....GlyProGlnAsn 256  
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256 LeThrLeuAsn.....HisThrAspLeuValPro 265  
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266 CysLeuCysIleGlnValTrpSerLeuGluProAsp..... 277  
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278 .....SerGluArg 280

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296 LeuThrPheIleAlaArgLeuArg...ValLeuSerProGlyValTrpG 311  
|||:::|||||  
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311 nLeuAspAlaProCysCysLeuProGlyLysValThrLeuCysTrpGln 328  
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583 .....CAGAGTATGAGTGAAGTCTGTT..... 603  
328 lArProAspGlnSerProCysGlnProLeuValProProValProGln 344  
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345 AsnAlaThrValAsnGluProGlnAspPheGlnLeuValAlaGlyHis 361  
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634 GACCCAAACCAAAATCCA.....AGAT 656  
361 roAsnLeuCysValGlnValSerThr..... 369  
657 CATCTTGTGCTGCTGACTGTGAGACAGACAGATGAGATGACTCAAT 706  
370 .....TrpGluLysVal 373  
707 GCGTGAGCTCAGAGCCTTTGGATCCACATCATCTGTGGAGACTTG 756  
373 lGlnLeuGlnAlaCysSerTrpAlaSerLeuGlyProPheLysAsp 390  
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390 spMetLeuLeuValGluMetLysThrGlyLeuAsnAsnThrSerValCys 406  
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779 .....ACTTACCTCT 790  
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436 rGSerHisGlnCysMetGlnLeuTrpAsnAspAsnMetGlySerLeu 452  
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891 AGAAGAATTCATCAGCAGAGCTAATGTCATCACTCTACACAGTTTC 940  
453 ..TrpAlaCys..... 455  
941 ACTGTGCTGCCATCACACGTCGAGTCCAGCCCTCTTCAGACAGTCC 990  
455 ..... 455  
991 CTAAATGACTTTGAGACAGCTGTGACTGTG.....GCCCGAATATCTC 1040  
456 .....PrometAspLysTyrIleHisArgArgTrp 466  
1041 AAATACACAGAGTCCCAAGCCAGTTGAGACTACATTT...CCCGTGG 1087  
466 al.....LeuValTrpLeuAlaCysLeuLeuAlaAlaLeuPhe 480  
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1088 TGTATGGCTTCATCATCACTCATTCGCTGCTGCTGAGTCTGATC 1137  
481 PhePheLeu.....LeuLeuLysLysAspArgArg 491  
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1138 GTGCTGATCATCTGTATGACCTGAGGCTTCTGCGCGGATCAGAGAA 1187  
491 sAlaAlaArgGlySer..... 496

documentation block:  
sequence 1, Application US/09022255  
agent No. 6072033  
GENERAL INFORMATION:  
APPLICANT: Yao, Zhenqin  
APPLICANT: Spriggs, Melanie  
APPLICANT: Fenslow, William  
TITLE OF INVENTION: No. 6072033el Receptor That Binds IL-1  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle

alignment_scores:		
Quality:	184.50	Length: 655
Ratio:	0.666	Gaps: 32
Percent Similarity:	42.250	Percent Identity: 20.763
alignment_block:		
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Align seg 1/1	to: US-09-022-255-1	from: 1 ..to: 3288

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207 pLeuAsnValSerThrArgAlaAspAsnValLeuLeuThrLeuAspValS 224
    ||||| ..... ||||| M :::::
174 GCCT.....CTTCGCCTCAACGGTTC 166
    .....
224 erGIuGlInAspPheSerPheLeuLeuTyrlLeuArrProValPro... 239
    ..... ||| ..... |||||
197 TGCCGCCCGCGCCGCCCTCCCGCGCTCTCGACTTCGCCGCGCGGTC 246
    ..... ||| ..... |||||
240 .....AspAlaLeu 243
    .....
247 TGGCCGACGGAGGGGCTAGCTGCAGATCAAGAATAAGTACTGTGTGCA 256
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243 sSerLeuTrpTyrr.....LysAsnLeuThr.....GlyProGlnAsn 256
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224	erglgluglnaspheSerPheLeuTyrLeuArgProValPro...	239
197	TGGCCCGGCGCGGCCCTCCCGCGCCTTCGTGACTTCGGGCTCGGTC	246
240	.....AspIleLeu	243
247	TGCCGCAGAGGGGCTGAGCTGCAGAGTCAGAAGATAGTACTTGCTGGA	256
243	sSerIlePtyr.....LysAsnLeuThr.....GlyProGlnAsn	256
297	TGACAGCGTAGNTCCACCACCAAAACCCTGACCCCGCTTCCCAAAAACA	346
256	IerHLeuAsn.....HisThrAspLeuValPro	265
347	TCTATTATCAATCTTAGTTGTTTCCCTTACCCACAGCAGAGAATTAGTCCCT	366
266	CysLeuCysIleGlnValTrpSerLeuGluProAsp.....	277
397	GTTGTTCATGTTGAG...TGCACCTGCAGACAGATGCCAGCATCTGTA	443
278	.....SerGluArg..	280
444	CCTGAGGGTGCAGAGCTGTCCGCTCCGACGTGAACACCAATGACGGC	493
281	....ValGluPheCysProPheArgGluAspProGluAlaHisArgAsn	295
494	TGTGTGTAAGTTC..CAGTTTCTGTCCATGCTGTGAGCATACCGTAAG	540
296	LeuTrpHisIleAlaArgLeuArg...ValLeuSerProGluValTrpGlu	311
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583	.....CAGAGATGATAAGTACTGTT.....	603
328	IaProAspGlnSerProCysGlnProLeuValProProValProGlnLys	344
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634	GACCCAACCAACAATCCA.....AGAT	656
361	roAsnLeuCysValGlnValSerThr.....	369
657	CATTTTGTGCTGACTGTGAGGACAGACAGATGAGATGACTACTCAT	706
370	.....TrpGluLysVa	373
707	GCGTAGCTACGAGCGCTTTGGATGCCAACATCACTGTGGAGACTTC	756
773	IglnLeuGlnAlaCysSerTrpAlaAspSerLeuGlyProPheLysAspa	390
757	GACACACAGCATCTGCGAGTGG.....	778
390	spMetLeuLeuValGlnMetLysThrGlyLeuAsnAspThrValCys	406
779	.....ACTTCACCTGT	790
407	AlaLeuGluPro.....SerGlyCysThrProLeu...Proserme	419
791	GGATGGAATCCACCCCCTACACAGGCTCTGGGAAGTTTCTCCCACTCA	840
419	tAlaSerThrArgAlaAlaArgLeuGlyGlnGluLeuLeuGlnAspPhea	436
841	GAGAACCAACAGCTGCTTGGATGTCGTTAAACAATAATTGGCCCCCGACA	890
436	rgSerHisGlnCysMetGlnLeuTrpAsnAspAspAsmetGlySerLeu	452
991	AGAAGAATTCATCAGCAGGATATGTCAACATTCACCTTAAGCAAAGTTTC	940

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453 ..TTPAlaGys..... 455
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941 AGTGTGCTGCTGCATCCAGCAGTGCAGTCCAGCCCTTCTTACAGCAGCTGC 990
455 ..... 455
991 CTAAATGACTGTTGAGACAGCTGACTGTGCCCTGCCCAATATCTC 1040
456 .....PrometaspLysTyrIleHisArgArgTrrpV 466
1041 AATATACACAGTTCACAGCCAGTTCAGACATACAT...CCCTGTGGG 1087
466 al.....LeuValTrrpLeuAlaCysLeuLeuLeuAlaAlaAlaLeuPhe 480
1088 TGTATGCGCTCATCATCACTCATCGCCATCTCTGCTGGATCTGTCATC 1137
481 PhePheLeu.....LeuLeuLysLysAspArgArgLys 491
1138 GTGCTGATCATCTGATGACCTGGAGGCTTCTGGCCGATCAAGAGAA 1187
491 sAlaAlaArgGlySer..... 496
1188 ACATGTGATCATCTGATGACCTGGAGGCTTCTGGCCGATCAAGAGAA 1237
497 .....ArgTrrpAlaLeuLeuLeuHisSerAlaAsp 506
1238 CTGCCCCCAGCCCTGAGGCCAGGAGGCTGATCTGATCTGATCTGCGCCGAC 1287
507 G1ValaGlyTrrpGluArgLeuValGlyAlaLeuAlaSerAlaLeu...Se 522
1288 CACCCCTCTATGTGAGGCTGCTTAAAGTTCGCCAGTCTGATCAC 1337
522 rGlnMetProLeuArgValAlaValaAspLeuTrrpSerArgArgGluLeu 539
1338 TGCTGTGAGCAGTGAAGTACCTGCTGACCTCTGAGAAAGACAGTATCT 1387
539 erAlaHisGlyAlaLeuAlaTrrpPheHisGlnArgArgGlyLeu 555
1388 CTGAGTGGGGTCAATGACCTGAGTGGGAGCAGAGAGAGAGAGAGATGCTG 1437
556 GlnGluGlyValValIleLeuLeuPheSer..... 566
1438 GAGAGCACTCCAAATCATCTGCTGTTCCGAGGACCCAGCAAA 1487
567 .....ProAlaAlaValAlaGlnCysG 574
1488 GTGGAAAGCATCTTGGGTGGGCTGAGCCTCTGTCAGCTACGGGTG 1537
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1538 ACCACTGCT.....AAGCTGCT...GGGACCTTTTC 1566
591 AlaAlaTrrpLeuSerCysValLeuProAspPheLeuGlnGlyArgAlaTh 607
1567 ACTGCACCCATGATGATGATCTCTCCAGATCAAGAGCCAGCCCTT 1616
607 rGlyArgTrrpValGlyValTrrpPheAspGlyLeuLeuHisProAspSerV 624
1617 CGGCACTAGCTTCTTCTGCTCTCTCTGAGTGGCATCTGTACTGAGAGGATG 1666
624 alProSerProPheArgValAlaProLeuPheSerLeuPro...ThrGlnLe 640
1667 TCCCGCAGCTTCTTCAACATCACTCCAGTACCCACTATGACATATT 1716
640 uProAlaPheLeuAspAlaLeuGln.....GlyG 650
1717 GAGGAGGTTTACTTCCGATCCAGACCTGGAGATGTTTGAACCCGCGC 1766
650 LysSer.....ThrSerAlaGlyArgProAlaAspArgValGlu 663
1767 GATGCACCATGTCAGAGAGCTCACAGGGGACATTTACGTCAGAGCCCTA 1816
664 ArgValThrGlnAlaLeuArgSerAlaLeuAspSerCysThrSerSer 680

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seq\_name: /cgn2\_6/plodata/2/lna/6A\_COMB.seq:us-08-978-773-1

seq\_documentation\_block:

Sequence 1, Application US/08978773

Patent No. 6083906

GENERAL INFORMATION:

APPLICANT: Trout, Anthony

TITLE OF INVENTION: Method of Regulating Nitric Oxide Production

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunex Corporation

STREET: 51 University Street

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple PowerMacintosh

OPERATING SYSTEM: Apple Operating System 7.5.5

SOFTWARE: Microsoft Word for PowerMacintosh, Version 6.0.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/978,773

FILING DATE:

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: USSN 60/052,525

FILING DATE: 27 NOVEMBER 1996

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia Anne

REGISTRATION NUMBER: 34,693

REFERENCE/DOCKET NUMBER: 2623-A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 587-0430

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 3288 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Mouse

IMMEDIATE SOURCE:

CLONE: IL-17 receptor

FEATURE:

NAME/KEY: CDS

LOCATION: 121..2712

US-08-978-773-1

alignment\_scores: Quality: 184.50 Length: 655  
Ratio: 0.666 Gaps: 32  
Percent Similarity: 42.290 Percent Identity: 20.763

alignment\_block:

US-09-899-471-5 x US-08-978-773-1 ..

Align seg 1/1 to: US-08-978-773-1 from: 1 to: 3288

198 SerIleGlnSerCysTrrp.....ValLeuProTr 207

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seq\_documentation\_block:

Sequence 1, Application US/09022253  
 Patent No. 6096305

GENERAL INFORMATION:

APPLICANT: Yao, Zhengbin  
 APPLICANT: Spriggs, Melanie  
 APPLICANT: Fanslow, William  
 TITLE OF INVENTION: No. 6096305el Receptor That Binds IL-17  
 NUMBER OF SEQUENCES: 10  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Immunex Corporation  
 STREET: 51 University Street  
 CITY: Seattle  
 STATE: WA  
 COUNTRY: USA  
 ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
 COMPUTER: Apple Power Macintosh  
 OPERATING SYSTEM: Apple Operating System 7.5.5  
 SOFTWARE: Microsoft Word for Apple, Version 6.0.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/022,253  
 FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/620,694

FILING DATE: 21-MARCH-1996

APPLICATION NUMBER: USSN 08/538,765

FILING DATE: 7 AUGUST 1995

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: USSN 08/410,535

FILING DATE: 23 MARCH 1995

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia Anne

REGISTRATION NUMBER: 34,695

REFERENCE/DOCKET NUMBER: 2617-B

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206)587-0430

TELEFAX: (206)

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 3288 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

MOLECULE TYPE: cDNA to mRNA

HYPOTHEICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Mouse

STRAIN: HVS13 receptor

FEATURE:

NAME/KEY: CDS

LOCATION: 121..2715

US-09-022-253-1

alignment\_scores:  
 Quality: 184.50 Length: 655  
 Ratio: 0.666 Gaps: 32  
 Percent Similarity: 42.290 Percent Identity: 20.763  
 alignment\_block:  
 US-09-899-471-5 x US-09-022-253-1  
 Align seg 1/1 to: US-09-022-253-1 from: 1 to: 3288

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680 rGluAlaPro 683  
1867 CAGTCCCGCCG 1876  
seq\_name: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq:US-09-022-260-1  
seq\_documentation\_block:  
; Sequence 1, Application us/09022260  
; Patent No. 6100235  
; GENERAL INFORMATION:  
; APPLICANT: Yao, Zhengbin  
; APPLICANT: Spriggs, Melanie  
; APPLICANT: Fanslow, William  
; TITLE OF INVENTION: NO. 6100235el Receptor That Binds IL-17  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Power Macintosh  
; OPERATING SYSTEM: Apple Operating System 7.5.5  
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/022,260  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/620,694  
; FILING DATE:  
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; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USSN 08/410,535  
; FILING DATE: 23 MARCH 1995  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Perkins, Patricia Anne  
; REGISTRATION NUMBER: 34,695  
; REFERENCE/DOCKET NUMBER: 2617-B  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206)587-0430  
; TELEFAX: (206)  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3288 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single

TOPOLOGY: linear  
 MOLECULE TYPE: cDNA to mRNA  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 ORIGINAL SOURCE:  
 ORGANISM: Mouse  
 STRAIN: HVS13 receptor  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 121..2715  
 US-09-022-260-1

Alignment scores:  
 Quality: 184.50 Length: 655  
 Ratio: 0.666 Gaps: 32  
 Percent Similarity: 42.290 Percent Identity: 20.763

Alignment block:  
 US-09-899-471-5 x US-09-022-260-1 ..

Align seg 1/1 to: US-09-022-260-1 from: 1 to: 3288

198 SerIleGlnSerCysTrp.....ValLeuProTr 207  
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640 uProAlaPheLeuAspAlaLeuGln.....GlyG 650
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seq_documentation_block:
; Sequence 1, Application US/09022259
; Patent No. 6191104
;
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spirig, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6191104el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,259
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/620,694
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/410,535
; FILING DATE: 23 MARCH 1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:

```

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NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3288 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Mouse
STRAIN: HVS13 receptor
FEATURE:
NAME/KEY: CDS
LOCATION: 121..2715
US-09-022-259-1

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alignment\_scores:

Quality	Ratio	Length
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Percent Similarity: 42.290 Percent Identity: 20.763

alignment\_block:

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Align seg 1/7 to: US-09-022-259-1 from: 1 to: 3288

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207 PleuAsnValSerThrAspGlyAspAsnValLeuLeuThrLeuAsnValS 224
174 GCTG.....CTTCTGCTGTAACGCTTC 196
224 erGluGlnGlnAspPheSerPheLeuLeuTyrLeuArgProValPro... 239
197 TGGCCCGGCGCGCGCTCCCGCGCTCTCGACTCCCGGCTCGGTC 246
240 .....AspAlaLeuLy 243
247 TGCAGGAGGAGGCGCTGAGCTGACAGTCAAGATAGTACTGTGGA 296
243 sSerLeuTrpTyr.....LysAsnLeuThr.....GlyProGlnAsnI 256
297 TGACAGCTGATCCACCCCAAAACCTGACCCGCTTCCCAAAAACA 346
256 leuThrLeuAsn.....HisThrAspLeuValPro 265
347 TCTATATCAATCTAGTGTTCCTCTACCCACAGGAGATATGTCCT 396
266 CysLeuCysIleGlnValTyrSerLeuGluProAsp..... 277
397 GTTTGATGTTGAG...TGGACCTCGACAGATGCAATCTCTGA 443
278 .....SerGluArg 280
444 CTCGAGGAGTCACAGCTGCTCCGCTCCAGTGAACACCAAGAGCGCG 493
281 .....ValGluPheCysProPheArgGluAspProGlyAlaHisArgAsn 295
494 TGCTGTCAAGTTC...CAGTTTGTCCATGCTGCAGATACAGCTAG 540
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891 AGAAGAAATTCATCAGCGAGCTAATGCTCATCTTAAGCAAGTTTC 940
453 ..TrpAlaCys..... 455
941 ACTGCTGCTGCATCCACAGCTGACGTCACGCCCTTTCTCAGACGCTGC 990
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456 .....PrometAspLysTyrTyrLeuHisArgHisTrpV 466
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481 PhePheLeu.....LeuLeuLysAspArgArgLys 491
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491 salAlaAlaArgLysSer..... 496
1188 ACATGCTGATGACTCCAAATCAATGAGCATTTGCCGTAGACAGACCTGA 1237
497 .....ArgThrAlaLeuLeuLeuHisSerAlaAsp 506
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607 rGlyArgTyrValGlyValTyrPheAspGlyLeuLeuHisProAspSerV 624
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624 alProSerProPheArgValAlaProLeuPheSerLeuPro..ThrGlnLe 640
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seq\_name: /cgn2\_6/ptodata/2/lna/58\_COMB.seq:US-09-022-257-1

seq\_documentation\_block:

: Sequence 1, Application US/09022257

: Patent No. 6197525

: GENERAL INFORMATION:

: APPLICANT: Yao, Zhengbin

: APPLICANT: Spriggs, Melanie

: APPLICANT: Fanslow, William

: TITLE OF INVENTION: No. 6197525el Receptor That Binds IL-17

: NUMBER OF SEQUENCES: 10

: CORRESPONDENCE ADDRESS:

: ADDRESSEE: Immunex Corporation

: STREET: 51 University Street

: CITY: Seattle

: STATE: WA

: COUNTRY: USA

: ZIP: 98101

: COMPUTER READABLE FORM:

: MEDIUM TYPE: Floppy disk

: COMPUTER: Apple Power Macintosh

: OPERATING SYSTEM: Apple Operating System 7.5.5

: SOFTWARE: Microsoft Word for Apple, Version 6.0.1

: CURRENT APPLICATION DATA:

: APPLICATION NUMBER: US/09/022,257

FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/620,694  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: USSN 08/410,535  
 FILING DATE: 23 MARCH 1995  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Perkins, Patricia Anne  
 REGISTRATION NUMBER: 34,695  
 REFERENCE/DOCKET NUMBER: 2617-B  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (206)587-0430  
 TELEFAX: (206)  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 3288 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA to mRNA  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 ORIGINAL SOURCE:  
 ORGANISM: Mouse  
 STRAIN: HVS13 receptor  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 121..2715  
 US-09-022-257-1  
 Alignment\_scores:  
 Quality: 184.50 Length: 655  
 Ratio: 0.666 Gaps: 32  
 Percent Similarity: 42.290 Percent Identity: 20.763  
 Alignment\_block:  
 US-09-899-471-5 x US-09-022-257-1 ..  
 Align seg 1/1 to: US-09-022-257-1 from: 1 to: 3288

278 .....SerGluArg. 280  
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seq\_documentation\_block:  
 : Sequence 6, Application US/09188930A  
 : Patent No. 6150502  
 : GENERAL INFORMATION:  
 : APPLICANT: Watson, James D.  
 : APPLICANT: Strachan, Lorna  
 : APPLICANT: Sleeman, Matthew  
 : APPLICANT: Onrust, Rene  
 : APPLICANT: Morrison, James Greg  
 : TITLE OF INVENTION: Compositions Isolated From Skin Cells  
 : FILE REFERENCE: 11000.1011c1

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: CURRENT APPLICATION NUMBER: US/09/188,930A
: CURRENT FILING DATE: 1998-11-09
: NUMBER OF SEQ ID NOS: 348
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 6
: LENGTH: 1059
: TYPE: DNA
: ORGANISM: Mouse
: US-09-188-930-6

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alignment_scores:
  Quality: 152.00      Length: 305
  Ratio: 1.094        Gaps: 13
  Percent Similarity: 45.574  Percent Identity: 23.607

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alignment\_block:  
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709 GTGAGGCCGCAAAAGTGTCTCCAGAGAGTGGCTGACGTTATGGTTC 758
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1667 ..... 1667
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1668 .....ATGACACAGTTCGAGGAGTGTACTCTCCGATCCAG 1703
670 gSerAlaLeuAspSerCysThrSerSerSerGlnAlaProGlyCysCys 686
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seq_name: /cgn2_6/plodata/2/lna/5A_COMB.seq:us-09-022-255-9
seq documentation block:
: Sequence 9, Application US/09022255
: Patent No. 6072033
: GENERAL INFORMATION:
: APPLICANT: Yao, Zhengbin
: APPLICANT: Springs, Melanie
: APPLICANT: Fanslow, William
: TITLE OF INVENTION: No. 6072033el Receptor That Binds IL-17
: NUMBER OF SEQUENCES: 10
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Immunex Corporation
: STREET: 51 University Street
: CITY: Seattle
: STATE: WA
: COUNTRY: USA
: ZIP: 98101
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: Apple Power Macintosh
: OPERATING SYSTEM: Apple Operating System 7.5.5
: SOFTWARE: Microsoft Word for Apple, Version 6.0.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/022,255
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: USSN 08/620,694
: FILING DATE: 21 MARCH 1996

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Seq. documentation_block:
: Sequence 9, Application us/09022696
: Patent No. 6072037
: GENERAL INFORMATION:
: APPLICANT: Yao, Zhengbin
: APPLICANT: Spriggs, Melanie
: APPLICANT: Fanslow, William
: TITLE OF INVENTION: No. 6072037el Receptor That Binds IL-17
: NUMBER OF SEQUENCES: 10

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CORRESPONDENCE ADDRESS:
: ADDRESSEE: Immunex Corporation
: STREET: 51 University Street
: CITY: Seattle
: STATE: WA
: COUNTRY: USA
: ZIP: 98101
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: Apple Power Macintosh
: OPERATING SYSTEM: Apple Operating System 7.5.5
: SOFTWARE: Microsoft Word for Apple, Version 6.0.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/022,696
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/620,694
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: USSN 08/410,535
: FILING DATE: 23 MARCH 1995
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: Perkins, Patricia Anne
: REGISTRATION NUMBER: 34,695
: REFERENCE/DOCKET NUMBER: 2617-B
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (206)587-0430
: TELEFAX: (206)587-0430
: INFORMATION FOR SEQ ID NO: 9:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 3223 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA to mRNA
: HYPOTHEICAL: NO
: ANTI-SENSE: NO
: ORIGINAL SOURCE:
: ORGANISM: Human
: STRAIN: IL-17 R (hCTLA8 receptor)
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 93...2693
: US-09-022-696-9

alignment_scores:
: Quality: 151.50 Length: 703
: Ratio: 0.493 Gaps: 37
: Percent Similarity: 43.670 Percent Identity: 21.479

alignment_block:
: US-09-899-471-5 x US-09-022-696-9
Align seg 1/1 to: US-09-022-696-9 from: 36 to: 3223

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seq\_documentation\_block:  
Sequence 3, Application US/08978773

Patent No. 6083906

GENERAL INFORMATION:

APPLICANT: Trout, Anthony

TITLE OF INVENTION: Method of Regulating Nitric Oxide Production

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunex Corporation

STREET: 51 University Street

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple PowerMacintosh

OPERATING SYSTEM: Apple Operating System 7.5.5

SOFTWARE: Microsoft Word for PowerMacintosh, Version 6.0.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/978,773

FILING DATE:

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: USSN 60/052,525

FILING DATE: 27 NOVEMBER 1996

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia Anne

REGISTRATION NUMBER: 34,693

REFERENCE/DOCKET NUMBER: 2623-A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206)587-0430

TELEFAX: (206)

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 3223 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Human

IMMEDIATE SOURCE:

CLONE: IL-17R

FEATURE:

NAME/KEY: CDS

LOCATION: 93..2690

US-08-978-773-3

alignment\_scores:

Quality: 151.50 Length: 703

Ratio: 0.493 Gaps: 37

Percent Similarity: 43.670 Percent Identity: 21.479

alignment\_block:

US-09-899-471-5 x US-08-978-773-3 ..

Align seg 1/1 to: US-08-978-773-3 from: 1 to: 3223

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61 uValPro.....ThrArgLeuGlnThrGluLeuValLeuArgC 74  
170 GGGCCCGGCGGGCGCTCCCTGAGCTGAGCTGAGCTGAGCTGAGCT 219  
74 ySerProGlnThrAspCysAlaLeuArgValArgValValHisLeu 90  
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91 AlaValHisGlyHisTrpAlaGluProGlyGlnAlaGlyLysSerAsp 107  
261 TGCGTGGATGACAGCTGATTCACCTCGA..... 290  
107 rGluLeuGlnGluSerArgAsnAlaSerLeuGlnAlaGlnValValLeu 124  
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seq\_name: /cgn2.6/plodata/2/lna/6A\_COMB.seq:US-09-022-253-9  
seq\_documentation\_block:  
Sequence 9, Application US/09022253  
Patent No. 6096305  
GENERAL INFORMATION:  
APPLICANT: Yao, Zhengbin  
APPLICANT: Spriggs, Melanie  
APPLICANT: Fanslow, William  
TITLE OF INVENTION: NO. 6096305el Receptor That Binds IL-17  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Power Macintosh  
OPERATING SYSTEM: Apple Operating System 7.5.5  
SOFTWARE: Microsoft Word for Apple, Version 6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/022,253  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/620,694  
FILING DATE: 21-MARCH-1996  
APPLICATION NUMBER: USSN 08/538,765  
FILING DATE: 7 AUGUST 1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/410,535  
FILING DATE: 23 MARCH 1995  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia Anne  
REGISTRATION NUMBER: 34,695  
REFERENCE/DOCKET NUMBER: 2617-B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3223 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA to mRNA



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670 gSerAlaLeuAspSerCysThrSerSerGlnAlaProGlyCysCys 686
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1704 GACCTGAGAGATGTTCCAGCGCGGCGCGCATGCACCGCGTACGGGAGCTGT 1752
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Date: Sep 28, 2002 9:43 PM

About: Results were produced by the Gencore software, version 4.5,  
Copyright (c) 1993-2000 Compugen Ltd.

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-LIST=45 -DOCALIGN=200 -THR.SCORE=pct -THR.MAX=100 -THR.MIN=0  
-ALIGN=15 -MODE=LOCAL -OUTEXT=pfs -NORM=ext -HEAPSIZE=500  
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Search information block:

Query: US-09-899-471-5  
Query length: 698  
Database sequences: 13736207  
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Score list:

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clone 1110025H02, mRNA sequence.  
ACCESSION AV010326  
VERSION AV010326.2 GI:16356130  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus.  
Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 1039)

#### REFERENCE

Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Horii, F., Ishii, Y., Ito, M., Kawai, J., Kono, H., Kouda, M., Koyu, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toyu, T., Muramatsu, M. and Hayashizaki, Y.  
Riken Integrated sequence analysis (RISA) system -384-format  
unpublished (2001)  
On May 11, 1999 this sequence version replaced gi:4787313.  
Contact: Chie Owa  
Genome Science Laboratory  
RIKEN

tel: 81-298-36-9145  
fax: 81-298-36-9098  
Email: genome-res@r.riken.go.jp  
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new  
genes. Genome Res. 10 (10), 1617-1630 (2000)  
wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Matsuoka, Y., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunaga, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
Riken integrated sequence analysis (RISA) system -384-format  
sequencing pipeline with 384 multichannel sequencer. Genome Res. 10 (11), 1757-1771 (2000)  
Kono, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.  
Computer-based methods for the mouse full-length cDNA  
encyclopedia: real-time sequence clustering for construction of a  
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and Hayashizaki, Y.  
Computational analysis of full-length mouse cDNAs compared with  
human genome sequences. Mamm. Genome. 12, 673-677 (2001)  
Please visit our web site (<http://genome.gsc.riken.go.jp/>) for  
further details.  
cDNA library was prepared and sequenced in Mouse Genome  
Encyclopedia Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in Riken.  
Division of Experimental Animal Research in Riken contributed to  
prepare mouse tissues.  
Location/Qualifiers  
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/strain="C57BL/6J"  
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#### TITLE

JOURNAL

COMMENT

#### FEATURES

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/dev.stage="18-day embryo"
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624 lProSerProPheArgValAlaProLeuPheSerLeuProThrGlnLeuP 641
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DEFINITION BB609618 RIKEN full-length enriched, 18 days embryo Mus musculus
ACCESSION  BB609618
VERSION     BB609618.1 GI:16451334
KEYWORDS   EST.
SOURCE     house mouse.
ORGANISM   Mus musculus.

REFERENCE
  1 (bases 1 to 1006)
  Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.,
  Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Kono,H., Kouda
  M., Koye,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,
  Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki
  D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
  Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,
  Muramatsu,M. and Hayashizaki,Y.
  RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
  Unpublished (2001)
  contact: Yoshihide Hayashizaki
  Laboratory for Genome Exploration Research Group, RIKEN Genomic
  Sciences Center(GSC), Yokohama Institute
  The Institute of Physical and Chemical Research (RIKEN)
  1-7-22 Suenho-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
  Tel: 81-45-503-9222
  Fax: 81-45-503-9216
  Email: genome-res@sc.riken.go.jp
  URL: http://genome-gsc.riken.go.jp/
  Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
  M., Kono,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  Normalization and subtraction of cap-trapper-selected cDNAs to
  prepare full-length cDNA libraries for rapid discovery of new
  genes. Genome Res. 10 (10), 1617-1630 (2000)
  Wagi,K., Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
  Watabiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsunura
  S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
  Hayashizaki,Y.
  RIKEN integrated sequence analysis (RISA) system--384-format
  sequencing pipeline with 384 multicapillary sequencer. Genome Res.
  10 (11), 1757-1771 (2000)
  Kono,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
  Y. and Hayashizaki,Y.

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TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-remail.nih.gov  
Tissue Procurement: Jeffrey E. Green, M.D.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLAM1133 row: k column: 20  
High quality sequence stop: 697.  
Location/Qualifiers

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ACCESSION BG968034 GI:14355671
VERSION BG968034.1
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SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE 1 (bases 1 to 784)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLES National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10997 row: g column: 04
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Location/Qualifiers
1. 784
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 mRNA sequence.

ACCESSION BF237179  
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KEYWORDS EST.

SOURCE

ORGANISM

house mouse.  
 Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 722)

AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

CONTACT Robert Strausberg, Ph.D.

COMMENT Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)

## FEATURES

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 Site: 2; SalI; Cloned unidirectionally. Primer: Oligo dT.  
 Average insert size 1.9 kb. Constructed by Life  
 Technologies. Note: this is a NCI\_CGAP library."  
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<http://image.llnl.gov>  
 DNA Sequencing by: Incyte Genomics, Inc.  
 CNA Library Prepared by: The I.M.A.G.E. Consortium (LNL)  
 Tissue Procurement: Jeffrey E. Green, M.D.  
 CDNA Library Preparation: Life Technologies, Inc.

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579 GGGCTACAGCGCTGTGTGGAGACACTGCGCTGCTGCTGCTGCTGCTG 530
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399 GAGGAGAGCTGTGTCTGAGTGTCCACAGAGAGAGATGTGGCCCTGTGT 448
84 aAlaArgValValHisLeuAlaValHisGlyHisTrpAlaGluProGlu 100
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449 TCCGTGTGTGTGTCCACTTGGCCGTGCATGGCAGTGGCAGAGCCTGAA 498
101 GluAlaGlyLysSerAspSerGluLeuGlnGluSerArgAsnAlaSerLe 117
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499 GAGAGTGGGAAGTCTGATTCAGAACTCCAGAGAGTCTAGGAAGCCCTCT 548
117 uGlnAlaGlnValValLeuSerPheGlnAlaTyrProIleAlaArgCys 134
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549 CAGAGGCCAGGTGTGCTCTCTCTTCAGAGCCTACCCATGCCCGCTGTG 598
134 LeuLeuGluGluValGlnValProAlaAspLeuValGlnProGlyGlnSer 150
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599 CCTGTGTGGAGTCCAGGTGCCGTGACCTGTGTGACCTGTGTGACCTGC 648
151 ValGlySerAlaValPheAspCysPheGluAlaSerLeuGlyAlaGlu 167
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649 GTGGGTCTGTGGTATTGTACTTTCAGAGGCTAGTCTTGGGGCTAGAGT 698
167 LeuIleTrpSer.TyrThrLysProArgTyrGlnLysGluLeuAsnLeu 183
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699 ACGAGTCTGTGCTTACACAGAACCCAGGTACACAGAAAGCTCAACCTC 748
184 ThrGlnGlnLeuProAspCysArgGlyLeuGluValAlaArgAspSerIleG 200
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749 ACGACACACACTGCTGACTGCAG.GGTCTTGAAGTCCGGAGACGATCCA 797
200 nSerCysTrpValLeuProTrpLeuAsnValSerThrAsp.GlyAspAsn 216
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798 GAGCTGCTGTG.....GAATGTTGACAAAT 820
217 ValLeuLeu 219
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821 GTCTTCTGTG 829
seq_name: gb_est1.BB637050

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**TITLE** National Institutes of Health, Mammalian Gene Collection (MGC)  
**JOURNAL** Unpublished (1999)  
**COMMENT** Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Lohar Hemmighausen Ph.D., Robin Humphreys  
cDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.llnl.gov>  
Plate: LIM8516 row: f column: 07  
High quality sequence stop: 562.  
Location/Qualifiers  
1..562

**FEATURES**  
**Source**  
/organism="Mus musculus"  
/strain="C57/B6"  
/db\_xref="taxon:10090"  
/clone\_image="3484038"  
/clone\_lib="NCI\_CGAP\_Mam5"  
/tissue\_type="tumor, gross tissue"  
/dev\_stage="7 months"  
/lab\_host="DH10B"  
/note="Organ: mammary; Vector: pCMV-Sport6; Site\_1: SalI;  
Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dT.  
Library constructed by Life Technologies. Investigators  
providing samples: Lohar Hemmighausen/Robin Humphreys,  
NIH"

**BASE COUNT** 86 a 190 c 180 g 106 t

**ORIGIN**

**Alignment\_scores:**  
Quality: 999.00 Length: 187  
Ratio: 5.342 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

**Alignment block:**  
US-09-899-471-5 x BE290565 ..

**Align seg 1/1 to: BE290565 from: 1 to: 562**

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2 CACCACTGTATGACGCTGTGGAAAGCATGACACATGAGATCGTATGAGGC 51  
454 acysprometaspysrtyrllehisargatgtpvalleuvaitrpleua 471  
52 CTGCCCCATGACAACTACATCCACAGGGCGCTGGTCGTATGAGGCTG 101  
471 lacysleuleuleualaalaaleuPhphepheheuleuleulylys 487  
102 CTGGCTACTTTGGCTGGGGCTTTTCTTCTTCCTCCTTRAAAAG 151  
488 aspargatglyalaaiaaargelyserargthrAlaleuleuleuhisse 504  
|||  
152 GACCAGGAAGAACGGCCCGTGCTCCGACAGCGGCTTGCTCCCTCCACTC 201  
504 TALAAspGLAagLYTYrGLuArgLeuValGLyAlaaleuAlaSerAlaI 521  
|||||  
202 CGCGCACGAGAGCGGCTACGACGCTTGGTGGAGACACTGGCCGCGGT 251  
521 euSerGLMetProleuArGValAlaValaAspLeutrPseArGARGLu 537  
252 TGAGCCACAATGCCACTGGCGGTGGCGGTGACCTGTGAGCCGCCCGAG 301  
538 LeuSerAlaHisGLyAlaaleuAlatrPPHeHisHisGLnARgarGARgl 554  
|||||  
302 CTGACGCGGACGAGAGCCCTTAGCTGGTTCACACACAGCAGAGCCGCTAT 351  
554 eLengInGLuglyGVAlValIlleuleuPheserProAlaVala 571  
353 CTGCGAGGGGTGGCTGTATATCTTCTTCTTCGCCCGCGGCGGCTGG 401

	571	IAGLcysGlnGInTrpleuGlnLeuGlnIphrValGIupProGlyProHis	587
	402	GCGACTGTACGAGTGGCTGCACCTCCAGCACATGGAGCCCGGCCCAT	451
	588	ASPAALeAlAAlArpleuSerCysValleuProaspPheleuGlnG1	604
	452	GACGCCCTGGCCGCTGCAGCTGCCTCACTTCCTTGCAAGG	501
	604	yArGaIAthrGIyArGTyrValGIyValTyrrPheaspGlyLeuLeuHsp	621
	502	CCGGCCGACCGCCGCTACGTCGGGGTCTACTTCGACGGGCTGTCACC	551
	552	CAGACTGTGTG	562
	seq_name:	gb_ests2:BF160122	
	seq_documentation_block:		
	LOCUS	BF160122	635 bp mRNA linear EST 30-OCT-2000
	DEFINITION	60176782ZEF1 NCL_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3984149 5'	
	ACCESSION	mRNA sequence.	
	VERSION	BF160122	
	KEYWORDS	BF160122.1 GI:11040229	
	SOURCE	EST.	
	ORGANISM	house mouse.	
		Mus musculus	
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
		Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
	REFERENCE	NIH-MGC http://mgc.ncl.nih.gov/.	
	AUTHORS	1. (bases 1 to 635)	
	TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)	
	JOURNAL	Unpublished (1999)	
	COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapsb@mail.nih.gov Tissue Procurement: Gilbert Smith, Ph.D. CDNA Library Preparation: Life Technologies, Inc. CDNA library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a> Plate: LLAM9185 row: 1 column: 06 High quality sequence start: 2 High quality sequence stop: 632. Location/Qualifiers 1..635 /organism="Mus musculus" /strain="CZECH II (fetal)" /db_xref="taxon:10090" /clone_image="3984149" /clone_id="NCL_CGAP_Lu29" /tissue_type="spontaneous tumor, metastatic to mammary." stem_cell_origin="" /lab_host="DH10B" /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"	
	BASE COUNT	92 a 229 c 204 g 110 t	
	ORIGIN		
	alignment_scores:		
	Quality:	975.00	Length: 207
	Ratio:	4.924	Gaps: 4
	Percent Similarity:	95.652	Percent Identity: 93.237
	alignment_block:		
	US-09-899-471-5 x BF160122		
	Align seg 1/1	to: BF160122 from: 1 to: 635	

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494 ArgGlySerArgThrAlaLeuLeuHisSerAlaAspGlyAlaGlyTyr 510
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2 CGTGGCGCCGACGCGCTTGTCTCCATCCGCGCCGACGAGCGGCTA 51
510 rGluArgLeuValGlyAlaLeuAlaSerAlaLeuSerGlnMetProLeu 527
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52 CGAGGCTCTGGTAGAGACACTGGCGTCCGCTGAGCCAGATGCGCTGC 101
527 rGValAlaValAlaSplLeuTrpSerArgArgGluLeuSerAlaHisGlyAla 543
|||||
102 GCGTGGCGCTGAGACCTGTGAGCGCGCGAGCTGACGCGGACGAGACC 151
544 LeuAlaTrpPheHisHisGlnArgArgGlyLeuGlnGlnGlyAla 560
|||||
152 CTAGCGCTGGTCCACACACGCGCGCGCTATCTCGACGAGATGGCGT 201
560 lValIleLeuLeuPheSerProAlaAlaValAlaGlnGlnGlnTrpL 577
|||||
202 GGTATCTCTTCTCTCTCCCGCGCGCGCTGCGCAGTGTGACAGTGGC 251
577 eugLeuGlnThrValGluProGlyProHisAspAlaLeuAlaAlaTrp 593
|||||
252 TGACAGCTCCAGACAGTGGAGCCGCTCGCATGACGCGCTCGCGCTCG 301
594 LeuSerCysValLeuProAspPheLeuGlnGlyArgAlaThrGlyArgTyr 610
|||||
302 CTCAGCTCGTCTCTACCCGATTTCTGCAAGCGCGCGCGCGCTCA 351
610 rValGlyValTyrPheAspGlyLeuLeuHisProAspSerValProSerP 627
|||||
352 CGTGGCGCTCTCTCTCTCGAGCGCTGCTGCAACCACTGTGCTCTCC 401
627 rPheArgValAlaProLeuPheSerLeuProThrGlnLeuProAlaPhe 643
|||||
402 CGTCCGCGCTGCGCGCGCTCTCTCTCGCTGCGCTGCGCTGCGCTTC 451
644 LeuAspAlaLeuGlnGlyCysSerThrSerAlaGlyArgProAlaA 660
|||||
452 CTGAGTGCACCTGCAGGAGCTGCTCCACGCTCCCGCGCGCGCGCG 500
660 sParGValAlaArgValThrGlnAlaLeuArgSerAlaLeuAspSerC 676
|||||
501 ..CGGGTGAACAGAGTGGCCAGCGCTGC...AGTCCGCTGACACACTG 545
676 sThrSerSerSerGluAlaProGlyCysGlnGluGluTrpAspLeuGlyP 693
|||||
546 TACTTCTAGCTCGGAAGCCCGAGGCTGCTGCGAGATGGAGACTGGGAC 595
693 rOCysThrThrLeuGlu 698
|||||
596 CCTGCACACTACACTAGAA 612

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seq\_name: gb\_est2:BG761977

seq\_documentation\_block:

LOCUS BG761977 935 bp mRNA linear EST 15-MAY-2001  
DEFINITION 602718928F1 NIH\_MGC\_49 Homo sapiens cDNA clone IMAGE:4858806 5',  
mRNA sequence.

ACCESSION BG761977  
VERSION BG761977.1 GI:14072630

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 935)  
AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)  
Tissue Procurement: ATCC/DCTD/DRP

# FEATURES

## source

cDNA Library Preparation: Ling Hong/Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.llnl.gov>  
Plate: LNCM1713 row: h column: 07  
High quality sequence stop: 813.

## Location/Qualifiers

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/organism="Homo sapiens"  
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/clone="IMAGE:4858806"  
/clone\_lib="NIH\_MGC\_49"  
/tissue\_type="melanotic melanoma, high MDR (cell line)"  
/lab\_host="DH10B (phage-resistant)"  
/notes="Organ: skin; Vector: pOTB7; Site: 1: XhoI; Site: 2:  
EcoRI; cDNA made by oligo-dT priming. Directionally cloned  
into EcoRI/XhoI sites using the following 5' adaptor:  
GGCAGAG(G). Size-selected >500bp for average insert size  
1.8kb. Library constructed by Ling Hong in the laboratory  
of Gerald M. Rubin (University of California, Berkeley)  
using ZAP-cDNA synthesis kit (Stratagene) and Superscript  
II RT (Life Technologies). Note: this is a NIH\_MGC  
Library."

BASE COUNT 154 a 301 c 291 g 189 t

## ORIGIN

alignment\_scores:  
Quality: 912.50 Length: 307  
Ratio: 3.755 Gaps: 8  
Percent Similarity: 79.153 Percent Identity: 62.866

alignment\_block:  
US-09-899-471-5 x BG761977

Align seg 1/1 to: BG761977 from: 1 to: 935

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2 ACAGACCTGCTTCCCTGCTCTGATTTCAGGTGCGCTTGGAACTGCA 51
277 pSerGluArgValGluPheCysProPheArgGluAspProGlyAlaHis 293
|||||
52 CTCGGTTAGACCAACATCTGCCCTTCAGGGAGAGACCCCGCCACAC 101
294 ArgAsnLeuTrpHisIleAlaArgLeuArgValLeuSerProGlyValTyr 310
|||||
102 CAGAACCTCTGGCAAGCGCCGCGACTGCGTGCACCTGCGAGAGTGG 151
310 pGlnLeuAspAlaProCysCysLeuProGlyLysValThrLeuCysTrpP 327
|||||
152 GCTGCTGGAGCAGCAGCTGCTGCTGCGCCGCAAGAGGCGCTGCTGCG 201
327 lAlaProAspGlnSerProCysGlnProLeuValProProValProGln 343
|||||
202 GGGCTCGGGGTGGGAGACCTTGCACCACTGGGAGGCACTTCTCTGG 251
344 LysAsnAlaThrValAsnGluProGlnAspPheGlnLeuValAlaGlyHis 360
|||||
252 GAGAAATGTACACTG...GACGTTCTGAGTTCATTCGGAAGGCCA 298
360 sProAsnLeuCysValGlnValSerThrTrpGluLysValGlnLeuGlnA 377
|||||
299 CCTTAACCTCTGTGCTCAGTGAACACTCGAGAACCTGCACGTCGACG 348
377 lAcSerTrpAlaAspSerLeuGlyProPheLysAspAspMetLeuLeu 393
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349 AGTGTCTTGGGCTGACTCCTTGGGCTCTCAAGAGAGATGCTACTG 398
394 ValGluMetLysThrGlyLeuAsnAsnThrSerValCysAlaLeuGluPr 410
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1 MetPValSerTrpPheLeuSerLeuAlaLeuGlyArgAsnProVal 17  
163 ATGCTGTGTCTGGTCTCTGCTCTTGGCACTGGCCGAAACCTGT 212  
17 ValValSerLeuGluArgLeuMetIuProGlnAspThrAlaArgCysS 34  
213 GGTCTCTCTCTGGAGAGACTATGAGGCTCAGAGACATGCAGCTGCT 262  
34 erLeuGlyLeuSerCysHisLeuTrpAspGlyAspValLeuCysLeuPro 50  
263 CTATAGGCTCTCCCTGCACACCTTGGAGATGACATGCTCTCTGCTCT 312  
51 GlySerLeuGlnSerAlaProGlyProValLeuValProThrArgLeuG 67  
313 GGAACCTCCACAGTCTGCCAGGCCCTGTGTAGTGCCTACCCGGCTGCA 362  
67 nThrGluLeuValLeuArg.CysProGlnIlyThrAspCysAlaLeuArg 83  
363 GACGAGCTGTGGTGCATGAGGTGTCCACAAACAAACATTTGGCCCTCTGT 412  
84 ValArgValVal.ValHisLeu.AlaValHisGlyHisTrp.AlaGluPro 99  
413 GTCCGTGTGTGTGGTCCACTTGTGCGGTGCATAGGGCAGCTGGGCAAGCC 462  
99 oGluIuValGlyLysSerAspSerGluLeuGlnIuSerArgAsnAlas 116  
463 TGAAGAACTGGAAAGTGTGATTTCAGAAATCCAGGAGTGTAGAACGCTT 512  
116 erLeuGlnAlaGlnValValLeuSerPheGlnAlaArgProIleAlaArg 132  
513 CTCCTCAGGCCAGGTGGTGGTCTCTCTCCACAGACTACCCCAAGCCCGC 562  
133 CysAlaLeuLeuGluValGlnValProAla.AspSerValGlnProGlyG 149  
563 TGTGCCCTGTGGAGAGTCCAGGTGCCCGCTTACCTGAGGAGCCGTGTC 612  
149 InSerValGlySerIleValAlaPheAsp.CysPheGlnAlaSer.LeuGlyA 165  
613 AGTCCGTGGGTCTCGGTATTTGACTGTGTTCGAGGCTAGTCTTGGGG 662  
165 laGlu.ValGlnIleTrpSerTyThrLysProArgTyGlnGluLeu 181  
663 CTGAGGAGTACAGATGTGCTACACAGAAAGCCAGGGTTCACGAAGAAGAC 712  
181 uAsnLeuThrGlnGlnIleuProAspCysArgGlyLeuGluValAlaArgAs 198  
713 TCAACTCTACACAGACGTGGCTGACTGTGAGGGGTCTTGAAGTCCGGGACA 762

198 erleeglnsercysrtpvalleu 205  
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 763 GCATCCAGAGCTGCTGGATGTGTG 785

seq\_name: gb\_est2:B1765330

seq\_documentation\_block:

LOCUS B1765330 922 bp mRNA linear EST 25-SEP-2001  
 DEFINITION 603050641F1 NIH\_MGC\_116 Homo sapiens cDNA clone IMAGE:5190442 5',  
 mRNA sequence.

ACCESSION B1765330  
 VERSION B1765330.1 GI:15756908  
 KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 922)  
 NIH-MGC http://mgi.ncl.nih.gov/  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cga@phs-remail.nih.gov  
 Tissue Procurement: Life Technologies, Inc.  
 cDNA Library Preparation: Life Technologies, Inc.  
 DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLM11476 row: b column: 11  
 High quality sequence stop: 794.  
 Location/Qualifiers

# FEATURES

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 /db\_xref="taxon:9606"  
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 /clone\_lib="NIH\_MGC\_116"  
 /lab\_host="DH10B"  
 /note="Organ: pooled colon, kidney, stomach; Vector:  
 pCMV-Sport6; Site\_1: NotI; Site\_2: EcoRV (destroyed); RNA  
 source anonymous pool of 3 colons, age 26 yo male, 49 yo  
 female, 71 yo male colon; 46 yo male kidney, and pool of 2  
 stomachs, 62 yo male and 70 yo female. Library is  
 oligo-dT primed and directionally cloned (EcoRV site is  
 destroyed upon cloning). Average insert size 1.4 kb,  
 insert size range 1-3 kb. Library is normalized and  
 enriched for full-length clones and was constructed by C.  
 Gruber (Invitrogen). Research Genetics tracking code  
 023. Note: this is a NIH\_MGC Library."  
 BASE COUNT 147 a 297 c 272 g 206 t  
 ORIGIN

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Quality: 902.00 Length: 344  
 Ratio: 3.667 Gaps: 7  
 Percent Similarity: 71.512 Percent Identity: 56.977

## Alignment\_block:

us-09-899-471-5 x B1765330 ..

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 6 CCTCAGGAGGCTACCCACGTCCTCCGGGCTCTCCGCGCCCTGTGGA 55  
 43 pGlyaspValLeuProGlySerLeuGlnSerAlaProGlyProy 60  
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 56 CAGTACATACACTCTGCTGCTGGGACATGCTGCTCCGGGCCCCG 105

60 alleValProThrArgLeuGlnThrGluLeuValLeuArgCysProGln 76  
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 106 TGCTGAGCGCTACGACACGACAGACAGAGCTGCTGAGAGTGGACAG 155  
 77 LysThrAspCysAlaLeuArgValAlaValHisLeuAlaValH 93  
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 156 GAGACCGAGCTGTGACCTGTGCTGCTGCTGCTGCTGCTGCTGCTG 205  
 93 sGlyHisTrpAlaGluProGluGluAlaGlyLysSerAspSerGluLeu 110  
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 206 T..... 206  
 110 InGlnSerArgAsnAlaSerLeuGlnAlaGlnAlaValLeuSerPheGln 126  
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 207 .....GCCTCTCCAGGCCCAATCGCTCTCTCCAG 242  
 127 AlaTrpProIleAlaArgCysAlaLeuLeuGlnValGlnValProAla 143  
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 243 GCCTACCCCTACTGCCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 292  
 143 PheValGlnProGlyGlnSerValGlySerAlaValAlaPheAspCysPhe 160  
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 293 CTTGTGAGTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 342  
 160 IuAlaSerLeuGlnAlaGlnValGlnIleTrpSerTrpThrLysProArg 176  
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 343 AGCGTCCCTAGGAGTAGTGAATGATCTGCTCTACTGACCCAGG 392  
 177 TyrGlnLysGluLeuAsnLeuThrGlnLeuProAspCysArgLysLe 193  
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 393 TACGAGAGGAGGAGTCAACACACAGCAGCTGCTGCTGCTGCTGCTG 433  
 193 uGluValArgAspSerIleGlnSerCysTrpValLeuProTrpLeuAsn 210  
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 434 .....GCCTGCTCAAGC 446  
 210 alSerThrAspGlyAspAsnValLeuLeuThrLeuAspValSerGln 226  
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 447 TGTCAGCAGATGCTACACAGCTGATCTGCTGCTGCTGCTGCTGCTG 496  
 227 GlnAspPheSerPheLeuLeuThrLeuArgProValProAspAlaLeu 243  
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 497 CAGCACTTCGCGCTCTCCCTGAC..... 520  
 243 sSerLeuTrpTrpLysAsnLeuThrGlyProGlnAsnIleThrLeuAsn 260  
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 521 .....TGC.....AATCAGACTGAGCCGACGATCATTAACCTGAAC 557  
 260 IsthAspLeuValProCysLeuCysIleGlnValTrpSerLeuGln 276  
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 558 ACACAGACTGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGAC 607  
 276 oAspSerGluArgValGluPheCysProPheArgGlnAspProGlyAla 293  
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 608 TGACTGCTTAGGAGACATCTGCCCTTACAGGAGAGACCCCGGAC 657  
 293 IAspAsnLeuTrpHisIleAlaArgLeuArgValIleSerProGlyVal 309  
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 658 ACCAGAACCTCTGCGAACG.CGCCGACTGCGACTGCTGACCCGACAG 706  
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 707 TGCTGCTGAGGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 756  
 326 pGlnAlaProAspGlnSerProCysGlnProLeuValProValProG 343  
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 757 GCGGCTGCGGCTGAGGAGACCTGCGGAGCTG.....TCCACCGTT 800  
 343 IuLysAsnAlaThrValAsnGluProGlnAsp...PheGlnLeuValAla 358  
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 801 ACCTTGAGGACAGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 850  
 359 GlyHisProAsnLeuCysValGlnValSer 368

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851 GGGACACCTACCTCTGTCTGCTGAC 880

seq\_name: gb\_est2:B1282622

seq\_documentation\_block:

LOCUS B1282622 619 bp mRNA linear EST 19-JUN-2001  
DEFINITION UI-R-CW05-ccd-b-11-0-UI.s1 UI-R-CW05 Rattus norvegicus cDNA clone

ACCESSION UI-R-CW05-ccd-b-11-0-UI.3, mRNA sequence.

VERSION B1282622 GI:14933575

KEYWORDS EST.

SOURCE

ORGANISM Norway rat.

Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

REFERENCE 1 (bases 1 to 619)

AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.

TITLE Normalization and subtraction: two approaches to facilitate gene

JOURNAL Genome Res. 6 (9), 791-806 (1996)

COMMENT 9704447

Contact: Soares, MB

Program for Rat Gene Discovery and Mapping

University of Iowa

451 Eckstein Medical Research Building Iowa City, IA 52242, USA

Tel: 319 335 8250

Fax: 319 335 9565

Email: msoares@iuii.weeg.uiowa.edu

The sequence contained an oligo-dT track that was present in the

oligonucleotide that was used to prime the synthesis of first

strand cDNA and therefore this may represent a bonafide poly A

tail. The sequence tag present in the cDNA between the NotI site

and the oligo-dT track served to identify it as a clone from the

non-normalized rat aorta pool library cDNA library preparation:

M.B. Soares Lab Clone distribution: clones will be available

through Research Genetics (www.resgen.com)

Seq primer: M13 Forward

POLYA-Yes.

1. 619

Location/Qualifiers

/organism="Rattus norvegicus"

/strain="Sprague-Dawley"

/db\_xref="taxon:10116"

/clone="UI-R-CW05-ccd-b-11-0-UI"

/clone\_11b="UI-R-CW05"

/dev\_stage="ADULT"

/lab\_host="DH10B (Life Technologies)"

/note="Vector: pT73D-Pac (Pharmacia) with a modified

polylinker; Site\_1: Not I; Site\_2: Eco RI; The UI-R-CW05

library is a non-normalized library constructed from the

following rat aorta tissues: embryonic day 19, embryonic

day 21, adult day 1, adult day 12, adult day 75, adult day

200. For a detailed description of the library from which

this clone was derived, please visit our web site at

ratseq.eng.uiowa.edu. The subtraction has been previously

described in (Bonaldo, Lennon and Soares, Genome Research

6:791-806, 1996)

TAG\_LIB=UI-R-CW05

TAG\_TISSUE=rat aorta pool

TAG\_SEQ=CTGTAGATC"

BASE COUNT 105 a 197 c 211 g 106 t

ORIGIN

alignment\_scores:

Quality: 893.00 Length: 193

Ratio: 4.907 Gaps: 0

Percent Similarity: 94.301 Percent Identity: 89.119

Alignment block:

Align seg 1/1 to reverse of: B1282622 from: 1 to: 619

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619 GAGGAGACATACATACGAGCGCTGTGGCGCTGTGGCGCTGTAG 570  
|||||  
522 rGlnMetProLeuArgValAlaValAspLeuTrpSerArgArgGluLeu 539  
|||||  
569 CCAGATGCCACTGCGCGCTGTGGCGCTGTGGCGCTGTAG 520  
|||||  
539 exAlaHisGlyAlaLeuAlaTrpPheHisGlnArgArgGluLeu 555  
|||||  
519 CCGCGACGAGAGCCCTGCTGTCCACGACAGCGCGCGCGCATG 470  
|||||  
556 GluGluGlyValValAlaLeuLeuPheSerProAlaAlaValAlaG 572  
|||||  
469 CAGGAGATGGCGGTGCTATCTTCTTCCACCGCGCGCGCTG 420  
|||||  
572 nCysGlnGlnTrpLeuGlnLeuGlnTrpValGluProGlyProHisAsp 589  
|||||  
419 GTGTACACAGTGGCTGACGCTCCAGACGCTGAGCGCGCGCATG 370  
|||||  
589 IalaLeuAlaAlaTrpLeuSerCysValLeuProAspPheLeuGlnArg 605  
|||||  
369 CTCTGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 320  
|||||  
606 AlaThrGlyArgTrpValGlyValTrpPheAspGlyLeuLeuHisPro 622  
|||||  
319 GCGACCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 270  
|||||  
622 pSerValProSerProPheArgValAlaProLeuPheSerLeuProTrg 639  
|||||  
269 CACTGTACCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 220  
|||||  
639 IalaLeuAlaPheLeuAlaLeuGlnGlyCysSerThrSerAla 655  
|||||  
219 AGCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 170  
|||||  
656 GlyArgProAlaAspArgValGluArgValThrGlnAlaLeuArgSer 672  
|||||  
169 GGGGACCTGCGCGAGCGCGAGCGAGCGAGCGAGCGAGCGAG 120  
|||||  
672 alaAspSerCysThrSerSerSerGluAlaProGlyCysCysGluTr 689  
|||||  
119 CTAGAGACGCTGTACTTAGAGCTCGAAGCCCGAGCGCTGCGGAGAT 70  
|||||  
689 rPaspLeuGlyProCysThrThrLeuGlu 698  
|||||  
69 GGGACCTGGAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTG 41